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ORGANISM: Artificial Sequence
                                                                       OTHER INFORM
US-09-987-457-10
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i Sequence 10, Application US/09987457

i Sequence 10, Application US/09987457

i Publication No. US20030013150A1

i APPLICANT: Manosroi, Aranya

APPLICANT: Manosroi, Jiradej

CURRENT FILING DATE: 2001-11-14

PRIOR FILING DATE: 2001-11-14

NUMBER OF SEQ ID NOS: 18

SEQ ID NO 10

LENGTH: 354
                                                  ö
                                                                                                                                       126 TCYEDQGISYRGTWSTAESGAECTNWNSSALAQKPYSGRRPDAIRLGLGNHNYCRNPDRD 185
                                                                                                2 TCYEGNGHFYRGKASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNR 61
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                                                  Gaps
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                                                                                                                                                                                                                                                                                                     RESULT 28
US-10-057-951-3
| Sequence 3, Application US/10057951
| Publication No. US20020177213A1
| GENERAL INFORMATION:
| APPLICANT MOORE et al. |
| TITLE OF INVENTOR: | Fisue Plasminogen Activator-Like Protease FILE REFERENCE: PF778P1
| CURRENT APPLICATION NUMBER: US/10/057,951
| CURRENT PILING DATE: 1999-10-0.1-29
| PRIOR APPLICATION NUMBER: US 09/411,977
| PRIOR APPLICATION NUMBER: US 09/084,491
| PRIOR APPLICATION NUMBER: US 09/084,491
| PRIOR PILING DATE: 1998-05-27
| PRIOR FILING DATE: 1999-705-28
| NUMBER OF SEQ ID NOS: 31
| SEQ ID NO 3
| LENGTH: 326
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39.4%; Score 218.5; DB 14; Length 326;
Best Local Similarity 44.7%; Pred. No. 3.7e-17;
Matches 42; Conservative 10; Mismatches 41; Indels 1;
Length 562;
Query Match 40.8%; Score 226; DB 15; Length 5 Best Local Similarity 47.7%; Pred. No. 9e-18; Matches 41; Conservative 9; Mismatches 36; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63 RPWCYVQVGLKPLVQECMVHDCAD-GKKPSSPPE 95
                                                                                                                                                                                                                                        186 SKPWCYVFKAGKYSSEFCSTPACSEG 211
                                                                                                                                                                                            62 RRPWCYVQVGLKPLVQECMVHDCADG 87
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3 CYEGNGHFYRGKASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNRR 62
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APPLICANT: Aranya Manosroi
APPLICANT: Charchai Tyapiwatana
APPLICANT: Charchai Getz
APPLICANT: Rolf-Guenther Werner
TITLE OF INVENTION: Methods for Large Scale Production of Recombinant
TITLE OF INVENTION: Mothods for Large Scale Production
TITLE OF INVENTION: Mothods for Large Scale Production
FILE REFERENCE: 0652.2190001
FILE REFERENCE: 0652.2190001
PRIOR FILING DATE: 2001-01-15
PRIOR FILING DATE: 2001-11-14
PRIOR FILING DATE: 2000-11-14
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 11
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FEATURE: OTHER INFORMATION: Description of Artificial Sequence: part of the OTHER INFORMATION: recombinant K2S molecule
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: Description of Artificial Sequence: K2S 174-527
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                                                                                                                                                                  DB 11; Length 354;
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39.4%; Score 218.5; DB
Best Local Similarity 44.7%; Pred. No. 4e-17;
Matches 42; Conservative 10; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-987-455-11
. Sequence 11, Application US/09987455
. Publication No. US20030049729A1
. GENERAL INFORMATION
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Best Local Similarity 44.7%
Matches 42; Conservative
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No Ait
                                   GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                         OM protein - protein search, using sw model
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December 3, 2003, 14:33:02; Search time 63.482 Seconds (without alignments) 1007.637 Million cell updates/sec Run on:

2257 1 SNBLHQVPSNCDCLNGGTCV.....VSHFLPWIRSHTKEENGLAL 403 US-09-880-203-6 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1107863 Total number of hits satisfying chosen parameters: 1107863 seqs, 158726573 residues Searched:

Minimum DB seq length: 0 Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

A Geneseq 19Jun03:*

| SIDS1/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*
| SIDS1/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
| SIDS1/gcgdata/geneseq/geneseqp-embl/AA1982.DAT:*
| SIDS1/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
| SIDS1/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
| SIDS1/gcgdata/geneseq/geneseqp-embl/AA1986.DAT:*
| SIDS1/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
| SIDS1/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
| SIDS1/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
| SIDS1/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
| SIDS1/gcgdata/geneseqg/geneseqp-embl/AA1991.DAT:*
| SIDS1/gcgdata/geneseqg/geneseqg-embl/AA1991.DAT:*
| SIDS1

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Human urokinase-tv	Seguence encoded b	Urokinase precurso	Pro-urokinase, Ho	Urokinase plasmino	Human urokinase-tv	Sequence encoded b	Human urokinase.	Sequence of human
	ΠD	AAE16547	AAP50871	AAR06244	AAR62991	AAY92836	AAE16544	AAP50114	AAP60783	AAP70258
	DB	23	9	11	16	21	23	w	,	œ
	Match Length DB ID	403	411	411	411	411	411	431	431	431
On the Property	Match	100.0	4.66	99.4	99.4	99.4	99.4	99.4	99.4	99.4
	Score	2257	2243	2243	2243	2243	2243	2243	2243	2243
Result	No.	1	61	m	4	Ŋ	9	7	œ	σ

22 22 43 3 3 4 4 3 4 4 4 4 4 4 4 4 4 4 4	99. 4.60	431	c		Natural human prop
444444	:	421	7 -	AAP92119	
4444	σ	n	11	AAR07112	Human pro-Urokinas
222	6	431	15	AAR47903	
2.4 4.4	σ	431	15	AAR63141	Full length human
24	ď.	431	21	AAY99591	Human plasminogen
	σ	431	27	9	2
24	6	431	22	160	aci.
24	σ	431	53	φ	sc-uPA. Homo sapi
24	σ	431	23	AAU99228	Human plasminogen
24	σ	431	23	AAE17128	Human uPA protein.
24		431	24	ABUS6547	Lung cancer-associ
24	9	431	24	ABU56708	cancer-asso
24	σ	431	24	ABU11076	n urokinase
24	σ	434	13	AAR20537	ъ
24	σ	434	13	3	Amidated deriv. of
24	σ	436	13	AAR20536	d deriv.
24	σ	3	18	AAW24578	Inhibitor resistan
24	O)	3	10	AAP91886	Sequence of prouro
3		3		Q	Non-glycosylated p
23	σ	411	14	AAR34584	Mutant human prour
23	g	431		23	Human plasminogen
23	g	411		AAP96146	Sequence encoded b
23	ď	щ		Ø١	Pro-urokinase. Ho
23	σ	411		ω	Prourokinase prote
23	O,	m		22	Human plasminogen
23	σ	411		AAR62992	Pro-urokinase muta
23	O)	-		9	Pro-urokinase muta
23	σ	411		AAR62998	Pro-urokinase muta
23	g	411		AAR62999	Pro-urokinase muta
23	g	411	16	000	Pro-urokinase muta
23	g	411		AAY39343	Human pro-urokinas
23	σ	411		AAY42284	
23	g	411		AAB20489	

ALIGNMENTS

AAE16547 standard; Protein; 403 AA. AAE16547; RESULT 1 AAE16547

(first entry) 09-APR-2002

Human; urokinase-type plasminogen activator; uPA; therapy; hypertension; stroke; hypotension; atherosclerosis; heart attack; thrombotic disorder; microvascular occlusion; angiogenic disorder; pulmonary fibrosis; asthma; tumour cell metastasis; glanoma; diabetic retinopathy; wound healing; clotting disorder; uterine concraction disorder; respiratory disease; and in motion of a dult respiratory distress syndrome; scuPA deltal36-143; Human urokinase-type plasminogen activator scuPA delta136-143 mutant. male impotence, adult respiratory distr single chain urokinase, mutant, mutein.

Homo sapiens. Synthetic.

WO200197752-A2.

27-DEC-2001

13-JUN-2001; 2001WO-US18976.

20-JUN-2000; 2000US-212874P.

Cines DB, Higazi AA;

(UYPE-) UNIV PENNSYLVANIA.

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Arimura H,
                                                                                                                                                       189.
197.
293.
325.
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403; Conserv
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bond-
bond
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Disulfide-bond
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                                                    Key
Cleavage-site
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                          Homo sapiens.
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Best Local 9
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                                                                                                                          The invention relates to a composition comprising one or more domains of urokinase-type plasminogen activator (uPA). The composition is used to modulate the contractility and angiogenic activity of a mammalian muscle, endothelial cell or tissue. The composition is used for treating stroke, hypotension, hypertension, atherosclerosis, heart attack, microvascular occlusions, thrombotic microangiopathies, surgically induced thrombotic disorders, angiogenic disorders, pulmonary fibrosis, athma, tumour cell nisorders, pulmonary fibrosis, asthma, tumour cell ingogenesis, tumour cell metastasis, glaucoma, contraction disorder, male impotence, respiratory disease or condition such as asthma, adult respiratory distress syndrome, primary pulmonary hypertension, microvascular thrombotic occlusion, and a disorder associated with chronic intrapulmonary fibrin formation. The present casculate (uPA) single chain urokinase (scuPA) deletion mutant designated as scuPA deltal36-143.
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                                                 Composition for modulating muscle cell and tissue contractility for treating atherosclerosis, asthma, hypertension, glaucoma, impotence, comprising domains from urokinase-type plasminogen activator -
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0
                                                                                                                                                                                                                                                                                                                                                                 Length 403;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence encoded by cDNA sequence for human urokinase zymogen (Japanese Patent Application No.37119/84).
                                                                                                                                                                                                                                                                                                                                                                                       Indels
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100.0%; Pred. No. 8.1e-176;
ive 0; Mismatches 0;
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                                                                                                       Fig 1F; 117pp; English
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Best Local Similarity 100.
Matches 403; Conservative
                WPI; 2002-122240/16.
N-PSDB; AAD27080.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2ymogen AAP50871 is the inactive precursor form of human urokinase. Urokinase zymogen is cleaved into the two-chain form composed of characteristic urokinase H (molecular wt.of 20,000) and L (molecular wt.of 20,000) chains when traered with catalytic amounts of plasmin. The patentors claim a new urokinase zymogen which has mol. wt. ca. 50,000, a single chain molecular structure, and selective affinity for fibrin. It is a thrombolytic agent which manifests its plasminogen activator activity on cleavage by proteolytic enzymes of urokinase.
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the zymogen"
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Pred. No. 1.2e-174;
); Mismatches 0;
                                                    site
from
Location/Qualifiers
158..159
/note= "potential cleavage
the two-chain form
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98.1%;
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ENSTDYLYPEQLKMTVVKLISHRECQOPHYYGSEVTTKMLCAADPQWKTDSCQGDSGGPL
LHKDYSADTLAHHNDIALLKIRSKEGRCAQPSRTIQTICLPSMYNDPQFGTSCEITGFGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAR62991 is the wild type pro-urokinase, from which the new mutants described in AAR62992-R63008 were derived. These mutants retain the thrombolytic activity of the wild type protein, useful for the treatment of thromboembolism, but have a reduced fibrinogenolysis activity and non-specific plasminogen activation. The mutants can therefore be used for the lysis of fibrin clots without inducing systemic bleeding, as can be the case with the wild type protein. (Updated on 25-WAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pro-urokinase mutants - have thrombolytic activity but reduced fibrinogenolysis activity and non-specific plasminogen activation
                                                                                                       VCSLOGRMTLTGIVSWGRGCALKDKPGVYTRVSHFLPWIRSHTKEENGLAL 403
                                                                                                                    361 VCSLQGRMTLTGIVSWGRGCALKDKPGVYTRVSHFLPWIRSHTKEENGLAL
                                                                                                                                                                                                                                                                                                                         Pro-urokinase; thrombolysis; fibrin clot lysis.
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/note= "flexible loop"
11..19
13..31
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21-SEP-1995
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                     ENSTDYLYPEQLKMTVVKLISHRECQQPHYYGSEVTTKMLCAADPQWKTDSCQGDSGGPL
    ENSTDYLYPEQLKMTVVKLISHRECQQPHYYGSEVTTKMLCAADPQWKTDSCQGDSGGPL
                                                                                                                                                                                                                                                       Urokinase precursor; fibrinolysis; thrombolytic; cerebral thrombosis; myocardial infarction;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Urckinase precursor-lipid composite - used as thrombolytic agent, having prolonged half-life in the blood, enhanced bio:availability and improved activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       By forming a precursor-lipid composite, the half-life of this thrombolytic agent in the blood may be increaced, exhibiting improved activity without abnormal acceleration of fibrinolytic activity. Compound is useful as a thrombolytic agent in treatment of cerebral thrombosis, myocardial infarction etc.
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                                                        VCSLQGRMTLTGIVSWGRGCALKDKPGVYTRVSHFLPWIRSHTKEENGLAL
                                                                        VCSLOGRMTLTGIVSWGRGCALKDKPGVYTRVSHFLPWIRSHTKEBNGLAL
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89JP-0016406.
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tes 403; Conserv
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27-JAN-1989;
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29-OCT-1998;
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                                                                                                                                                                                                                                                                            SNELHQVPSNCDCLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFYRG
                                                                                                                                                                                                                                                   PLVQECMVHDCADGK-----LKFQCGQKTLRPRFKIIGGEFTTIENQPWFAAIYRRH
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                                                                         Gaps
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8
                                     Length 411;
                                                                     Indels
                                   Score 2243; DB 16;
Pred. No. 1.2e-174;
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0
                                                                         0; Mismatches
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                                     99.4%;
98.1%;
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Disulfide-bond
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The present sequence shows the wild-type urokinase plasminogen activator (UPA). Cyclic peptides based on the amino acids residues 20-30 (the receptor-binding region) of UPA are claimed. These cyclic peptides target the UPA receptor (UPAR), allowing therapeutic or diagnostic agents to be delivered to UPAR-expressing cells. The cyclic peptides are used, optionally when linked to a therapeutic agent, to inhibit migration, invasion and proliferation of cells, or angiogenesis, or to induce apoptosis. Particularly they are used, in human or veterinary medicine, or therat diseases characterized by these processes, e.g. solid tumors, contract diseases characterized by these processes, e.g. solid tumors, cleukaemia or lymphoma (or their metastases); benigh hyperplasis; atherosclerosis, restenosis; ischaemia; deep vein thrombosis; neovascular callacosis; ischaemia; deep vein thrombosis; neovascular callacosis; ischaemia; deep vein thrombosis; neovascular callacosis; pretrioristis; fibrosis; bone fracture etc., most particularly growth, invasion and metastasis of tumors. When cyclic peptides can be used for diagnostic detection of uPAR when immobilized they are used to isolate uPAR or cells that express them. The cyclic peptides are stable, soluble in water, bind strongly to uPAR, are relatively inexpensive to produce and may be derivatized by attachment of therapeutic or diagnostic agents without significantly affecting their binding. Since they target uPAR, they should have the relatively low systemic toxicity and only low doses are required.
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                                                                                                                                                                                                                                 New cyclic peptide, useful for treatment or diagnosis of e.g. and other diseases involving cell proliferation or migration, the urokinase plasminogen activator receptor
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98.1%; Pred. No. 1.2e-174;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Fig 1; 93pp; English.
(ANGS-) ANGSTROM PHARM INC
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Matches 403, Conservative
                                                                                     Jones TR;
                                                                                                                                                         WPI; 2000-365605/31
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241 LHKDYSADTLAHHNDIALLKIRSKEGRCAQPSRTIQTICLPSMYNDPQFGTSCEITGFGK 300
                                                                                                                                                                                                  301 ENSTDYLYPEQLKMTVVKLISHRECQQPHYYGSEVTTKMLCAADPQWKTDSCQGDSGGPL 360
                         RGGSVTYVCGGSLISPCWVISATHCFIDYPKKEDYIVYLGRSRLNSNTQGEMKFEVENLI
                                                                                                                                                              293 ENSTDYLYPEQLKMTVVKLISHRECQQPHYYGSEVTTKMLCAADPQWKTDSCQGDSGGPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence encoded by the signal sequence and noncoding region of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The inventors claim a method of producing single-chain pro-urokinase by using as template, mRNA obtd. from cells of an established human kidney-derived cell line. The urokinase is used treat thrombosis and embolic diseases as well as in the treatment diseases in combination with anticancer agents.
                                                                                                                                                                                                                                                                   353 VCSLQGRMTLTGIVSWGRGCALKDKPGVYTRVSHFLPWIRSHTKEENGLAL
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animal cells transformed by DNA prepd. from m RNA
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Pred. No. 1.2e-174;
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                                                                                LHKDYSADTLAHHNDIALLKIRSKEGRCAQPSRTIQTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Enzyme; thrombosis therapy; embolic disease; single-chain pro-urokinase.
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/label= signal peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /label= A chain
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/label= B chain
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98.1%;
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84JP-0037119.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-FEB-1985;
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    173
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to a composition comprising one or more domains of urokinase-type plasminogen activator (uPA). The composition is used to modulate the contractility and angiogenic activity of a mammalian muscle, endothelial cell or tissue. The composition is used for treating stroke, hypotension, hypertension, atherosclerosis, heart attack, microvascular occlusions, thrombotic microangiopathies, surgically induced thrombotic disorders, angiogenic disorders, pulmonary fibrosis, asthma, tumour cell invasion, tumour cell angiogenesis, tumour cell metastasis, glaucoma, disorder, male impotence, respiratory discress syndrome, primary pulmonary hypertension, microvascular thrombotic occlusion, and a disorder sequence as the condition contraction disorder thrombotic occlusion, and a disorder sequence is human urokinase-type plasminogen activator (UPA) two
                                                                                                                                                          Human, urokinase-type plasminogen activator; uPA; therapy; hypertension; stroke; hypotension; atherosclerosis; heart atteak; thrombotic disorder; microvascular occlusion; angiogenic disorder; pulmonary fibrosis; asthma; tumour cell metastasis; glaucoma; diabetic retinopathy; wound healing; clotting disorder; uterine contraction disorder; respiratory disease; male impotence; adult respiratory distress syndrome; touPA; scuPA; two chain urokinase; aingle chain urokinase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PLVQECMVHDCADGKKPSSPPEELKFQCGQKTLRPRFKIIGGEFTTIENQPWFAAIYRRH 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Composition for modulating muscle cell and tissue contractility for treating atherosclerosis, asthma, hypertension, glaucoma, impotence, comprising domains from urokinase-type plasminogen activator
                                                                                                                        Human urokinase-type plasminogen activator tcuPA and scuPA protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ..
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98.1%; Pred. No. 1.2e-174;
ive 0; Mismatches 0;
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      standard; Protein; 411
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                                                                                      entry)
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nes 403; Conservative
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host, for the efficient production of high molecular human urokinase. The N-terminal of the protein expressed by the transforming plasmid is replaced with a codon frequently used in E.coli. (Updated on 25-MAR-2003 to correct PA field.)
                                                                                    Length 431;
                                                                                                           Indels
                                                                                  Score 2243; DB 7;
Pred. No. 1.2e-174;
0; Mismatches 0;
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98.1%;
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(NIPS ) NIPPON
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30-JAN-1987;
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19-MAY-1991
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                                                SNELHQVPSNCDCLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFYRG 80
                                                                                                                                       RGGSVTYVCGGSLISPCWVISATHCFIDYPKKEDYIVYLGRSRLNSNTQGEMKFEVENLI
                                                                         KASTDIMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVGLK
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                           SNELHQVPSNCDCLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFYRG
     Gaps
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SAGAMI CHEM RES CENTRE.
CENTRAL GLASS CO LTD.
NIPPON SODA CO.
TOYO SODA MFG CO LTD.
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used in Escherichia coli
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N-PSDB; AAN60703.
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23-OCT-1991
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                                                    1 SNELHQVPSNCDCLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFYRG
                                                                                                 SNELHOVPSNCDCLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFYRG
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  Gaps
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The patent is for the prodn. of human single chain urokinase-type plasminogen activator (UTPA). Mutants of scu-PA are especially those which render the protein protease resistant. Such scu-PA mutants are covalently modified at sites of proteolysis by proteases occuring in blood such as thrombin or plasmin, so that thay are no longer susceptable to protease hydrolysis at these locations. The target sites include Lysils to Lysils (cleavage at this site generates the so-called low molecular weight form of scu-PA or LUK), Argiss to Phel57 (susceptible to thrombin attack) and Lysils to liel59 (cleavage at this site by plasmin generates tuc-PA). Suitable scu-PA mutants have site site by plasmin generates tuc-PA). Suitable scu-PA mutants have site specific substitutions, insertions or deletions of residues at come or more of these target sites. Especially preferred are those mutants in which one amino acid residues forming the target sites are deleted or in which at least one of these mutants are resistant to proteolytic attack. The UTPA proteins exhibit the biological activity of natural human UTPA without the refolding procedure being necessary. They can be used as for known PAs in humans for the prevention or treatment of thrombosis or other contains the protein or treatment of thrombosis or other contains the proteins who was a for known pass in humans for the prevention or treatment of thrombosis or other contains the proteins while the proteins or other contains the proteins or other proteins the proteins or other contains the proteins or other contains the proteins or other contains the proteins the proteins or other contains the proteins the proteins or other proteins the proteins t
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     glyceraldehyde-3-phosphate dehydrogenase gene; thrombosis prevention;
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by culturing yeast strain transformed with hybrid vector contg
yeast expression control sequences
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98.1%; Pred. No. 1.2e-174;
live 0; Mismatches 0;
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                                                                                                                      Location/Qualifiers
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                                thrombosis treatment
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       141 PLVQECMVHDCADGKKPSSPPEELKFQCGQKTLRPRFKIIGGEFTTIENQPWFAAIYRRH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RGGSVTYVCGGSLISPCWVISATHCFIDYPKKEDYIVYLGRSRLNSNTQGEMKFEVENLI
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                                                                                                                                                                                                                                                                                                                                                                               The TPA portion of the claimed hybrid polypeptide (see FT) may consist of 2 kringles from N-terminal first serine to 219th glycine of human TPA, 1 kringle from 128th serine to 219th glycine of human TPA or half a kringle from 161st methionine to 219th glycine (see AAP70257). The C-terminal half of the hybrid polypeptide may contain an AA sequence from 150th glutamine to C-terminal 411th leucine of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VCSLQGRMTLTGIVSWGRGCALKDKPGVYTRVSHFLPWIRSHTKEENGLAL 403
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                                                                                                                                                                                                                                        Hybrid plasminogen activator-like polypeptide - having a region for affinity to fibrin from tissue plasminogen activator and a region from prourokinase
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                                                                                                                         Хокоуата М,
                                                                                                                                                                                                                                                                                                                                         Disclosure; Fig 2(1-5); 64pp; English
CENTRAL GLASS CO LTD.
TOYO SODA MFG CO LTD.
NISSAN CHEM IND LTD.
NISSAN CHEMICAL INDS KK.
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                                                                                                                         Yamada M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (see AAP70258).
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Best Local Similarity 98.1%;
Matches 403; Conservative
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N-PSDB; AAN70390.
                                                                                                                         Wada M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        431 AA;
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                                                                                                                            Tagawa M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
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                                              21 SNEIHQVPSNCDCLNGGTCVSNKYPSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFYRG
                                                                                                                                                    PLVQECMVHDCADGKKPSSPPEELKFQCGQKTLRPRFKIIGGEFTTIENQPWFAAIYRRH
                                                                             KASTDIMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVGLK
                                                                                                                                                                                                    RGGSVTYVCGGSLISPCWVISATHCFIDYPKKEDYIVYLGRSRLNSNIQGEMKFEVENLI
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                          SNELHQVPSNCDCLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFYRG
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Misc-difference 156
 Indels
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/note="Incorporated into new deriv."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human prourokinase; antithrombotic; derivative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Optional in new deriv."
 Mismatches
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HODGGAYA CHEM KK.
NIPPON SODA CO.
NISSAN CHEM IND LTD.
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(first entry)
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29-JUN-1990
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                                                                   LHKDYSADTLAHHNDIALLKIRSKEGRCAQPSRTIQTICLPSMYNDPQFGTSCEITGFGK
RGGSVTYVCGGSLISPCWVISATHCFIDYPKKEDYIVYLGRSRLNSNTQGEMKFEVENLI
               RGGSVTYVCGGSLISPCWVISATHCFIDYPKKEDYIVYLGRSRLNSNTQGEMKFEVENLI
                                                   LHKDYSADTLAHHNDIALLKIRSKEGRCAQPSRTIQTICLPSMYNDPQFGTSCEITGFGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The Arg at position 2 is encoded by TGA(sic). Possible error in the specification. Should read CGA? The pro-UK gene was derived from plasmid pUK13. The CDNA was The pro-UK gene was derived from plasmid pUK13. The CDNA was synthesised using urokinase mRNA isolated from a human kidney cell line. Pro-UK was cloned into a SV40 promoter-contg. plasmid down-stream of the promoter. This plasmid was then ligated to a DHFR-gene contg. plasmid so that pro-UK and DHFR are inserted in opposite directions. The recombinant plasmid was used to transform CHO-K1 cell derived DHFR gene-deficient host cells to produce (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                       VCSLQGRMTLTGIVSWGRGCALKDKPGVYTRVSHFLPWIRSHTKEENGLAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Glycosylated single-chain pro-urokinase prodn - by cultivating DHFR gene-deficient CHO-Kl cells transformed with a plasmid contg cDNA, SV40 promoter and DHFR gene.
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                                                                                                                                                                                                                                                                                                                                                                    (pro-UK); plasminogen activator; pUK33; ss
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Pred. No. 1.2e-174;
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/label=signal peptide
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/label=pro-urokinase
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(first entry)
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Best Local Similarity
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03-DEC-1990
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N-PSDB; AAQ04107.
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Best Local Similarity
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                                                              Brandazza A,
06-OCT-1989;
                     11-OCT-1988;
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24-JAN-1991
                                                                                                                                                                                                                                                                               403;
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                                                                                                                                                                                                                                                Gaps
                                                                                                                          A human prounokinase (PU) deriv. is new which is based upon residues 2-155 of natural human prounokinase. The new deriv. is produced by E. coli J103/pMUT9Q-RPK in culture. It is a fast-acting drug for the treatment and prevention of thrombosis. (Updated on 25-MAR-2003 to correct PA field.) (Updated on 25-MAR-2003 to correct PI field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Non-glycosylated; pro-urokinase; E. coli; Ptrp promoter; MS-2 RBS
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                                                            Antithrombotic fast-acting pro-urokinase deriv. - produced by culture of E. coli transformant contg. new plasmid of PMUT9Q family.
                                                                                                                                                                                                                          Length 431;
                                                                                                                                                                                                                                               Indels
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                                                                                                                                                                                                                       tch
39.4%; Score 2243; DB 10;
al Similarity 98.1%; Pred. No. 1.2e-174;
403; Conservative 0; Mismatches 0;
                                                                                                        Disclosure; Fig 1; 75pp; Japanese
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            Yamada
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(first entry)
           Omori M,
                               WPI; 1989-068869/09
                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                       431 AA;
                                           N-PSDB; AAN91075
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12-SEP-1990
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                                                                                                                                                                                                                                                                                                        on 21 is the start of the mature proUK. (MW 45kD) produced by E.coli B strain containing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SNELHQVPSNCDCLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFYRG
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                                                                                                                                                                                              Non-glycosylated pro-urokinase prodn. - using E.coli B strains and promoter Ptrp and Shine-Dalgarno sequence MS-2.
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Pred. No. 1.2e-174;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                      SER residue at position 21 is the start of the Non-glycosylated proUK (MW 45kD) produced by Ethe Sequence.

The Sequence.

(Sea also AAQ04101-07.

(Updated on 25-MAR-2003 to correct PA field.)
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llarity 98.1%;
Conservative
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                                         (FARM ) FARMITALIA ERBA SPA
88GB-0023833
                                                                                     Sarmientos P,
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17-OCT-1991;
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                                                                                                                                                                     of recombinant protein, esp. human pro:urokinase - from transgenic animals using promoter of bovine alpha Sl casein
                                                                                                                                                                                                                              E.coli strain C6008F8 was transformed with recombinant plasmid containing ds DNA derived from human pharynx cancer cell strain Detroit 562. 10000 colonies were screened and one positive clone was identified. Plasmid pUKI was isolated and found to contain the coding region and 3' non-coding region of pro-UK downstream of Cys(11). Four silent substitutions were identified c.f. Holmes et al., Biotechnology, vol.3, p.923 (1985) as follows: (sic) Asn(254), AAC to AAT; Leu(340), CTA to CTG; Pro(345), CCC to CCA, GJN(346), CAA to CAG.

(Updated on 25-MAR-2003 to correct PA field.)
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Pred. No. 1.2e-174;
                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                      (KYOW) KYOWA HAKKO KOGYO KK.
(EXPE-) CENT INST EXPER ANIMALS.
(JIKK-) JIKKEN DOBUTSU CHUO KENK.
                                                                                                                                                                                                              Example; Table 1; 55pp; English
                                                                                                                  Katsuki M;
                                                                                                                                                                                                                                                                                                                                                                                     99.48;
98.18;
                                                   89JP-0078574.
                              90EP-0303445
                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                     of recombinant
                                                                                                                                      WPI; 1990-299492/40.
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Best Local Similarity
                                                                                                                  Sekine S, Ito S,
                                                                                                                                                                                                                                                                                                                                                                431 AA;
                                                                                                                                                                                           chromosomal gene.
                                                                                                                                                  N-PSDB; AAQ06049
                               30-MAR-1990;
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                                                                                                       Pro-urokinase; half-life; thrombolytic; thrombosis; fibrinolytic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       403
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel human pro-urokinase derivs. having long half-life - with high thrombolytic activity, useful for treatment of thrombosis
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Pred. No. 1.2e-174;
0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (KYOW ) KYOWA HAKKO KOGYO KK
                                                                                                                                                                                                                                                                                                                                                                                                                  91JP-0269615.
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(first entry)
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                                                     Pro-urokinase derivative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1994-030907/04.
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Matches 403; Conserv
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N-PSDB; AAQ55772
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AAR63141
ID AAR631
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AAR63141 standard; Protein; 431

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AAR47903 standard; Protein; 431

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KASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVGLK
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(Updated on 25-MAR-2003 to correct PP field.)
                                                                                                                                                                                                                                                                                          "clevage of this site produces a bioactive two chain form of urokinase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Prodn. of human urokinase glycoproteins - using a recombinant expression system used for the treatment of vascular diseases or conditions.
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                                                                                       Human urokinase glycoproteins; cardiovascular diseases; pulmonary embolism.
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llarity 98.1%; Pred. No. 1.2e-174;
Conservative 0; Mismatches 0;
                                                                  full length human urokinase protein.
                                                                                                                                                Location/Qualifiers
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83US-0474930.
83EP-0103629.
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                                             (first entry)
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168..299
209..225
217..288
313..382
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372..400
179..180
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                                  (updated)
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403; Conserv
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                                                                                                                                                            Sig_peptide
Disulfide-bond
Disulfide-bond
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Disulfide-bond
Cleavage-site
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14-APR-1983;
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                                                                                                                           Homo sapiens
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                                 25-MAR-2003
09-JUN-1995
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            AAR63141;
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Indels

1 SNELHQVPSNCDCLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFYRG SNELHQVPSNCDCLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFYRG

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The present sequence is human plasminogen activator urokinase (u-PA), a serine protease which hydrolyses a peptide bond in human plasminogen to convert it to its active form, plasmin. Plasminogen is the principal serine protease zymogen in the extracellular fluids of vertebrates. Plasmin is implicated in pericellular proteolysis associated with a wide range of physiological and pathological processes. Plasminogen activators regulate plasminogen expression either by hydrolysing a activators ragulate plasminogen expression either by hydrolysing a complexes with plasminogen to spontaneously convert it to plasmin, Review of sequence homologies of several plasminogen activators and chymotrypsin has identified a six amino acid peptide involved in plasminogen
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                                                                                                                                                                                                                                                                                                                                   321 ENSTDYLYPEQLKMTVVKLISHRECQQPHYYGSEVTTKMLCAADPQWKTDSCQGDSGGPL
                        261 LHKDYSADTLAHHNDIALLKIRSKEGRCÄQPSRTIQTICLPSMYNDPQFGTSCEITGFGK
                                                                                                                                                                                                                                                                                                              ENSTDYLYPEQLKMTVVKLISHRECQOPHYYGSEVTTKMLCAADPQWKTDSCQGDSGGPL
                                                                           PLVQECMVHDCADGK------LKFQCGQKTLRPRFKIIGGEFTTIENQPWFAAIYRRH
                                                                                                  RGGSVTYVCGGSLISPCWVISATHCFIDYPKKEDYIVYLGRSRLNSNTQGEMKFEVENLI
                                                                                                                                                                               201 RGGSVTYVCGGSLISPCWVISATHCFIDYPKKEDYIVYLGRSKLNSNTQGEMKFEVENLI
                                                                                                                                                                                                                                  LHKDYSADTLAHHNDIALLKIRSKEGRCAQPSRTIQTICLPSMYNDPQFGTSCEITGFGK
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This invention describes a novel thrombolytic agent comprising streptokinase where at least one nonessential portion has been modified. The invention also describes a method of forming a thrombolytic agent comprising determining a nonessential portion of streptokinase and modifying the nonessential portion to render the resulting protein less antigenic. The modified streptokinase is used to treat blood clot disorders, such as heart attacks. The modified streptokinase has less antigenicity than streptokinase but is still able to complex plasminogen and lead to plasminogen activation. Modified streptokinase with the monessential portions removed or truncated simplify the molecule. Such smaller proteins are cheaper and easier to produce. This sequence represents a fragment of the human urokinase protein which is used in the description of the method of the invention.
            Disclosure; Page 46-48; 55pp; English.
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activation. This peptide is particularly useful when inserted between amino acid residues 644 and 645 of full length human plasminogen. Novel plasminogen activators have been made based upon the plasminogen activation/recognition site of plasminogen binding proteins. The polypeptides are useful in preparing thrombolytic agents for treating blood clotting disorders such as heart attack.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New thrombolytic agents derived from modified humanized streptokinase, useful for treating blood clot disorders -
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                                                                                                                       Length 431;
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                                                                                                                     Score 2243; DB 21;
Pred. No. 1.2e-174;
0; Mismatches 0;
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Best Local Similarity 98.1%;
Matches 403; Conservative
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blood clot; heart
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                                               Length 431;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VCSLQGRMTLTGIVSWGRGCALKDKPGVYTRVSHFLPWIRSHTKEENGLAL
                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Amino acid sequence of urokinase plasminogen activator.
                                               Score 2243; DB 21;
Pred. No. 1.2e-174;
0; Mismatches 0;
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                                                     99.4%;
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                                                                            al Similarity 98.1
403; Conservative
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431 AA;
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431 AA;
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                                                                                                                                                                                                                                                                                                                   Protein
                                                                                                                                                                                                                                                     Peptide
                                                                                                                                                                                                                                                                              Protein
                                                                                                            sc-uPA
                                            The specification describes a pharmaceutical composition, comprising a growth factor, an inhibitor agent, i.e. a protease. The inhibitor agent, i.e. a protease. The inhibitor agent inhibits the action of at least one specific adverse protein, i.e. a protease, that is upregulated in a damaged tissue such as a wound environment. Growth factors which are included in the composition of the invention are platelet-derived growth factor (PGF), inconsective dissue derived growth factor (FGF), connective tissue derived growth factor (GGF), connective dissue derived growth factor (KGF), transforming growth factor (GGF), consection of protein agrowth factor (KGF), transforming growth factor (GGF), and chrysalin. Inhibitors which are included in the composition of the invention include inhibitors of urokinase-type composition is useful for the treatment of chronic damaged tissue, i.e. wounds and dermal ulcers. The present sequence represents a human uPA, and is used to produce the composition of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RGGSVTYVCGGSLISPCWVISATHCFIDYPKKEDYIVYLGRSRLMSNTQGEMKFEVENLI 260
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PLVQECMVHDCADGK------LKFQCGQKTLRPRFKIIGGEFTTIENQPWFAAIYRRH 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               261 LHKDYSADTLAHHNDIALLKIRSKEGRCAQPSRTIQTICLPSMYNDPQFGTSCEITGFGK 320
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                                                                                                                                                                                                 Composition for the treatment of damaged tissue i.e. chronic wounds and dermal ulcers comprises an inhibitor agent i.e. a protease and a growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PLVQECMVHDCADGKKPSSPPEELKFQCGQKTLRPRFKIIGGEFTTIENQPWFAAIYRRH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SNELHOVPSNCDCLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFYRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RGGSVTYVCGGSLISPCWVISATHCFIDYPKKEDYIVYLGRSRLNSNTQGEMKFEVENLI
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98.1%; Pred. No. 1.2e-174;
tive 0; Mismatches 0; Indels 8;
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                                                                                                                                    Occleston NL;
                                                                                                                                    Mcintosh FS,
                                                                                                                                                                                                                                                     Disclosure; Page 550; 572pp; English.
                                              21-DEC-2000; 2000WO-IB01935.
                                                                       99GB-0030768
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Best Local Similarity 98.1
Matches 403; Conservative
                                                                                                                                      Huggins JP,
                                                                                                                                                              WPI; 2001-418351/44
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                                                                                                (PFIZ ) PFIZER
(PFIZ ) PFIZER
                                                                         29-DEC-1999;
                                                                                                                                      Davies MJ,
                       12-JUL-2001
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This sequence represents single chain prepro-urckinase (sc-upA).

Pro-urckinase (amino acids 21-431) with a cleavage between amino acids 178 and 179 gives high molecular weight urckinase-type classinogen activator (HWW-upA). HWW-upA is a protein consisting of two peptide chains linked by a di-sulphide bond. The chains, close and 179 of pro-urckinase. HWW-upA is obtain acids in a kringle domain and a urckinase receptor (CDB) binding domain. HWW-upA is then cleaved between amino acids 155-178 and 179-60 plasminogen activator (LWM-upA) at then cleaved between amino acids 155-178 and 179-411, that has no plasminogen activator activity. Sc-upA, or fragments of it, may be used in the anti-HIV agents of the invention which comprise a ligand molecule that binds to CDB7. The agents are useful for treating HIV-infected humans for suppression of reproduction of HIV. The anti-HIV agents act by a mechanism of action different from those of conventional drugs, widening the choice of therapeutics agents and avoiding problems of
                                                                                                                                                                                                                                                                                                                              Single chain prepro-urokinase; sc-uPA; pro-urokinase; HIV; high molecular weight urokinase-type plasminogen activator; HWW-uPA; long A; long B; ESF-like domain; kringle domain; urokinase receptor; low molecular weight urokinase-type plasminogen activator; LMW-uPA; CD87; binding domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'note= "With a cleavage between amino acids 178-179"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "With a cleavage between amino acids 178-179"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Anti-HIV agents, comprises ligand molecule that binds to CD87, e.g. high molecular weight urokinase-type plasminogen activator, amino-terminal fragment or an anti-CD87 antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21..431
/label= Pro-urokinase/HMW-uPA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
AAG79460 standard; Protein; 431 AA
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/label= LMW-uPA
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19-JUN-2001; 2001JP-0184284.
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N-PSDB; ABA00207.
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DB 23;

99.4%; Score 2243;

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200
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                                                                                          KASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVGLK 120
                                                                                                          KASTDIMGRPCLPWNSATVLQQIYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVGLK 140
                                                                                                                                              PLVQECMYHDCADGK-----LKFQCGQKTLRPRFKIIGGEFTTIENQPWFAAIYRH 172
                                                                                                                                                                                                                                                                                                          ENSTDYLYPEQLKMTVVKLISHRECQQPHYYGSEVTTKMLCAADPQWKTDSCQGDSGGPL 352
                                                              90
                                      60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genetic variants of Plasminogen activator, Urokinase (PLAU) isogenes, useful for improving efficiency and reliability in drug development for treating thrombolytic disorders and cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to a polynucleotide comprising a first nucleotid sequence (NSI) comprising a PLAU (plasminogen activator, urokinase, a serine protease) isogene selected from isogenes 1-9 and 11-20 given
                                                                                                                                                                       PLVQECMVHDCADGKKPSSPPEELKFQCGQKTLRPRFKIIGGEFTTIENQPWFAAIYRRH
                                                                                                                                                                                                                                                      LHKDYSADTLAHHNDIALLKIRSKEGRCAQPSRTIQTICLPSMYNDPQFGTSCEITGFGK
                                                                SNELHQVPSNCDCLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFYRG
                                                                                                                                                                                                 RGGSVTYVCGGSLISPCWVISATHCFIDYPKKEDYIVYLGRSRLNSNTQGEMKFEVENLI
                                     SNELHQVPSNCDCLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFYRG
            Gaps
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            Indels
Pred. No. 1.2e-174;
; Mismatches 0;
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N-PSDB; ABK86597, ABK86598.
98.1%;
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              Conservative
  Best Local Similarity
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              403;
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in the specification, where each isogene comprises the regions of the PLAU gene or CDNA and is further defined by the corresponding sequence of polymorphisms (Gefining single nucleotide polymorphisms, SNP). Also included are methods of haplotyping/genotyping (and predicting the abjotype/genotype of the PLAU gene of an individual, identifying an association between a trait and at least one haplotype or haplotype pair of the PLAU gene, an isolated oligonucleotide for detecting a complexity of the PLAU gene, a recombinant non-human organism transformed or transfected with the gene or CDNA, fragments of the polymorphic variant PLAU protein or fragment of sie, an isolated polymorphic variant PLAU protein or fragment for sie, an isolated polymorphic variant PLAU a computer system for storated and analysing polymorphism data for the PLAU a computer system for cancers. The malysing polymorphism data for the PLAU gene and a genome cancers. The methods are useful for improving the efficiency and diseases associated with PLAU activity, in validating PLAU as a drug diseases as sociated with PLAU activity, in validating PLAU as a drug condition of disease associated with PLAU activity. The antibody is useful in diagnostic, prognostic and therapeutic methods. PLAU or candidate or useful in studying the expression and function of PLAU, and in expressing PLAU protein for use in screening for candidate drugs to treat diseases related to pLAU activity. The gene for PLAU is a plant of the discovery and eventual protein for use in screening for candidate or an interpretation for use in screening for pLAU in an interpretation of the pLAU protein for use in screening for PLAU in an interpretation of the pLAU protein for use in screening for PLAU in an interpretation of the pLAU protein for use in screening for PLAU in an interpretation of the pLAU protein for use in screening for PLAU in an interpretation of the pLAU protein for use in screening for PLAU in an expressing pLAU protein for use useful in the pLAU protein for the pLAU a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 SNELHQVPSNCDCLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFYRG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          141 PLVQBCMVHDCADGKKPSSPPEELKFQCGQKTLRPRFKIIGGEFTTIENQPWFAAIYRRH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99.4%; Score 2243; DB 23;
ilarity 98.1%; Pred. No. 1.2e-174;
Conservative 0; Mismatches 0;
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les 403; Conserv
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23
                                   ABU56547
                       RESULT
                                                The invention relates to a method of identifying a compound for treating cancer. The method involves detecting the expression of a panel of sequences selected from transcription factor Etel, urokinase-type plasminogen activator (uPA), Nacetylglucosaminyltransferase V (GnT-V), matrix-type metalloproteinase (MMP)-1 and MMP-3 in the cell. The method cancer cell or identifying a compound that affects a cell, particularly a cancer cell or identifying a compound that affects a cell, particularly a Li s used for diagnosing and/or treating cancer or other conditions that are affected by one or more members of a panel of genes or that protein product. The method is also useful for drug discovery, drug safety evaluations and in gene therapy. The present sequence is human uPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KASTDIMGRPCLPWNSAIVLQQIYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVGLK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ENSTDYLYPEQLKMTVVKLISHRECQQPHYYGSEVTTKMLCAADPQWKTDSCQGDSGGPL 352
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SNELHQVPSNCDCLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFYRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVGLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PLVQECMVHDCADGK-----LKFQCGQKTLRPRFKIIGGEFTTIENQPWFAAIYRRH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PLVQECMVHDCADGKKPSSPPEELKFQCGQKTLRPRFKIIGGEFTTIENQPWFAAIYRRH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RGGSVTYVCGGSLISPCWVISATHCFIDYPKKEDYIVYLGRSRLNSNTQGEMKFEVENLI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LHKDYSADTLAHHNDIALLKIRSKEGRCAQPSRTIQTICLPSMYNDPQFGTSCEITGFGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ENSTDYLYPEQLKMTVVKLISHRECQQPHYYGSEVTTKMLCAADPQWKTDSCQGDSGGPL
                                                                                                                                                                                                                                        Identifying a compound for treating cancer, comprises detecting transcription factor Ets-1, N-acetylglucosaminyltransferase V, urokinase-type plasminogen activator, matrix-type metalloproteinase-1
Ets-1 transcription factor; N-acetylglucosaminyltransferase V; {\tt GnT-V}_i matrix-type metalloproteinase; {\tt MMP-1}_i; {\tt MMP-3}_i gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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8
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Pred. No. 1.2e-174;
0; Mismatches 0; Indels 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VCSLQGRMTLTGIVSWGRGCALKDKPGVYTRVSHFLPWIRSHTKEENGLAL
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                                                                                                                                                                                                                                                                                                      Example 1; Page 62-63; 63pp; English.
                                                                                                                                                       (NYXI-) NYXIS NEURO THERAPIES INC.
                                                                                                                                                                                Moskal JR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99.4%;
98.1%;
                                                                                                          14-JUN-2001; 2001WO-US19248.
                                                                                                                                 14-JUN-2000; 2000US-0593488.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                               and -3 gene expression
                                                                                                                                                                                famamoto H, Kroes R,
                                                                                                                                                                                                        2002-130746/17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      431 AA;
                                                                                                                                                                                                                  N-PSDB; AAD27855
                                     Homo sapiens
                                                                                   20-DEC-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    403;
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Best Local S
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The invention relates to a method for detecting a lung cancer-associated transcript in a cell from a patient, comprising concacting a biological cample from the patient with a polynucleotide that selectively hybridises to a sequence that is at least 80 % identical to a gene that exhibits concer-associated expression in lung cancer samples. Lung cancer-associated polynucleotides and polypeptides are used for cancer-associated polynucleotides and polypeptides are used for concer-associated proliferation of a lung cancer-associated cell to treat lung cancer in a patient and for treating a mammal having coll to treat lung cancer in a patient and for treating a mammal having coll to treat lung cancer by administrating a modulatory compound identified. The methods are useful for treating lung cancer, such as small cell lung cancer or other benign or precancerous cancer, non-small cell lung cancer or other benign or precancerous cultations, e.g. atelectasis, emphysema, bronchtis, chronic obstructive pulmonary disease, fibrosis, apphysema, bronchtis, interstitial cultang pulmonary fibrosis, asthma and bronchiectasis. The genes, polynucleotides conditions are useful for diagnostic purposes and as targets for screening for therapeutic compounds that modulate lung cancer, such as antibodies. Sequences ABUS6745 represent lung cancer, such as an colypeptides of the invention.
                                                                                                                                                                                                                                                                                                      Lung cancer-associated polypeptide; cytostatic; emphysema; antiinflammatory; antiaethmatic; non-small cell lung cancer; atelectasis small cell lung cancer; benign lesion; precancerous lesion; bronchitis; chronic obstructive pulmonary disease; hypersensitivity pneumonitis; interstitial pulmonary fibrosis; asthma; bronchiectasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Detecting a lung cancer-associated transcript in a cell from a patient for treating lung cancer, by contacting a biological sample from the patient with a polynucleotide that exhibits increased or decreased expression in lung cancer.
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Pred. No. 1.2e-174;
0; Mismatches 0;
                                                                                                                                                                                                                               Lung cancer-associated polypeptide #140.
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ABUS6547 standard; Protein; 431
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10-MAY-2001; 2001US-290492P.
09-NOV-2001; 2001US-339245P.
13-NOV-2001; 2001US-350666P.
29-NOV-2001; 2001US-334370P.
12-APR-2002; 2002US-372246P.
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Best Local Similarity
Matches 403; Conserv
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                                                                                                                                                         02-APR-2003
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                                                                          ABU56547;
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                                                                                                                                                                                                                                                                                                                                              lung cancer-associated polypeptide, cytostatic, emphysema, antinflammatory, antiasthmatic; non-small cell lung cancer; atelectasis; small cell lung cancer, benign lesion; precancerous lesion; bronchitis; chromic obstructive pulmonary disease; hypersensitivity pneumonitis; interstitial pulmonary fibrosis; fibrosis; asthma; bronchiectasis.
                                                                                                                 292
                                                                                                                                                      LHKDYSADTLAHHNDIALLKIRSKEGRCAQPSRTIQTICLPSMYNDPQFGTSCEITGFGK 320
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                                                                                                                                                                            ENSTDYLYPEQLKMTVVKLISHRECQOPHYYGSEVTTKMLCAADPQWKTDSCQGDSGGPL 352
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Detecting a lung cancer-associated transcript in a cell from a patient for treating lung cancer, by contacting a biological sample from the patient with a polynucleotide that exhibits increased or decreased expression in lung cancer -
                                                                                                                                                                                      ENSTDYLYPEQLKMTVVKLISHRECQQPHYYGSEVTTKM.CAADPQWKTDSCQGDSGGPL
                                             PLVQECMVHDCADGK------LKFQCGQKTLRPRFKIIGGEFTTIENQPWFAAIYRRH
                                                                                 SNELHQVPSNCDCLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFYRG
                                                                                                        RGGSVTYVCGGSLISPCWVISATHCFIDYPKKEDYIVYLGRSRLNSNTQGEMKFEVENLI
                                                                                                                                          LHKDYSADTLAHHNDIALLKIRSKEGRCAQPSRTIQTICLPSMYNDPQFGTSCEITGFGK
                                   KASTDIMGRPCLPWNSAIVLOOIYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVGLK
SNELHQVPSNCDCLNGGTCVSNKYFSNIHWCNCPKKFGGQHCBIDKSKTCYEGNGHFYRG
                                                                                                                                                                                                                         VCSLOGRMTLTGIVSWGRGCALKDKPGVYTRVSHFLPWIRSHTKEENGLAL 403
                                                                                                                                                                                                                                                                                                                               cancer-associated polypeptide #301.
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                                                                                                                                                                                                                                                                             standard; Protein; 431
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10-MAY_2001; 2001US_290492P
09-NOV_2001; 2001US_339245P
13-NOV_2001; 2001US_350666F
29-NOV_2001; 2001US_37370P
12-APR_2002; 2002US_372246P
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                                                                                                                                                                                                                                                                                                               (first entry)
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N-PSDB; ABX76437.
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The invention relates to a method for detecting a lung cancer-associated transcript in a cell from a patient, comprising contacting a biological casmple from the patient with a polymicleotide that selectively hybridises to a sequence that is at least 80 % identical to a gene that exhibits concreased or decreased expression in lung cancer samples. Lung cancer-associated polymoleotides and polymeptides are used for identifying a compound that modulates a lung cancer-associated for inhibiting proliferation of a lung cancer-associated coll to treat lung cancer in a patient and for treating a mammal having cancer hy administering a modulatory compound identified. The methods are useful for treating lung cancer, such as small cell lung cancer or other benign or precancerous cancer, non-small cell lung cancer or other benign or precancerous concern, at electasis, emphysem, bronchitis, chronic obstructive pulmonary fibrosis, asthma and bronchites. The genes, polymicleotides cond polypeptides are useful for diagnostic purposes and as targets for screening for therapeutic compounds that modulate lung cancer, such as antibuted as a published that modulate lung cancer, such as antibuted as a published that modulate lung cancer, such as a polymored as the second and promotive and polymerated and as targets for antibodies. Sequences ABUS6745 represent lung cancer sesociated
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99.4%; Score 2243; DB 24;
Best Local Similarity 98.1%; Pred. No. 1.2e-174;
Matches 403; Conservative 0; Mismatches 0;
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LHKDYSADTLAHHNDIALLKIRSKEGRCAQPSRTIQTICLPSMYNDPQFGTSCEITGFGK 320
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The protein has fibrinolytic activity and can be used in the same way as PUK, e.g. for treating acute myocardial infarction, lung membolism and deep venous thrombosis. It has greater affinity for plasminogen bound to fibrin than for circularing plasminogen, so have high selectivity for thrombi with reduced chance of bleeding. Compared with the COM+terminated cpds., it has a better stability against most carboxypeptidases and prolonged half life. See also AAQC0360, AAQC0364-58 and AARC0336-38. (Updated on 25-WAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                                                                                                                 New amidated derivs. of human pro-urokinase - are fibrinolytic and can be used to treat acute myocardial infarction, pulmonary embolism or deep vencus thrombosis
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                                                              plasminogen activator;
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                                                                                                                        Location/Qualifiers
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                                Amidated deriv. of pro-urokinase
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91GB-0014846.
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nes 403; Conservative
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                                                                                                                                                                                                                                                                                                                                                        Visco C,
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                                                              Pro-urokinase;
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21-MAY-1992
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                                                                                                                                                                                                                              New antisense compound, useful for preparing a composition for treating hyperproliferative disorders, cancer e.g., breast, colon, bone, brain, ovary, cervix, endometrium, stomach or kidney cancer, or tumor
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                                                                                                                                                                                                                                                                                                                                      A new compound, which is 8-50 nucleobases in length targeted to a nucleic acid molecule encoding urokinase plasminogen activator, specifically hybridises with and inhibits the expression of urokinase plasminogen activator. The compound is useful for preparing a composition for treating (e.g. by gene therapy) hyperproliferative disorder, cancer e.g., breast, colon, bone, brain, ovary, cervix, endometrium, scomach or kidney cancer, or tumour metastasis. This is the amino acid sequence of a urokinase plasminogen activator.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VCSLQGRMTLTGIVSWGRGCALKDKPGVYTRVSHFLPWIRSHTKEENGLAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
99.4%; Score 2243; DB 24;
Best Local Similarity 98.1%; Pred. No. 1.2e-174;
Matches 403; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                              Disclosure; Page 101-102; 153pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ā
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                                                                                                                                                         AT;
                                                               18-MAR-2002; 2002WO-US08112.
                                                                                              2001US-0821972.
                                                                                                                                                           Watt
                                                                                                                          (ISIS-) ISIS PHARM INC
                                                                                                                                                         Freier SM,
                                                                                                                                                                                      WPI; 2003-058441/05.
N-PSDB; ABX17681.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  431 AA;
    WO200279515-A1
                                                                                              30-MAR-2001;
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                                   10-OCT-2002
                                                                                                                                                                                                                                                                               metastasis
                                                                                                                                                           Baker BF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  353
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                                                                                                                                                          321 ENSTDYLYPEQLKMTVVKLISHRECQQPHYYGSEVTTKMLCAADPQWKTDSCQGDSGGPL 380
232
               LHKDYSADTLAHHNDIALLKIRSKEGRCAQPSRTIQTICLPSMYNDPQFGTSCEITGFGK
RGGSVTYVCGGSLISPCWVISATHCFIDYPKKEDYIVYLGRSRLNSNTQGEMKFEVENLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The protein has fibrinolytic activity and can be used in the same way as PUK, e.g. for treating acute myocardial infarction, lung embolism and deep venous thrombosis. It has greater affinity for plasminogen bound to fibrin than for circulating plasminogen. So have high selectivity for thrombi with reduced chance of bleeding. Compared with the COOM-terminated cpds., it has a better stability against most carboxypeptidases and prolonged half life.

See also AAQC0356, AAQC0754-58 and AAR20536-38.
(Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                              VCSLOGRMTLTGIVSWGRGCALKDKPGVYTRVSHFLPWIRSHTKEENGLAL 403
                                                                                                                                                                                                              /note= "may be any amino acid, pref. Lys or Arg, or 0-4 amino acids may be omitted"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New amidated derivs. of human pro-urokinase - are fibrinolytic and can be used to treat acute myocardial infarction, pulmonary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sarmientos
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/label= pro-UK
/note= "the amidated form of pro-UK is
claimed in claim 1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Roncucci
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pro-urokinase; plasminogen activator; ss
                                                                                                                                                                                                                                                                                                                                                                                                                          Amidated deriv. of pro-urokinase (1)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        embolism or deep venous thrombosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (FARM ) FARMITALIA ERBA SRL CARLO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1,4,7; Page 8; 18pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Perego R,
                                                                                                                                                                                                                                                                                                               AAR20536 standard; Protein; 436
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91GB-0014846.
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(first entry)
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21-MAY-1992
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173
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PLVQECMVHDCADGK------LKFQCGQKTLRPFKIIGGEFTTIENQPWFAAIYRRH 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SNELHQVPSNCDCLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFYRG
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(Updated on 25-MAR-2003 to correct PA field.)
                                431
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Best Local Similarity 98.1%; Pred. No. 1.2e-174;
Matches 403; Conservative 0; Mismatches 0;
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S
                                                                                                                                                                                                                                                              plasminogen activator;
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                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
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                                                                                                                  AAR20538 standard; Protein; 434
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/label= pro-UK
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91GB-0014846.
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(first entry)
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                                                                                                                                                                                                                                                                Pro-urokinase;
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10-JUL-1991;
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21-MAY-1992
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92US-0942157.

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                                                                                                   KASTDIMGRPCLPWNSATVLQQIYHAHRSDALQLGLGKRNYCRNPDNRRRPWCYVQVGLK 140
                                                                                                                                                                                   260
                                                                                                                                                                                                                                           ENSTDYLYPEQLKMITVVKLISHRECQOPHYYGSEVTTKMLCAADPQWKTDSCQGDSGGPL 352
                                                                                                                          PLVQECMVHDCADGK-----LKFQCGQKTLRPRFKIIGGEFTTIENQPWFAAIYRRH 172
                                                                                                                                      PLVQECMVHDCADGKKPSSPPEELKFQCGQKTLRPRFKIIGGEFTTIENQPWPAAIYRH 200
                                                                                                                                                              RGGSVTYVCGGSLISPCWVISATHCFIDYPKKEDYIVYLGRSRLNSNTQGEMKFEVENLI 232
                                                                                                                                                                                                      LHKDYSADTLAHHNDIALLKIRSKEGRCAQPSRTIQTICLPSMYNDPQFGTSCEITGFGK 292
                                                                                                                                                                                                                       LHKDYSADTLAHHNDIALLKIRSKEGRCAQPSRTIQTICLPSMYNDPQFGTSCEITGFGK 320
                                                                                                                                                                                                                                                             ENSTDYLYPEQLKMTVVKLISHRECQOPHYYGSEVTTKMLCAADPQWKTDSCQGDSGGPL 380
                                                                                   KASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVGLK 120
                                               9
                                                                 SNELHQVPSNCDCLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFYRG 80
                                                                                                                                                                                                                                                                                                                                                                                                                                       Urokinase, inhibitor resistant, plasminogen; human, whey acid protein; plasminogen activator inhibitor-1; plasminogen activator; protease; WAP; plasmin; proteolytic enzyme; clot lysis; heart attack; heart muscle.
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198 .203
/note= "deleted in modified urokinase of the invention"
                                              SNELHQVPSNCDCLNGGTCVSNKYFSNIHWCNCPXKFGGQHCEIDXSKTCYEGNGHFYRG
                                                                                                                                                                                  RGGSVTYVCGGSLISPCWVISATHCFIDYPKKEDYIVYLGRSRLNSNTQGEMKFEVENLI
                            Gaps
                                                                                                                                                                                                                                                                                             VCSLQGRWTLTGIVSWGRGCALKDKPGVYTRVSHFLPWIRSHTKEENGLAL 431
                                                                                                                                                                                                                                                                               VCSLQGRMTLTGIVSWGRGCALKDKPGVYTRVSHFLPWIRSHTKEENGLAL 403
                           8
          Length 436;
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'note= "whey acid protein signal peptide"
                          Indels
          DB 13;
        Score 2243; DB 13;
Pred. No. 1.2e-174;
0; Mismatches 0;
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/note= "Kringle-1 domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                   AAW24578 standard; Protein; 430 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "urokinase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "E-domain"
                                                                                                                                                                                                                                                                                                                                                                                                                     Inhibitor resistant urokinase.
         99.4%;
98.1%;
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(first entry)
                  al Similarity 98.1
403; Conservative
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/note= "u
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11-NOV-1997
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         Query Match
Best Local S:
Matches 403
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This sequence represents the full length urokinase, including the whey acid protein (WAP) signal peptide. This sequence has residues 179-184 of the urokinase sequence deleted to create the modified urokinase (see AAW24579) cleaves plasminogen, and has a lower binding affinity for plasminogen activator inhibitor-1 than the corresponding unmodified urokinase. (Urokinase is one of two types of mammalian plasminogen activators (PA), the other being tissue type PA. PAS catalyse the conversion of the circulating zymogen plasminogen to the broad spectrum protease plasmin by infinited proteolysis. The modified urokinase and be used for old lysis, specifically to dissolve heart attack-causing clots before they cause permanent damage to heart muscle. The urokinase mutant is more resistant to inhibition by plasminogen activator inhibitors than the unmodified urokinase. It can be selectively expressed and secreted from the mammary glands of transgenic animals.
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Pred. No. 2.1e-174;
1; Mismatches 0;
                                                                                                                                                                                                                                                                      Disclosure; Column 15-18; 16pp; English.
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Best Local Similarity 97.8%;
Matches 402; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A low mol. wt. polypeptide plasminogen activator (PA) is claimed which is formed from authon acids 150-411 of prounsokinase. The preferred intiation region for the low mol. wt. PA is indicated (see FT). A low mol wt. PA can be injected into blood in the body in vivo to dissolve clots
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 KASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVGLK 120
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                                                                                                                                   21..431
/note= "Mature prourokinase."
170..19
/note= "Preferred initiation region for the low mol. wt.
plasminogen activators."
                                                                 Low mol. wt. plasminogen activator; prourokinase; dissolve blood clot.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21 SNELHQVPSNCDCLNGGTCVSNKYFSNIHWCNCPKKFGQHCEIDKSKTCYEGNGHFYRG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tch 39.2%; Score 2240; DB 10; al Similarity 97.8%; Pred. No. 2.1e-174; 402; Conservative 1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 without harm.
(Updated on 31-OCT-2002 to add missing OS field.)
(Updated on 25-MAR-2003 to correct PR field.)
(Updated on 25-MAR-2003 to correct PI field.)
                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                             (COLB ) COLLABORATIVE RES INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fig 1; Page -; 27pp; English.
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88US-0248727.
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(updated)
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                                       Sequence of prourokinase
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N-PSDB; AAN91740.
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27-SEP-1988;
                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                           07-OCT-1988;
31-OCT-2002
16-APR-1990
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5219569-2
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; APPLICANT: BLABER, MICHAEL; HEYNEKER, HERBERT L.; VEHAR,
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TITLE OF INVENTION: PROTEASE RESISTANT UROKINASE
NUMBER OF SEQUENCES: 6
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/766,858
FILING DATE: 16-AUG-1985
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 725,468
FILING DATE: 22-APR-1985
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61 KASTDIMGRPCLPWNSATVLQQIYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVGLK 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LHKDYSADTLAHHNDIALLKIRSKEGRCAQPSRTIQTICLPSMYNDPQFGTSCEITGFGK 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 SNELHQVPSNCDCLNGGTCVSNKYPSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFYRG
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361 VCSLQGRMTLTGIVSWGRGCALKDKPGVYTRVSHFLPWIRSHTKEENGLAL 411
                                                                                                                                                                                                                                         APPLICANT: Victor Gurewich
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DELIVERY
TITLE OF INVENTION: OF BRUGS BY PLATELETS FOR THE TREATMENT OF
TITLE OF INVENTION: OF BRUGS BY PLATELETS FOR THE TREATMENT OF
TITLE OF INVENTION: CARDIOVASCULAR AND OTHER DISEASES
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 411;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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Local Similarity 99.1%; Pred No. 1.9e-1189,
Cosal Similarity 99.1%; Pred No. 1.9e-1189,
Conservative 0, Mismatches 0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 50Z or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
PRILING DATE: AUGUST 5, 1994
PLING DATE: AUGUST 5, 1994
PRILING PAPELCATION DATA:
APPLICATION UNBER:
FILING DATE:
FILING DATE:
FILING DATE:
AMMENT AUGUST 10 PROGRATION:
AMMENT TO AUGUST 10 PROGRATION:
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REGIGTRATION NUMBER: 32,983
REFERENCE/DOCKET NUMBER: 04547/013001
TELEPHONE: (617) 542-5070
                                                                                                                                                             Sequence 18, Application US/08286748B; Patent No. 5759542; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (617) 542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEX: 200154
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
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STRANDEDNESS: single
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ZIP: 02110-2804
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CITY: Boston
STATE: Massach
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US-08-286-748B-18
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                                                                                                                                                                                                                                                                   CORRESPONDED ADDRESS:
CORREST: 225 Franklin Street
CITY: Boston
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZID: 0.2110-2804
CONFUTER: EADABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 553X
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURENT APPLICATION DATA:
APPLICATION NUMBER: US/08/087,163
FILING DATE: 07/02/93
CLASSIFICATION DATA:
APPLICATION DATA:
RELING DATE: WINDBER:
FILING DATE: WINDBER:
FILING DATE: WINDBER:
                                                                                                                                   APPLICANT: Liu, Jian-Ning
APPLICANT: Liu, Jian-Ning
APPLICANT: Gurewich, Victor
TITLE OF INVENTION: PRO-UROKINASE MUTANTS
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            04353/003001
                                                          Sequence 1, Application US/08087163
Patent No. 5472692
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNAY DATE:
ATTORNAY AGENT INFORMATION:
NAME: Fasse, J. Peter
REGISTRATION NUMBER: 32, 983
REFERENCE/DOCKET NUMBER: 0435:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 411
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Best Local Similarity 98.1
Matches 403; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS: N/
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293 ENSTDYLYPEQLKMTVVKLISHRECQOPHYYGSEVTTKMLCAADPQWKTDSCQGDSGGPL 352
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                             PLYQECMYHDCADGK-----LKFQCGQKTLRPRFKIIGGEFTTIENQPWFAAIYRH 172
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                                                                                                                                                                                                                                                                            233 LHKDYSADTLAHHNDIALLKIRSKEGRCAQPSRTIQTICLPSMYNDPQFGTSCEITGFGK
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                                                                                                                                                      173 RGGSVTYVCGGSLISPCWVISATHCFIDYPKKEDYIVYLGRSRLNSNTQGEMKFEVENLI
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FEATURE:
NAME/KEY: mat peptide
LOCATION: (21). ()
OTHER INFORMATION:
LOCATION: (20). ()
LOCATION: (20). ()
OTHER INFORMATION: Urokinase-type plasminogen activator (uPA)
US-09-101-272G-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICAMY NISSIN Food Products Co., Ltd.
TITLE OF INVENTION: CANCEROUS METASTASIS INHIBITOR
FILE REFERENCE: QSO979
CURRENT APPLICATION NUMBER: US/09/101,272G
CURRENT FILING DATE: 1998-07-08
PRIOR APPLICATION NUMBER: UP 1059/1996
RIOR FILING DATE: 1996-01-08
NUMBER OF SEQ ID NOS: 107
SOFTWARE: Patentin version 3:1
LENGTH: 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1, Application US/09101272G; Patent No. 6509445; GENERAL INFORMATION:
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                                    301 ENSTDYLYPEQLKMTVVKLISHRECQQPHYYGSEVTTKMLCAADPQWKTDSCQGDSGGFL 360
ENSTDYLYPEQLKMTVVKLISHRECQQPHYYGSEVTTKMLCAADPQWKTDSCQGDSGGPL 352
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                                                                                                                                                      361 VCSLQGRMTLTGIVSWGRGCALKDKPGVYTRVSHFLPWIRSHTKEENGLAL 411
                                                                                                                      353 VCSLQGRMTLTGIVSWGRGCALKDKPGVYTRVSHFLPWIRSHTKBENGLAL 403
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS.
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/153,799
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: R Hain Swope, BOC Health Care Inc
STREET: 100 Mountain Avenue
CITY: Murray Hill
STATE: New Jersey
COUNTRY: USA
ZIP: 07974
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CLASSIFICATION: 435
PRIOR APPLICATION DATE:
APPLICATION NUMBER: US 07/847975
FILING DATE: 06-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 8909916.2
FILING DATE: 29-APR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB90/00650
FILING DATE: 26-APR-1990
PRIOR APPLICATION NUMBER: PCT/GB90/00650
FILING DATE: 29-OCT-1991
ATPOREY. FAGENT UNFORMATION:
NAME: SWOPE, R Hain
REGISTRATION NUMBER: 24864
REFREENCE/DOCKET NUMBER: 92H832
TELECOMMUNICATION INFORMATION:
THE TELECOMMUNICATION INFORMATION:
THE TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Ballance, David J
APPLICANT: Goodey, Andrew R
TITLE OF INVENTION: POLYPEPTIGES
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                              Sequence 18, Application US/08153799
Patent No. 5766883
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELERA: (908)
TELERA: 19484
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 411 amino acids
"VPE: amino acids
''near
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US-08-153-799-18
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                  ENSIDYLYPEQLKMIVVKLISHRECQQPHYXGSEVITKMLCAADPQWKTDSCQGDSGGPL 380
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ENSTDYLYPEQLKMTVVVKLISHRECQQPHYYGSEVTTKMLCAADPQWKTDSCQGDSGGPL 352
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99.4%; Score 2243; DB 6; Length 431;
Best Local Similarity 98.1%; Pred. No. 2e-188;
Matches 403; Conservative 0; Mismatches 0; Indels 8
                                                                  VCSLQGRMTLTGIVSWGRGCALKDKPGVYTRVSHFLPWIRSHTKEENGLAL
                                                                                                                                                                                                 APPLICANT: KOBAYASHI, YO-ICHI,OMORI, MUNEKI;YAMADA, CHIKAKO TITLE OF INVENTION: RAPIDLY ACTING PROUROKINASE UUMBER OF SEQUENCES: 23 CURRENT APPLICATION DATA: APPLICATION DATA: APPLICATION NUMBER: US/07/340,007 FILING DATE: 18-AUG-1988
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2e-188;
-haq 0; Indels
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Patent No. 5648253
GENERAL INFORMATION:
APPLICANT: Wei, Cha-Mer
TITLE OF INVENTION: Inhibitor-Resistant Urokinase
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
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STREET: 1100 Peachtree Street Suite 2800
CITY: Atlanta
STATE: Georgia
COUNTRY: USA
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                      ;Patent No. 5188829
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SEQ ID NO:1:
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LENGTH: 431
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US-07-942-157A-3
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61 KASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVGLK 120
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CHER INFORMATION: /label= modified
CHER INFORMATION: /note= "six amino acids deleted in 178.07.942.157A.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99.2%; Score 2240; DB 1; 97.8%; Pred. No. 3.7e-188;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION: 1.19
OTHER INFORMATION: /label= peptide
OTHER INFORMATION: /note= "WAP signal"
                                                                 TSI108Cont
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US-09-181-816-1
Sequence 1, Application US/09181816
Patent No. 6277818
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                           : 430 amino acids
AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
NAME/KEY: Modified-site
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Matches 402, Conservative
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MOLECULE TYPE: protein
HYPOTHETICAL: NO
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: P 44 40 892.7
FILING DATE: 17-NOV-1994
ATTOCNEY/AGENT INFORMATION:
NAME: EVANS, JOSEPH D.
REGISTRATION NUMBER: 148/42448
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-8800
                                                                                                                                        148/42448
                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 48: SEQUENCE CHARACTERISTICS: ELENTH: 411 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
      17-NOV-1995
                                                                                                                                                                                                                                                                                             single
                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                        TYPE: amino acid
STRANDEDNESS: sin
                                                                                                                                                                                                                                                                                                                   linear
      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                    US-08-560-098A-48
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US-08-560-098A-47
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STATE: DO
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                                                                                                                                                                                                                                                                                                                                                                                                                                               61 KASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVGLK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 KASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVGLK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PLVQECMVHDCADGK-----LKFQCGQKTLRPRFKIIGGEFTTIENQPWFAAIYRRH 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12 LLVQECMVHDCADGKKPSSPPEELKFQCGQKTLRPRFKIIGGEFTTIENOPWFAAIYRRH 180
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APPLICANT: MAZAR, Andrew P.

APPLICANT: JONES, Terence R.

TITLE OF INVENTION: CYCLIC PEPTIDE LIGANDS THAT TARGET UROKINASE
TITLE OF INVENTION: PLASMINOGEN ACTIVATOR RECEPTOR
TITLE OF INVENTION: PLASMINOGEN ACTIVATOR RECEPTOR
CURRENT APPLICATION WUMBER: US/09/181,816
CURRENT APPLICATION WUMBER: US/09/181,816
CURRENT FILING DATE: 1998-10-29
SOFTWARE: PATENTIN VET: 2.0
SEQ ID NO 1
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                                                                                                                                                                                                                                                                                       98.9%; Score 2233; DB 3; Length 411; 97.8%; Pred. No. 1.4e-187;
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US-08-48
US-08-560-098A-48
Sequence 48, Application US/08560098A
Sequence 18, Application US/08560098A
Sequence 18, Sequence 18, Sequence 18, Sequence 19, Sequence 19, Sequence 19, Sequence 19, Sequence 19, STEPTERS, Getd Josef, APPLICANT: STEPTERS, Getd Josef, APPLICANT: STEPTERS, Getd Josef, TITLE OF INVENTION: Coagulation-inhibiting Properties 17TLE OF SEQUENCES: CORRESPONDENCE ADDRESS: CORRESPONDENCE ADDRESS: ADDRESSEE: Evenson, Edwards & Lenahan
                                                                                                                                                                                                                                                                                                                               1; Indels
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (BPO)
APPLICATION NUMBER: US/08/560,098A
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                                                                                                                                                                                                                                                                                                           Pred. No. 1.4e
0; Mismatches
                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 97.8
Matches 402; Conservative
                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                               LENGTH: 411
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US-09-181-816-1
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                                                                                                                                             Gaps
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       Length 411;
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Patent No. 5976841
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: WIENDEL-WIELAND, Regina
APPLICANT: STEFFENS, Gerd Josef
ATTLE OF INVENTION: Proteins having Fibrinolytic and
TITLE OF INVENTION: Coagulation-inhibiting Properties
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: Evenson, MCKeown, Edwards & Lenahan
STREET: 1200 G Street, N.W., Suite 700
CITY:
COMMANDER OF SEQUENCES OF STREET: 200 G Street, N.W., Suite 700
COTY:
CO
                                                                                                                                     Indels
Query Match
98.3%; Score 2219; DB 2;
Best Local Similarity 97.3%; Pred. No. 2.4e-186;
Matches 400; Conservative 0; Mismatches 3;
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Sequence 83, Application US/08720012
Patent No. 5747291
APPLICANT: STEFFENS, GERD J.
APPLICANT: WIRNOT, STEFFAN
APPLICANT: WIRNOT, STEFFAN
APPLICANT: HEINZEL-WIELAND, REGINA
                                                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER: 26,269
REFERENCE/DOCKET NUMBER: 146
TELECOMMUNICATION:
TELEPHONE: (202)628-8800
              STREET: 1200 G Street, N.
CITY: Washington, D.C.
COUNTRY: U.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              87.0%;
97.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                365 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFEX: (202) 628-8844
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 357; Conserv
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  ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 73 PWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVGLKPLVQECMVHDCA 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVGLKPLVQECMVHDCA 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   154 DGKKPSSPPEELKFQCGQKTLRPRFKIIGGEFTTIENQPWFAAIYRRHRGGSVTYVCGGS 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LISPCWVISATHCFIDYPKKEDYIVYLGRSRLNSNTQGEMKFEVENLILHKDYSADTLAH 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HNDIALLKIRSKEGRCAQPSRTIQTICLPSMYNDPQFGTSCEITGFGKENSTDYLYPEQL 304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DGK------LKFQCGQKTLRPRFKIIGGEFTTIENQPWFAAIYRRHRGGSVTYVCGGS 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      334 KMTVVKLISHRECQQPHYYGSEVTTKMLCAADPQWKTDSCQGDSGGPLVCSLQGRWTLTG 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13 CLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFYRGKASTDTMGRPCL 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            40 CVTGEGTPKPESHNNGDFEEIPEEY-----LQISKTCYEGNGHFYRGKASTDTMGRPCL 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: STEFFENS, GERD J.
APPLICANT: WINNIN, STEFFENS
APPLICANT: WINNIN, STEFFENS
APPLICANT: SCHNEIDER, JOHNNES
APPLICANT: SAUDERE, JOHNNES
APPLICANT: SAUDERE, JOHNNES
APPLICANT: SAUDERE, JOHNNES
APPLICANT: SAUDERE, JOHNNES
TITLE OF INVENTION: IMPROVED FIBRINOLYTIC CHARACTERISTICS AND THROMBIN
TITLE OF INVENTION: INHIBITING EFFECT
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 432;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16; Indels
COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO) CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   394 IVSWGRGCALKDKPGVYTRVSHFLPWIRSHTKEENGLAL 432
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 1965; DB 2;
Pred. No. 4.5e-164;
8; Mismatches 16;
                                                                      APPLICATION NUMBER: US/08/560,098A
FILING DATE: 17-NOV-1995
PRIOR APPLICATION NUMBER: US/08/560,098A
APPLICATION NUMBER: P 44 0 892.7
FILING DATE: 17-NOV-1994
ATTORNEY-KAGENT INFORMATION:
NAME: EVANS, JOSEPH D.
REGISTRATION NUMBER: 148/42448
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-8800
TELEPHONE: (202) 628-8804
INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHRACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 83, Application US/08093741
Patent No. 5681721
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             87.1%;
                                                                                                                                                                                                                                                                                                                                                           432 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 90.5
Matches 361; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                             , MOLECULE TYPE: protein US-08-560-098A-47
                                                                                                                                                                                                                                                                                                                                                                         amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                     linear
                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS
                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY:
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US-08-093-741-83
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181 NIQGEMKFEVENLILHKDYSADTLAHHNDIALLKIRSKEGRCAQPSRTIQTICLPSMYND 240
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                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/093,741
FLING DATE: 20-JUL-1993
CLASSIFICATION 1435
PROGRAPPLICATION DATE: DE P43 23 754.1
APPLICATION NUMBER: DE P43 23 754.1
APPLICATION NUMBER: DE P43 23 754.1
FILING DATE: 15-JUL-1993
ATTONNEY/AGENT INPOMMATION:
NAME: EVANS, JOSEPH D.
REGISTRATION NUMBER: 26,269
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Pred. No. 4.4e-164;
0; Mismatches 0;
Edwards &
Suite 700
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ADDRESSEE:
  US-08-560-098A-44
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APPLICANT: SAUNDERS, DEREK J.

TITLE OF INVENTION: BIFUNCTIONAL UROKINASE VARIANTS WITH
TITLE OF INVENTION: IMPROVED FIBRINOLYTIC CHARACTERISTICS AND THROMBIN
TITLE OF INVENTION: INHIBITING BFFECT
NUMBER OF SEQUENCES: 83
CORRESPONDENCE ADDRESS:
ADDRESSE: Evenson, McKeown, Edwards & Lenahan
STREET: 1200 G Street, N. W. Suite 700
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Pred. No. 4.4e-164;
0; Mismatches 0; Indels
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COMPUTER: Flappy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC Compatible
COMPANING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/720,012
FILING DATE: 27-SEP-196
FILING DATE: 20-JUL-1993
APPLICATION NUMBER: US 08/093,741
FILING DATE: 12-JUL-1993
APPLICATION NUMBER: DE P43 23 754.1
FILING DATE: 15-JUL-1993
APPLICATION NUMBER: 26,269
REGISTRATION NUMBER: 26,269
REGISTRATION NUMBER: 26,269
REGISTRATION NUMBER: 26,269
REGISTRATION NUMBER: 148/41345
TELEPHONE: (202)628-8800
                                                                                                                 SSEE: Evenson, McKeown, F: 1200 G Street, N. W. Washington, D.C.
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Best Local Similarity 97.8%;
Matches 357; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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RESULT 13

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible COURENT APPLICATION DATA: PAPLICATION NUMBER: US/08/560,098A FILING DATE: 17-NOV-1995 PRIOR APPLICATION NUMBER: P 44 40 892.7 FILING DATE: 17-NOV-1994 ATTORNYAGETY INFORMATION: NAME: EVANS, JOSEPh D. REGISTRATION NUMBER: 26,269 REFERENCE/DOCKET NUMBER: 148/42448 TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION:
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                                                                                     APPLICANT: WNENDT, Stephan
APPLICANT: HEINZEL-WIELAND, Regina
APPLICANT: HEINZEL-WIELAND, Regina
APPLICANT: STEPFENS, Gerd Josef
ITILE OF INVENTION: Proteins having Fibrinolytic and
ITILE OF INVENTION: Coaquilation-inhibiting Properties
CORRESPONDENCES: 60
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Pred. No. 4.9e-164;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                         E: Evenson, McKeown, Edwards & 1200 G Street, N.W., Suite 700
Sequence 44, Application US/08560098A Patent No. S976841
GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
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amino acid
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                CITY: Washington
STATE: DC
COUNTRY: USA
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47 SKTCYEGNGHFYRGKASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPD 106
339 WKTDSCQGDSGGPLVCSLQGRMTLTGIVSWGRGCALKDKPGVYTRVSHFLPWIRSHTKEE 398
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                            302 WKIDSCQGDSGGPLVCSLQGRMILIGINGHINGHINGHINGHINGHINGHINGHINGHINSHIKEE 361
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 107 NRRRPWCYVQVGLKPLVQECMVHDCADGK-----LKFQCGQKTLRPRFKIIGGEFTT
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60
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                                                                                                                                                                                                                                                                                                                  APPLICANT: WRENDT, Stephan
APPLICANT: STEFFENS, Gerd Josef
APPLICANT: STEFFENS, Gerd Josef
APPLICANT: JANOCHA, Elke
APPLICANT: HINZEL-WIELAND, Regina
TITLE OF INVENTION: Chimeric Proteins having Fibrinolytic
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Revenson, McKeown, Edwards & Lenahan
STREET: 1200 G Street, N.W., Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Rloppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
ROTREMY APPLICATION NATA:
APPLICATION NUMBER: US/08/967,024C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match

87.0%; Score 1964; DB 3;
Best Local Similarity 97.8%; Pred. No. 4.9e-164;
Matches 357; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 05/06/30/2012 FILING DATE: 05/06/30/2012 FILING DATE: 05/06/30/2012 FILING DATE: 06/06/2012 FILING DATE: 30-NOV-1994 ATORNEY AGENT INFORMATION: NAME: EVANS, Joseph D. REGISTRATION NUMBER: 26,269 REPERSENCE/DOCKET NUMBER: 148/42444 TELECOMMUNICATION INFORMATION: TELEPHONE: (202) 628-8800
                                                                                                                                                                                                                                               Sequence 25, Application US/08967024C Patent No. 6133011 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (202) 628-8844
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 393 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                               399 NGLAL 403
                                                                                                                                        362 NGLAL 366
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CITY: WAL
STATE: DC
TAL 20005
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US-08-967-024C-25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PQFGTSCEITGFGKENSTDYLYPEQLKMTVVKLISHRECQQPHYYGSEVTTKMLCAADPQ 301
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                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                               ZITE: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/967,024C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 1964; DB 3;
Pred. No. 4.9e-164;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 94 42 665.8
APPLICATION NUMBER: 90.804.1994
ATTORNEY/AGENT INFORMATION:
NAME: EVANS, JOSEPH D.
REGISTRATION NUMBER: 26,269
REFERRNCE/DOCKET NUMBER: 148/42444
TELECOMMUNICATION INFORMATION:
                                                                                                                                   Sequence 24, Application US/08967024C Patent No. 6133011 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    87.08;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (202) 628-6844
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          393 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 97.8
Matches 357; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    / MOLECULE TYPE: protein US-08-967-024C-24
                                                                                                                                                                                                                                                                                                                                                                                        STREET: 1200 G St
CITY: Washington
STATE: DC
       ||||||
NGLAL 366
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE:
                                                                                               RESULT 14
US-08-967-024C-24
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103 RNPDNRRRP-WCYVQVGLKPLVQECMVHDCADGKLKFQCGQKTLRPRFKIIGGEFTTIEN 161
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125 GEMKFEVENLILHKDYSADTLAHHNDIALLKIRSKEGRCAQPSRTIQTICLPSMYNDPQF 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            222 GEMKFEVENLILHKDYSADTLAHHNDIALLKIRSKEGRCAQPSRTIQTICLPSMYNDPQF 281
                                                                              185 GISCEIIGEGKENSTDYLYPEQLKMTVVKLISHRECQQPHYYGSEVTTKMLCAADPQWKT
                                                                                                                                                                   245 DSCQGDSGGPLVCSLQGRMTLTGIVSWGRGCALKDKPGVYTRVSHFLPWIRSHTKEENGL
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                                                                                                                                          342 DSCQGDSGGPLVCSLQGRMTLTGIVSWGRGCALKDKPGVYTRVSHFLPWIRSHTKEENGL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: WRENDT, Stephan
APPLICANT: HEINZEL-WIELAND, Regina
APPLICANT: STEFFENS, GERT JOSEF
TITLE OF INVENTION: Proteins having Fibrinolytic and
TITLE OF INVENTION: Coagulation-inhibiting Properties
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: Evenson, MCKeown, Edwards & Lenahan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: FIDEPY disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPANING SYSTEM: DPC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPG
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/560,098A
FILING DATE: 17-NOV-1994
ATONEN APPLICATION DATA:
APPLICATION NUMBER: P4 40 892.7
FILING DATE: 17-NOV-1994
ATONENYAGATI INFORMATION:
NAME: EVANS, JOSSEPH 26,269
REGISTRATION NUMBER: 26,269
REGISTRATION NUMBER: 26,269
REGISTRATION NUMBER: 148/42448
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. 1.4e-120;
6; Mismatches 12;
                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 46, Application US/08560098A Patent No. 5976841 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                larity 91.1%;
Conservative
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS LENGTH: 331 amino aci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
Matches 275; Conserv
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                                                                                                                      WKTDSCOGDSGGPLVCSLOGRMTLTGIVSWGRGCALKDKPGVYTRVSHFLPWIRSHTKEE 398
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                           PQFGTSCEITGFGKENSTDYLYPEQLKMTVVKLISHRECQQPHYYGSEVTTKMLCAADPQ 338
                                                                                                                                               WKTDSCQGDSGGPLVCSLQGRMTLTGIVSWGRGCALKDKPGVYTRVSHFLPWIRSHTKEE 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GEMKFEVENLILHKDYSADTLAHHNDIALLKIRSKEGRCAQPSRTIQTICLPSMYNDPQF 281
                                                                    PQFGTSCEITGFGKENSTDYLYPEQLKMTVVKLISHRECQQPHYYGSEVTTKMLCAADPQ 301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLUM INC.

COMPUTER:

COMPUTER:

SYSTEM: PC-DOS/MS-DOS

SOSTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:

APPLICATION DATA:

APPLICATION DATA:

FILING DATE: 17-NOV-1995

PILING DATE: 17-NOV-1994

ATTORNEY/AGENT INFORMATION:

NAME: EVANS, JOSEPh D:

REGISTRATION NUMBER: 26,269

REGISTRATION NUMBER: 26,269

REGISTRATION NUMBER: 148/42448

TELEPHONE: (202) 628-8840

TELEPHONE: (202) 628-8844

INFORMATION POR SEQ ID NO: 45:

SEQUENCE CHARACTERISTICS:

LENGTH: 306 amino acids

TURED OF THE COMPANIAN OR SEQ ID NO: 45:

LENGTH: 306 amino acids

TURED OF THE COMPANIAN OR SEQ ID NO: 45:

LENGTH: 306 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: WNENDT, Stephan
APPLICANT: HEINZEL-WIELAND, Regina
APPLICANT: STEFFENS, Gerd Josef
TITLE OF INVENTION: Coagulation-inhibiting Properties
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: Evenson, McKeown, Edwards & Lenahan
STREET: 1200 G Street, N.W., Suite 700
                                                                                                                                                                                                                                                                                                                                                                             Sequence 45, Application US/08560098A Patent No. 5976841
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
PC compatible
PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Washington
STATE: DC
COUNTRY: USA
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                                                                                                                                                                                                                                                              362 NGLAL 366
                                                                                                                                                                                                                 NGLAL 403
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US-08-560-098A-45
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61 LGRSRLNSNTQGEMKFEVENLILHKDYSADTLAHNDIALLKIRSKEGRCAQPSRTIQTI 120
                                                                                                                                                                                                    331 MLCAADPQWKTDSCQGDSGGPLVCSLQGRMTLTGIVSWGRGCALKDKPGVYTRVSHFLPW 390
    151 IIGGEFTTIENQPWFAAIYRRHRGGSVTYVCGGSLISPCWVISATHCFIDYPKKEDYIVY 210
                                                                                                                                                                           271 CLPSMYNDPQFGTSCEITGFGKENSTDYLYPEQLKMTVVKLISHRECQQPHYYGSEVTTK 330
                             1 IIGGEFTTIENOPWFAAIYRRHRGGSVTYVCGGSLISPCWVISATHCFIDYPKKEDYIVY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    211 IGRSRLNSNTQGEMKFEVENLILHKDYSADTLAHHNDIALLKIRSKEGRCAQPSRTIQTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           150 KIIGGEFTTIENQPWFAALYRRHRGGSVTYVCGGSLISPCWVISATHCFIDYPKKEDYIV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/560,098A
FILING DATE: 17-NOV-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: P 44 40 892.7
FILING DATE: 17-NOV-1994
ATTORNYAGENT INFORMATION:
NAME: EVANS, JOSEPH D.
REGISTRATION NUMBER: 148/42448
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 19
US-08-560-098A-49

US-08-560-098A-69

Sequence 49, Application US/08560098A

Patent No. 597641

GENERAL INFORMATION:
APPLICANT: WIEDLY Stephan
APPLICANT: HEINZEL-WIELAND, Regina
APPLICANT: STEFFENS, Gard Josef

TITLE OF INVENTION: Proteins having Fibrinolytic and
TITLE OF INVENTION: Coagulation-inhibiting Properties
NUMBER OF SEQUENCES: 60

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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STREET: 1200 G Street, N.W., Suite 700
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 1374; DB 2;
Pred. No. 1.3e-112;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 99.2%;
Matches 252; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (202) 628-881
INFORMATION FOR SEQ 1D NO: 4
SEQUENCE CHARACTERISTICS:
LENGTH: 254 amino acids
                                                                                                                                                                                                                                                                                                                                                  391 IRSHTKEENGLAL 403
                                                                                                                                                                                                                                                                                                                                                                                           241 ÍRSHÍKÉENGLÁL 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: protein
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MEDIUM TYPE: Floppy
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US-08-560-098A-49
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                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: COLPITS, TRACEY L.
APPLICANT: COLDITTS, TRACEY L.
APPLICANT: RISEAN, PAULA N.
APPLICANT: RASS, MICHAEL R.
APPLICANT: RUSSELL, JOHN C.
APPLICANT: STEWARD N.
APPLICANT: STEWARD D.
TITLE OF INVENTION: NOVEL SERINE PROTEASE REAGENTS
TITLE OF INVENTION: OF THE PROSTATE
NUMBER OF SEQUENCES: 76
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                                                                                                                                                                             245 DSCQGDSGGPLVCSLQGRMTLTGIVSWGRGCALKDKPGVYTRVSHFLPWIRSHTKEENGL 304
125 GEMKFEVENLILHKDYSADTLAHHNDIALLKIRSKEGRCAQPSRTIQTICLPSMYNDPQF
                                                                                                      185 GTSCEITGFGKENSTDYLYPEQLKMTVVKLISHRECQQPHYYGSEVTTKMLCAADPQWKT
                                                                                                                                                    342 DSCQGDSGGPLVCSLQGRMTLTGIVSWGRGCALKDKPGVYTRVSHFLPWIRSHTKEENGL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/944,483
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING APPLICATION NUMBER:
ATTORNEY, AGENT INFORMATION:
NAME: BECKEY, Cheryl L.
NAME: BECKEY, Cheryl L.
REGISTRATION NUMBER: 35,441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6183.US.01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: 1L
                                                                                                                                                                                                                                                                                                                                                                                       Sequence 73, Application US/08944483
Patent No. 6232456
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 61
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: No. 6232456e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : 253 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.(
Matches 253; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 847/938-2623
TELEX:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM CON OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS:
TOPOLOGY: lin
                                                                                                                                                                                                                                       402 AL 403
                                                                                                                                                                                                                                                                                  305 AL 306
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US-08-944-483-73
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Query Match
38.4%; Score 867.5; DB 2;
Best Local Similarity 43.7%; Pred. No. 6.1e-68;
Matches 178; Conservative 60; Mismatches 148;
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Patent No. 5840533
GENERAL INFORMATION:
APPLICANT: NIWA, MINEO
APPLICANT: SAITO, YOSHIMASA
APPLICANT: SASAKI, HIYOSHI
APPLICANT: HAYASHI, MASAKO
APPLICANT: NOTANI, JOUJI
                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                           TELEFAX.

TELEFAX.

INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 477 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: protein
                               COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
STRANDEDNESS: si
                 20005
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US-08-811-949-39
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                          61 YLGRSRLNSNTQGEMKFEVENLILHKDYSADTLAHHNDIALLKIRSKEGRCAQPSRTIQT 120
                                                               ICLPSMYNDPQFGTSCEITGFGKENSTDYLYPEQLKMTVVKLISHRECQQPHYYGSEVTT 329
                                                                                  121 ICLPSMYNDPQFGTSCEITGFGKENSTDYLYPEQLKMTVVKLISHRECQQPHYYGSEVTT 180
                                                                                                                               KMLCAADPQWKTDSCQGDSGGPLVCSLQGRMTLTGIVSWGRGCALKDKPGVYTRVSHFLP 389
                                                                                                                                                    YLGRSRLNSNTQGEMKFEVENLILHKDYSADTLAHHNDIALLKIRSKEGRCAQPSRTIQT 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   81 KASTDIMGRPCLPWNSAIVLQQIYHAHRSDALQLGLGGGHNYCRNPDNRRRPWCYVQVGLK 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       141 PLVQECMVHDCADGKKPSSPPEELKFQCGQKTLRPRFKIIGGEFTTIENQPWFAAIYRRH 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 KASTDIMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVGLK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PLVQECMVHDCADGK-----LKFQCGQKTLRPRFKIIGGEFTTIENQPWFAAIYRRH 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21 SNELHQVPSNCDCLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFYRG 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 SNELHOVPSNCDCLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFYRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 200;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Nissin Food Products Co., Ltd.
TITLE OF INVENTION: CANCEROUS METASTASIS INHIBITOR
FILE REFERENCE: 505079
CURRENT APPLICATION NUMBER: US/09/101,272G
CURRENT FILING DATE: 1998-07-08
PRIOR PELING DATE: 1996-01-08
NUMBER OF SEQ ID NOS: 107
SOFIWARE: Patentin version 3.1
SEQ ID NO 733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             43.6%; Score 983; DB 4;
95.6%; Pred. No. 1.6e-78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
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                                                                                                                                                                                                                                                                    RESULT 20
US-09-101-272G-73
; Sequence 73, Application US/09101272G
7-101-100, 6509445
                                                                                                                                                                                              WIRSHTKEENGLAL 403
                                                                                                                                                                                                                          241 WIRSHTKEENGLVL 254
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 172; Conserva
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59 RGKASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVG 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               253 ERFLCGGILISSCWVLTAAHCFQERYPPQHLRVV-LGRTYRVKPGKEEQTFEVEKCIVHE 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   236 DYSADTLAHHNDIALLKIRSKEGRCAQPSRTIQTICLPSMYNDPQFGTSCEITGFGKENS 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            370 SSPFYSEQLKEGHVRLYPSSRCTSKFLFNKTVTKNMLCAGDTRSGEIHPNVHDACQGDSG 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     197 SKFILEFCSVPVCS----KATCGLRKYKEPQLHSTGGLFTDITSHPWQAAIFAQNRRSSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              78 OCHTVPVKSCSELRCFNGGTCWQAASFSDF-VCQCPKGYTGKQCEVDTHATCYKDQGVTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        119 LKPLVQECMVHDCADGKLKFQCG-QXTLRPRFKIIGGEFTTIENQPWFAAIYRRHRGGS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                296 TDYLYPEQLKMTVVKLISHRECQQPHYYGSEVTTKMLCAADPQWKT-----DSCQGDSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 ELHQVP----SNCDCLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 477;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/560,098A
FILING DATE: 17-NOV-1995
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: P 44 40 892.7
FILING DATE: 17-NOV-1994
ATTORNYAGENT INFORMATION:
NAME: EVANS, JOSEPH D.
REGISTRATION NUMBER: 148/42448
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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54; Mismatches 153;
                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                              38.1%; Score 859.5; DB (37.7%; Pred. No. 3.5e-67.
                                                                                                                                                                           NUMBER OF SEQUENCES: 35
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/88,451
FILING DATE: 06-JUL-1993
FRIOR APPLICATION NUMBER: 770,510
FILING DATE: 03-OCT-1991
                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 384,608
FILING DATE: 24-JUL-1989
APPLICATION NUMBER: 240,856
FILING DATE: 02-SEP-1988
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Best Local Similarity 37.7%
Matches 184, Conservative
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   DWIRDNMR
                                                                                         ;Patent No. 5520913
                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 527
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                                                       RESULT 23
5520913-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 527;
APPLICANT: KOBAYASHI, MASAKAZU
TITLE OF INVENTION: TISSUE PLASMINOGEN ACTIVATOR
NUMBER OF SEQUENCE: 67
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400 CITY: ARLINGTON
                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/811,949 FILING DATE: 05-MAR-1997 CLASSIPICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  38.3%; Score 865.5; DB 2; 37.7%; Pred. No. 1e-67; iive 56; Mismatches 151;
                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REPERENCE/DOCKET NUMBER: 18-9
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-220
INPORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : 527 amino acids
amino acid
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Matches 184; Conservative
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                                                                                         ADDRESSEE:
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                                                                                                                                         STATE: V. COUNTRY:
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| Sequence 16, Application US/07609510B
| Patent No. 5326700
| GENERAL INFORMATION:
| APPLICANT: Barg et al.
| TITLE OF INVENTION: Method for Altering Post-Translational Processing of Tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100
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221 AQALGLGKHNYCRNPDGDAKPWCHVLKNRRLTWEYCDVPSCSTCGLRQYSQPQFRIKGGL 280
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APPLICANT: ANDERSON, STEPHEN, BENNETT, WILLIAM F., BOTSTEIN, DAVID, HIGGINS, DEBORAH L.; PAONI, NICHOLAS F., ZOLLER, MARK J. TITLE OF INVENTION: TISSUE PLASMINOGEN ACTIVATOR HAVING ZYMOGENIC PROPERTIES
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221 AQALGLGKHNYCRNPDGDAKPWCHVLKNRRLTWEYCDVPSCSTCGLRQYSQPQFRIKGGL 280
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                                                                                                                                                                                            CCMPUTER READBLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: 1EM PC compatible
OPERATING SYSTEM:
PC-DOS/MS-DOS
SOFTWARE: Patin (Genetech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US31/01025A
FILING DATE: 19910314
FLING DATE: 19910314
FLING DATE: 19910314
FLING DATE: 19910314
FLING DATE: 1 March 1990
ATTORNEY/ACENT NUMBER: 07/486,657
FILING DATE: 1 March 1990
ATTORNEY/ACENT NUMBER: 28,616
REGISTRATION NUMBER: 28,616
REGISTRATION NUMBER: 28,616
REGISTRATION NUMBER: 454P2
TELECOMMUTCATION INFORMATION:
TELEPHONE: 415/266-1896
TELEFRAX: 415/252-9881
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    Specific Properties
TITLE OF INVENTION: Specific Pro
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Bl
CITY: South San Francisco
STATE: California
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TOPOLOGY: 1:-
91-010
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INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
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Matches 183, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     42 OCHSVPVKSCSEPRCFNGGTCQQALYFSDF-VCQCPEGFAGKCCEIDTRATCYEDOGISY 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RGKASTDIMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVG 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              101 RGTWSTAESGAECTNWNSSALAQKPYSGRRPDAIRLGLGNHNYCRNPDRDSKPWCYVPKA 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        161 GKYSSEFCSTPACSEGNSDCYFGNGSAYRGTHSLTESGASCLPWNSMILIGKVYTAQNPS 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -- KLKFQ-----CG-QKTLRPRFKIIGGE 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                341 YRVVPGEEEGKFEVEKYIVHKEFDDDT--YDNDIALLQLKSDSSRCAQESSVVRTVCLPP 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      399 ADLQLPDWTECELSGYGKHEALSPFYSERLKEAHVRLYPSSRCTSQHLLNRTVTDNMLCA 458
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 215 RINSNTQGEMKFEVENLILHKDYSADTLAHHNDIALLKIRSKEGRCAQPSRTIQTICLPS 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  335 AD----PQWKT-DSCQGDSGGPLVCSLQGRMTLTGIVSWGRGCALKDKPGVYTRVSHFL 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     459 GDTRSGGPQANLHDACQGDSGGPLVCLNDGRMTLVGIISWGLGCGQKDVPGVYTKVTNYL 518
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 ELHQVP-SNCD---CLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFY
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PCT-US91-01025A-2
; Sequence 2. Application PC/TUS9101025A
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; TITLE OF INVENTION: Tissue Plasminogen Activator Having Fibrin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 527;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                        Mb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
38.0%; Score 858.5; DB 1;
Best Local Similarity 37.5%; Pred. No. 4.3e-67;
Matches 183; Conservative 56; Mismatches 152;
                                                                                                                                                 ZIP: 46285
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.0 GOMPUTER: Macintosh
OPERATING SYSTEM: Macintosh
OPERATING SYSTEM: Macintosh
                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/609,510B
FILING DATE: 19901106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             119 LKPLVQECMVHDCADG------
                CORRESPONDENCE ADDRESS:
ADDRESSEE: Eli Lilly and Company STREET: Lilly Corporate Center CITY: Indianapolis STATE: IN. COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 527 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein
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DWIRDNMR 526
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  SEQUENCES:
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    NUMBER OF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      221 AQALGLGKHNYCRNPDGDAKPWCHVLKNRRLTWEYCDVPSCSTGGLRQYSQPQFRIKGGL 280
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     341 YRVVPGEEEQKFEVEKXIVHKEFDDDT--YDNDIALLQLKSDSSRCAQESSVVRTVCLPP 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             399 ADLQLPDWTECELSGYGKHEALSPFYSERLKEAHVRLYPSSRCTSQHLLNRTVTDNMLCA 458
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                                                                                                nt No. 5185259
APPLICANT: GOEDDEL, DAVID V.;KOHR, WILLIAM J.;PENNICA,
                                                                                                                                 R, GORDON A.
TITLE OF INVENTION: TRUNCATED HUMAN TISSUE PLASMINOGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 38.0%; Score 858.5; DB 6; Best Local Similarity 37.5%; Pred. No. 4.3e-67; Matches 183; Conservative 56; Mismatches 152;
                                                                                                                                                   ACTIVATOR

NUMBER OF SEQUENCES: 15

CURRENT APPLICATION DATA:

APPLICATION UMBER: US/07/489,855

FILING DATE: 02-MAR-190

PRIOR APPLICATION DATA:

APPLICATION UMBER: 12,694

FILING DATE: 09-FEB-1987

APPLICATION NUMBER: 483,052

FILING DATE: 07-ARK-1983

APPLICATION NUMBER: 399,003

FILING DATE: 14-JUL-1982

APPLICATION NUMBER: 398,003

FILING DATE: 05-MAY-1982
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||| : :
DWIRDNMR 526
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;Patent No.
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Sequence 43, Application US/08811949 Patent No. 5840533

RESULT 27 US-08-811-949-43

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 136 RGTWSTAESGAECTINWNSSALAQKPYSGRRPDAIRLGLGNHNYCRNPDRDSKPWCYVFKA 195
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             275 MYNDPQFGTSCEITGFGKENSTDYLYPEQLKMTVVKLISHRECQQPHYYGSEVTTKMLCA 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 BLHQVP-SNCD---CLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 562;
                                                                                                                                                                                           ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, ADDRESSEE: P.C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
CITY: ARLINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/811,949 FILING DATE: 05-MAR-1997
APPLICANT: SAITO, YOSHIMASA
APPLICANT: SASAKI, HITOSHI
APPLICANT: HAYASHI, MASAKO
APPLICANT: HOTANI, JOUJI
APPLICANT: KOBAYASHI, MASAKAZU
ATITLE OF INVENTION: TISSUE PLASMINOGEN ACTIVATOR
NUMBER OF SEQUENCES: 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    38.0%; Score 858.5; DB 2;
37.5%; Pred. No. 4.6e-67;
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                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET VMBER: 18-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     : 562 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 37.55
Matches 183; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein
                                                                                                                                                                                                                                                                                                                                    ZIP: 22202
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                              USA
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                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-811-949-43
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316 FADIASHPWQAAIFAKHRRSPGERFLCGGILISSCWILSAAHCPQERFPPHHLTVILGRT 375
                                                                                                                                                                                           376 YRVVPGEEEQKFEVEKYIVHKEFDDDT--YDNDIALLQLKSDSSRCAQESSVVRTVCLPP 433
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       215 RLNSNTQGEMKFEVENLILHKDYSADTLAHHNDIALLKIRSKEGRCAQPSRTIQTICLPS 274
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                                 FTTIENQPWFAAIYRRH-RGGSVTYVCGGSLISPCWVISATHCFIDYPKKEDYIVYLGRS
                                                                                                                                                                                                                                                                                                                                            434 ADLOLPDWİECELSGYGKHEALSPFYSERLKEAHVRLYPSSRCTSQHLLNRTVTDNMLCA
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Patent No. 5885607
CENERAL INFORMATION:
CENERAL INFORMATION:
CENERAL INFORMATION:
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CENERAL CANDENCES:
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
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ZIP: MSH 3YZ

COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/883,795A
FLING DATE: 27-JUN-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Gravelle, Micheline
REGISTRATION NUMBER: 40,261
REFERENCE/DOCKET NUMBER: 784,261
REGISTRATION INFORMATION:
TELECOMMUTCATION INFORMATION 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             38.0%; Score 858.5; DB 2;
37.5%; Pred. No. 4.6e-67;
tive 56; Mismatches 152;
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40 King Street West
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INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
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TYPE: amino acid
STRANDEDNESS: single
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554 DWIRDNMR 561
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CITY: Toronto
STATE: Ontario
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AD-----PQWKT-DSCQGDSGGPLVCSLQGRMTLTGIVSWGRGCALKDKPGVYTRVSHFL 388
                              494 GDTRSGGPQANLHDACQGDSGGPLVCLNDGRWTLVGIISWGLGGGQKDVPGVYTKVTNYL 553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----KLKFQ-----CG-QKTLRPRFKIIGGE 155
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ZIP: 20005
COMPUTER READABLE FORM:
MEDLIUM TYPE: Floppy disk
MEDLIUM TYPE: Floppy disk
COMPUTER: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.30 (EPO)
SOFTWARE: Patentln Release #1.0, Version #1.30 (EPO)
SOFTWARE: Patentln Release #1.0, Version #1.30 (EPO)
SOFTWARE: PATENTON DATA:
PRILING DATE: 17-NOV-1995
PRILING DATE: 17-NOV-1994
PRILING DATE: 17-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: EVANS, JOSEPH D.
REGIGIERATION NUMBER: 148/42448
TELEPHONDE: (202) 628-8800
TELEPHONDE: (202) 628-8800
TELEPHONDE: (202) 628-8800
TELEPHONE: SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
LENDTH: 562 amino acids
TYPE: amino acid
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                 Sequence 50, Application US/08560098A
Patent No. 5976841
GENERAL INFORMATION:
APPLICANT: WREND: Stephan
APPLICANT: STEFFENS, Gerd Josef
TITLE OF INVENTION: Proteins having Fibrinolytic and
TITLE OF INVENTION: Coagulation-inhibiting Properties
NUMBER OF SQUENCES: 60
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Evenson, McKeown, Edwards & Lenahan
STREET: 1200 G Street, N.W., Suite 700
CITY: Washington
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Best Local Similarity 37.5'
Matches 183; Conservative
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554 DWIRDNMR 561
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STATE: DO
COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RGKASTDIMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVG 118
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                                                                             196 GKYSSEFCSTPACSEGNSDCYFGNGSAYRGTHSLTESGASCLPWNSMILIGKVYTAQNPS 255
                                                                                                            -----KLKFQ-----CG-QKTLRPRFKIIGGE 155
                                                                                                                                                                        FTTIENQPWFAAIYRRH-RGGSVTYVCGGSLISPCWVISATHCFIDYPKKEDYIVYLGRS 214
                                                                                                                                                                                                                                     215 RLNSNTQGEMKFEVENLILHKDYSADTLAHHNDIALLKIRSKEGRÇAQPSRTIQTICLPS 274
                                                                                                                                                                                                                                                                                                275 MYNDPQFGTSCBITGFGKENSTDYLYPBQLKMTVVKLISHRECQQPHYYGSBVTTKMLCA 334
                                                                                                                                                                                                                                                                                                                                                           335 AD-----PQWKT-DSCQGDSGGPLVCSLQGRMTLTGIVSWGRGCALKDKPGVYTRVSHFL 388
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38.0%; Score 858.5; DB 6; Length 562;
Best Local Similarity 37.5%; Pred. No. 4.6e-67;
Matches 183; Conservative 56; Mismatches 152; Indels 97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;Patent No. 5185259
; APPLICANT: GOEDDEL, DAVID V.;KOHR, WILLIAM J.;PENNICA, DIANE;
;VEHAR, GORDON A.
; IIILE OF INVENTION: TRUNCATED HUMAN TISSUE PLASMINOGEN
;ACTIVATOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 15
CURRENT APPLICATION DATA:
FILING DATE: 02-MAR-1990
PRIOR APPLICATION DATA:
APPLICATION DATE: 12,694
FILING DATE: 09-FEB-1987
APPLICATION NUMBER: 12,694
FILING DATE: 09-FEB-1987
APPLICATION NUMBER: 396,003
FILING DATE: 14-UL-1982
APPLICATION NUMBER: 374,860
FILING DATE: 05-MAY-1982
                                               119 LKPLVQECMVHDCADG------
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DWIRDNMR 561
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Db 256 AQALGLGKHNYCRNPDGDAKPWCHVLKNRRLTWEYCDVPSCSTCGLRQYSQPQFRIKGGL 315

Qy 156 FTTIENQPWFAALYRRH-RGGSVTYVCGGSLISPCWVISATHCFIDYPKKEDYLVYLGRS 214

Db 316 FADLASHPWQAALFAKHRSPGSFFLCGGILISSCMILSAHCFQERFPHHLTVILGRT 375

Qy 215 RLNSNTQGEMKFEVENLILHKDYSADTLAHNDIALLKIRSKEGRCAQPSRTIQTICLPS 274

Db 376 YRVVPGEEQLFFVENLILHKDYSADTLAHNDIALLKIRSKEGRCAQPSRTIQTICLPS 274

Qy 275 MYNDPQFGSCEITGFGKENSTDYLYPEQLKNTVVKLISHRECQQPHYYGSEVTTKALCA 493

Qy 275 MYNDPQFGSCEITGFGKENSTDYLYPEQLKNTVVKLISHRECQQPHYYGSEVTTKALCA 493

Qy 335 AD----PQWKT-DSCQGDSGGPLVCSLQGRMTLTGIVSWGRGCALKDKPGVYTRVSHFL 388

Qy 335 AD----PQWKT-DSCQGDSGGPLVCLNDGRMTLTGIVSWGRGCALKDKPGVYTRVTNYL 553

Qy 389 PWIRSHTK 396

Db 554 DWIRDNWR 561

Search Completed: December 3, 2003, 14:45:37
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2257
1 SNELHQVPSNCDCLNGGTCV.....VSHFLPWIRSHTKEENGLAL 403
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                         283308 seqs, 96168682 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                               - protein search, using sw model
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UKBAY
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A36
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Match Length DB
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1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
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Perfect score:
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                                                                                                                                                                                                                                                                                               Sequence:
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No.
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plasmin (EC 3.4.21	brain-specific ser	plasmin (EC 3.4.21	prostasin (EC 3.4.	plasma kallikrein	hepsin (EC 3.4.21.	plasma kallikrein	hepsin (EC 3.4.21.	membrane-bound ard	trypsin (EC 3.4.21	trypsin (EC 3.4.21	trypsin (EC 3.4.21	chymotrypsin (EC 3	coaqulation factor	plasma kallikrein	protein C (activat
A61545	JC5759	146260	A57014	KOMSPL	S00845	KOHUP	S33777	JC7731	S55066	TRBOTR	S13813	A21195	KFBO7	KORTPL	KXHII
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•				18.1 638		-		_				. ,			
•		19.1	18.1	-	17.9	17.8		17.6	17.5		17.3	17.3			

ALIGNMENTS

	RESULT 1
	UKHU
	u-plasminogen activator (EC 3.4.21.73) precursor [validated] - human
	A vittetinate inames: certuriat prasminogen activator; uroxinase; uroxinase-rype plasminogen N.Confains: uroxinase-true nlasminomen activator chain a uroxinase-true nlasminomen activator.
	C;Species: Homo sapiens (man)
	C.Accession: A00931; IS2209; UT0102; A37561; I38102; S65783; A37562; A37563; A37564; A? R:Riccio A : Grimald: G : Verde D : Cebseric C : Dlack
	Nucleic Acids Res. 13, 2759-2771, 1985
	A, Title: The human urokinase plasminogen activator gene and its promoter.
	331; MUID:85215647; PMID:2987867
	A.Accession: Accession: A.Accession: A.Accession: A.Accession: A.Accession: Accession: A.Accession: A.Accessi
	A:rolecule Lype: DAA A:Residues: 1-431 <ric></ric>
	A,Cross-references: GB:X02419; NID:q37601; PIDN:CAA26268.1; PID:q1834524
	I G
	;
	A/little: Exon-intron boundary sliding in the generation of two mRNAs coding for porcine a betarance mumber. TESSES MITTER GROUNDS DATE: DRIVER SPECIAL PROPERTY.
-	PARCHAGENCE INTERCET: LOLKEON; MOID: COCCUCONY; FAIR CANAGOOD
_	A:Status: preliminary: translated from GR/EMBL/DDR.
	A; Molecule type: DNA
	027; NID:g340174; PIDN:AAA61257.1; PID:g340175
	985
	Alltie: Molecular cloning of cDNA coding for human preprourokinase.
	A;Keresence number: JT0102; MUID:86056954; PMID:2415429
	A.A.C.C.S.J.C.L.U.Z.C.C.C.C.C.C.C.C.C.C.C.C.C.C.C.C.C.C
	A:Residues: 1-213./1/ 214-473.
	A.Cross-references: GB:K03226: NID:g340155: PIDN:AAC97138.1: PID:g340158: GB:D00244: NI
	Proc. Natl. Acad. Sci. U.S.A. 81, 4727-4731, 1984
	A; Title: Identification and primary sequence of an unspliced human urokinase poly(A) + 1
	A; Vererence number: A3/561; MUID:84272706; PMID:6589620
	A:Molecule tyme: mPNA
	A. Residues: 66-431 <ver></ver>
	A;Cross-references: GB:D00244; NID:g220138
	R;Jacobs, P.; Cravador, A.; Loriau, R.; Brockly, F.; Colau, B.; Chuchana, P.; van Elser
	A/Title: Molecular cloning, sequencing, and expression in Escherichia coli of human pre
	A;Status: preliminary
	A; Molecule type: mRNA
	A; Residues: 1-150, W', 152-213, 'I', 215-385, 'C', 387-429, 'V', 431 <jac></jac>
_	A; Cross-reterences: EMBL:X02760; NID:g35297; PIDN:CAA26535.1; PID:g35298

ä

9 80 200 232 292

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u-plasminogen activator (EC 3.4.21.73) precursor - yellow baboon
C;Species: Papio cynocephalus, Papio hamadryas cynocephalus (yellow baboon)
C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 18-Jun-1999
C;Accession: S14687; S08651
R;Au, Y.P.T.; Wang, T.W.; Clowes, A.W.
Nucleic Acids Res. 18, 311, 1990
A;Title: Nucleotide and deduced amino acid sequences of baboon urokinase-type plasmino;
A;Title: Nucleotide and deduced amino acid sequences of baboon urokinase-type plasmino;
A;Reference number: S14687; MUD: 90287734; PMID: 2113276
A;Residuces: 1433 < AUY.
A;Residuces: 1433 < AUY.
A;Residuces: 1433 < AUY.
A;Cevencias: EMBL:X51935; NID: 938130; PIDN: CAA36200.1; PID: 938131
C;Superfamily: urokinase-type plasminogen activator; EGF homology; Kringle homology; C;Superfamily: urokinase-type plasminogen activator chain A #status predicted <ACH.>
F;12.0.50Domain: signal sequence #status predicted <ACH.>
F;21.176/Product: plasminogen activator chain A #status predicted <BCH.>
F;30-61/Domain: kringle homology <ARG>F;178-421/Domain: kringle homology <ARG>F;178-421/Domain: trypsin homology <ARG>F;178-421/Domain: prypsin homology <ARG>F;178-421/Dom
                C;Keywords: fibrinolysis; glycoprotein; heterodimer; hydrolase; kringle; serine proteir f?1-20/Domain: signal sequence #status predicted <SIG> f?1-20/Domain: signal sequence #status predicted <SIG> f?1-431/Product: urokinase-type plasminogen activator chain A #status experimental <MF 531-6.70Domain: BGF homology <EGF> f?31-6.70Domain: BGF homology <ERGS F;70-151/Domain: kringle homology <ERGS F;156-177/Product: urokinase-type plasminogen activator chain A #status experimental <F;156-177/Product: urokinase-type plasminogen activator chain B #status experimental <F;179-419/Domain: trypsin homology <TRY> F;179-419/Domain: trypsin homology <TRY> F;31-39;33-51,53-62,70-151,91-133,122-146,168-299,209-225,217-288,313-382,345-361,372-47,38/Binding site: carbohydrate (Thr) (covalent) #status predicted F;178-179-179-179,01a-avage site: Lys-Ile (plasmin) #status experimental <F;224,275,376/Active site: Lys-Ile (plasmin) #status experimental
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LHKDYSADTLAHHNDIALLKIRSKEGRCAQPSRTIQTICLPSMYNDPQFGTSCEITGFGK 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PLVQECMVHDCADGK-----LKFQCGQKTLRPRFKIIGGEFTTIENOPWFAAIYRRH 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ENSTDYLYPEQLKMTVVKLISHRECQQPHYYGSEVTTKMLCAADPQWKTDSCQGDSGGPL 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SNELHQVPSNCDCLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFYRG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          F;322/Binding site: carbohydrate (Asn) (covalent) #status experimental
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Pred. No. 2.3e-166;
1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 99.2%;
Best Local Similarity 97.8%;
Matches 402; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                81
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Brochim Boobhe Agrae, Y. Ushkynea, Y. Sakii, M. Tamaki, S.; Hara, H.; Takahashi, K.; Sawasaki, Brochim Brochim Boobhe Agraer 132, 43-59, 196; Tamaki, S.; Hara, H.; Takahashi, K.; Sawasaki, Aritilla: Caracterization of single chain urokinase-type plasminogen activator with a no Aritilla: Caracterization of single chain urokinase-type plasminogen activator with a no Aritilla: Caracterization of single chain urokinase-type plasminogen activator with a no Aritilla: Caracterization single caracterization 
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A;Introns: 19/3; 29/1; 65/1; 123/2; 154/1; 227/2; 277/1; 324/1; 373/3
C;Function: C;Function: proteolytically activates plasminogen
A;Description: proteolytically activates plasminogen
A;Pathway: fibrinolysis
C;Superfamily: urokinase-type plasminogen activator; EGF homology; kringle homology; try
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A; Title: Bovine urokinase-type plasminogen activator and its receptor: cloning and independence number: JN0560; MUD:93216119; PMID:8385052
A; Reference number: JN0560; MUD:93216119; PMID:8385052
A; Accession: JN0560; MUD:93216119; PMID:8385052
A; Accession: JN0560; MUD:93216119; PMID:8385052
A; Accession: JN0560; MUD:93216119; PMID:836062
A; Accession: JN0560; MUD:9163800; PIDN:AAA51419.1; PID:9163801
C; Superfamily: urokinase-type plasminogen activator; EGF homology; kringle homology; t C; Keywords: glycoprotein; heterodimer; hydrolase; kringle; serine proteinase
F; 120/Domain: signal sequence #status predicted <AGI>F; 21-179/Product: plasminogen activator chain A #status predicted <AGI>F; 21-179/Product: urokinase-type plasminogen activator chain A #status predicted <AGI>F; 21-179/Product: plasminogen activator chain B #status predicted <AGI>F; 181-413/Product: plasminogen activator chain B #status predicted <AM2>F; 181-413/Promain: trypsin homology <ARC>F; 181-413/Promain: trypsin homology <ARC>F; 181-411/Domain: Activator chain B #status predicted
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C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 16-Jul-1999
                                                                                                                                                                                                     SHELHQESGASNCGCLNGGKCVSYKYFSNIQRCSCPKKFQGEHCEIDTSQTCFEGNGHSY
                                                                                                                                                                 -----KLKFQCGQKTLRPRFKIIGGEFTTIEN
                                                                                                                                                                                                                                                                              QPWFAA1YRRHRGGSVTYVCGGSL1SPCWV1SATHCF1DYPKKEDY1VYLGRSRLNSNTQ
                                                                                                                                                                                                                                                                                                               201 OPWFAAIYRRHRGGSVTYVCGGSLISPCWVVSATHCFINYOOKEDYIVYLGROTLHSSTH
                                                                                                                                                                                                                                                                                                                                                                                                                           261 GEMKFEVEKLILHEDYSADSLAHHNDIALLKIRTDKGQCAQPSRSIQTICLPPVNGDAHF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Accession: JN0560
R;Kraetzschmar, J.; Haendler, B.; Kojima, S.; Rifkin, D.B.;
Gene 125, 177-183, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        u-plasminogen activator (EC 3.4.21.73) precursor - bovine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 76.6%; Score 1728; DB 1; Sest Local Similarity 73.8%; Pred. No. 1.3e-126; Matches 305; Conservative 44; Mismatches 54;
                                                                                                                                                                    LKPLVQECMVHDCADG------
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UVFGG
UVP3
UVFGG
UVP18EATHORGEN activator (EC 3.4.21.73) precursor - pig
UVP18EATHORGEN activator (EC 3.4.21.73) precursor - pig
UVP18EATHORGEN SUB SCIENCE domestica (domestic pig)
UVP18EACESSION 3.08 SCIENCE ACREA domestica (domestic pig)
UVP18EACESSION A00932.
UVP18EACESSION A00932.
UVC18EACESSION A00933.
UVC18EACESSION A00932.
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                                                                                                                                                                                                                                                                                                                                                              PLVQECMVHDCADGK-----LKFQCGQKTLRPFKIIGGEFTTIENQPWFAAIYRRH 172
                                                                                                                                                                                                                                                                                                                                                                                                 QRVQECMVHNCADGKKPSSPPEELQFQCGQRTLRPRFKIVGGEFTTIENQPWFAAIYRRH 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RGGSVTYVCGGSLISPCWVVSATHCFINYPKKEDYIVYLGRSRLNSNTQGEMKFEVENLI 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FCKENSTDYLYPEQLKMTVVKLISHRECQQPHYYGSEVTTKMLCAADPQWKTDSCQGDSG 349
                                                                                                                                                                                                                                                 KASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVGLK 120
                                                                                                                                                                                SREL-QVPSDCGCLNGGTCMSNKYFSSIHWCNCPKKFGGQHCBIDKSKTCYEGNGHFYRG 79
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                                                                                                                                    SNELHQVPSNCDCLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFYRG
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                             Length 433;
                                         ;
le-154;
has 10; Indels
                    ; Score 2090; DE
; Pred. No. 1e-15
17; Mismatches
                          92.6%;
                    Query Match
Best Local Similarity 90.6
Matches 375; Conservative
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Best Local Similarity
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A) Journal 19/3; 30/1; 66/1; 124/2; 155/1; 229/2; 279/1; 326/1; 375/3
C) Superfamily: urokinase-type plasminogen activator; EGF homology; kringle homology; t C; Superfamily: urokinase-type plasminogen activator; EGF homology; kringle homology; t C; Keywords: glycoprotein; heterodimer; hydrolase; kringle; serine proteinase C; Keywords: glycoprotein; bequence #status predicted <SIG>F; 1-178/Product: urokinase-type plasminogen activator chain A #status predicted <ACH>F; 32-63/Domain: EGF homology <EGF>F; 180-433/Product: urokinase-type plasminogen activator chain B #status predicted <BCH F; 180-433/Product: urokinase-type plasminogen activator chain B #status predicted <BCH F; 180-421/Domain: trypsin homology <TRY>F; 180-421/Domain: trypsin homology <TRYP>F; 180-421/D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cDNAs encoding mouse urokina
                                                                                                                                        208
                                                                                                                                                                                                                   180 VCGGSLISPCWVISATHCFIDYPKKEDYIVYLGRSRLNSNTCGEMKFEVENLILHKDYSA 239
                                                                                                                                                                                                                                                                                 DTLAHHNDIALLKIRSKEGRCAQPSRTIQTICLPSMYNDPQFGTSCEITGFGKENSTDYL 299
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HDCADGKLK------FQCGQKTLRPRFKIIGGEFTTIENQPWFAAIYRHRGGS-VTY 179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Y.; Reich,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 u-plasminogen activator (EC 3.4.21.73) precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 18-Jun-1999
C;Accession: A29420; A24615
R;Degen, S.J.F.; Heckel, J.L.; Reich, E.; Degen, J.L.
Biochemistry 26, 8270-8279, 1987
A;Title: The murine urokinase-type plasminogen activator gene.
A;Reference number: A29420; MUID:88163489; PMID:2831940
                                                                                                                       149 QDCSLSKKPSSTVDQQGFQCGQKALRPRFKIVGGFFTVVENQPWFAAIYLKNKGGSPPSF
                                                                                            HDCADGKLK-----FQCGQKTLRPRFKIIGGEFTTIENQPWFAAIYRHRGGS-VTY
                                                                                                                                                                                                                                                                                                                                                                             YPEQLKMTVVKLISHRECQQPHYYGSEVTTKMLCAADPQWKTDSCQGDSGGPLVCSLQGR
                                                                                                                                                                                                                                                                                                                                                                                                                     329 YPKDLKMSVVKIISHEQCKQPHYYGSEINYKMLCAADPEWKTDSCSGDSGGPLICNIDGR
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A;Residues: 1-433 <DEG>
A;Cross-references: GB:NL7922; NID:g202296; PIDN:AAA40539.1; PID:g202297
A;Cross-references: GB:NL7922; NID:g202296; Bolin, D.; Vassalli, J.D.; Combepine, C.; Godeau, F.; Nagamine, Y.; Re:Eur. J. Biochem. 148, 225-232, 1985
A;Ittle: Cloning, nucleotide sequencing and expression of cDNAs encoding A;Reference number: A24615; MUID:85179474; PMID:2985383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Molecule type: mRNA
A;Residues: 1-433 <BEL>
A;Cross-references: GB:X02389; NID:g55127; PIDN:CAA26231.1; PID:g55128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       360 MTLTGIVSWGRGCALKDKPGVYTRVSHFLPWIRSHTKEENGLA
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Matches 283;
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                                                                                                                                                                                                                                       GKENPSDYRYSDELKMTFVSLVSHEVCQQPHYYGAEVTDKMLCAADPQWETDSCQGDSGG
                      RHRGGSVTYVCGGSLISPCW1SATHCF1DYPKKEDY1VYLGRSRLNSNTQGEMKFEVEN
                                                 RHRGGSITYLCGGSLISPCWVVSATHCFIDHPKKENYIVYLGQSRLNSDTRGEMQFEVEK
                                                                                                                LILHKDYSADTLAHHNDIALLKIRSKEGRCAQPSRTIQTICLPSMYNDPQFGTSCEITGF
                                                                                                                                      261 LILHEDYSAESLAHHNDIALLKIRTSRGQCAQPSRSIQTICLPPEHEDAHSRTRCEIIGF
                                                                                                                                                                                                         GKENSTDYLYPEQLKMTVVKLISHRECQQPHYYGSEVTTKMLCAADPQWKTDSCQGDSGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
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A. Molecule type: mRNA
A. Residues: 1-477 < KRA>
C. Superfamily: tissue plasminogen activator; EGF homology; fibronectin type I repeat homology is a signal sequence #status predicted < SIG>
C. Reywords: Eibrinolysis; glycoprotein; hydrolase; kringle; serine proteinase
F. 22-36/Domain: propebtide #status predicted < PRO>
F. 22-36/Domain: propeptide #status predicted < PRO>
F. 22-36/Domain: BGF homology < RRC>
F. 22-97/Domain: BGF homology < RRC>
F. 22-97/Domain: kringle homology < RRC>
F. 22-47/Domain: trypsin homology < RRC>
F. 22-47/Domain: trypsin homology < RRC>
F. 24-27/Domain: trypsin homology < RRC>
F. 26-47/Domain: trypsin homology < RRC>
F. 26-47/Domain: dispersion homo
                                                                                                                                                                                                                                                                                                                                                                                      bat
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t-plasminogen activator (EC 3.4.21.68) precursor - false vampire bat (Megaderma lyra)
C;Species: Megaderma lyra
                                                                                                                                                                                                                                                                                                           C;Accession: JS0598
R;Kraetzschmar, J.; Haendler, B.; Langer, G.; Boidol, W.; Bringmann, P.; Alagon,
Gene 105, 229-237, 1991
                                                                                                                                                                                                                                                                                                                                                                                         vampire
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         311
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                                                                                                                                                                                                                                       N'Alternate names: tissue plasminogen activator
C'Species: Desmodus rotundus (common vampire bat)
C'Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 16-Jul-1999
            LMSATVNLISQDDCKNKYYDSTRVTDNMVCAGDPLWETDACKGDSGGPMVCEHNGRMTLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    177 VTYVCGGSLISPCWVISATHCFID-YPKKEDYIVYLGRSRLNSNTQGEMKFEVENLILHK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 78 OCHTVPVKSCSELRCFNGGTCWQAASFSDF-VCQCPKGYTGKQCEVDTHATCYKDQGVTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SKFILEFCSVPVCS----KATCGLRKYKEPQLHSTGGLFTDITSHPWQAAIFAQNRRSSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SSPFYSEQLKEGHVRLYPSSRCTSKFLFNKTVTNNMLCAGDTRSGELYPNVHDACQGDSG

    common vampire

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 ELHQVP----SNCDCLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DYSADTLAHHNDIALLKIRSKEGRCAQPSRTIQTICLPSMYNDPQFGTSCEITGFGKENS
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                                                                                                                                                                                                                                                                                                                                                                               A,Title: The plasminogen activator family from the salivary gland of the A,Reference number: JS0597; MUID:92039036; PMID:1937019
A,Accession: JS0598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 477;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |||||| GPLVCMNDNHMTLLGIISWGVGCGEKDIPGVYTKVTNYLGWIRDNMR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ,225-226/Cleavage site: His-Ser (plasmin) #status predicte
;272,321,428/Active site: His, Asp, Ser #status predicted
                                                                                                                                                                                                                      -plasminogen activator (EC 3.4.21.68) alpha-2 precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
38.5%; Score 868.5; DB 2;
Best Local Similarity 43.7%; Pred. No. 7.8e-60;
Matches 178; Conservative 60; Mismatches 148;
                                                                                  389 GIVSWGDGCAKKNKPGVYTRVTRYLNWIDSN 419
                                                       364 GIVSWGRGCALKDKPGVYTRVSHFLPWIRSH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         210 KCGGSLISPCWVASAAHCFIQLPKKENYVVYLGQSKESSYNPGEMKFEVEQLILHEYYRE 269
                                                                                                                                                                                             VCGGSLISPCWVISATHCFIDYPKKEDYIVYLGRSRLNSNTQGEMKFEVENLILHKDYSA 239
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              || |: :|:: || | :| :| || | CANTALOLGEGRANYCENPNGESEPPACYTK--RRYSIQETPCS 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VHDCADGKLKFQCGQKTLRPRFKIIGGEFTTIENQPWFAAIYRRHRGGSVTYVCGGSLIS 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PCWVISATHCFID----YPKKEDYIVYLGRSRLNSNTQGEMKFEVENLILHKDYSADTLA 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HHNDIALLKIRSKEGRCAQPSRTIQTICLPSMYNDPQFGTSCEITGFGKENSTDYLYPEQ 303
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DTLAHHNDIALLKIRSKEGRCAQPSRTIQTICLPSMYNDPQFGTSCEITGFGKENSTDYL
                                                                                                                                                                                                                                                          YPEQLIMITVVKLISHRECOOPHYYGSEVTTKMLCAADPOWKTDSCOGDSGGPLVCSLQGR
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                                                                                                                                                                                                                                                                                                                                                                                                  432
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                                                                                                                                                                                                                                                                                                                                                  360 MTLTGIVSWGRGCALKDKPGVYTRVSHFLPWIRSHTKEENGLA 402
                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 47.8
ses 187; Conservative
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Nyflernate names: t-PA; tissue plasminogen activator
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Accession: A94004; A25529; J70562; A93293; S02125; A91343; A93951; A91322; A54645; I(R;NY, T.; Elgh, F.; Lund, B.
Proc. Natl. Acced. Sci. U.S.A. 81, S355-359; 1984
A;Title: The structure of the human tissue-type plasminogen activator gene: correlation
A;Reference number: A94004; MUID:84298137; PMID:6089198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     is inconsistent with the authors' translat
                                            F;22-66/Domain: propeptide #status predicted <PRO>F;27-46/Domain: propeptide #status predicted <PRO>F;37-431/Product: plasminogen activator beta #status predicted <PLA>F;37-441/Pomain: EGF homology <EGF>F;82-163/Domain: EGF homology <EGF>F;82-163/Domain: trypsin homology <TRY>F;180-425/Domain: trypsin homology <TRY>F;180-425/Domain: trypsin homology <TRY>F;181-52,46-63,65-74,82-163,103-145,134-158,168-299,211-227,219-288,313-388/Disulfide F;1819-180/Cleavage site: His-Ser (plasmin) #status predicted F;179-180/Cleavage site: His-Ser (plasmin) #status predicted F;256,275,382/Active site: His, Asp, Ser #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SPCWVISATHCFID-YPKKEDYIVYLGRSRLNSNTQGEMKFEVENLILHKDYSADTLAHH 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NDIALLKIRSKEGRCAQPSRTIQTICLPSMYNDPQFGTSCEITGFGKENSTDYLYPEQLK 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        274 NDIALLQLKSGSPQCAQESDSVRAICLPEANLQLPDWTECELSGYGKHKSSSPFYSEQLK 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SELRCFNGGTCWQAASFSDF-VCQCPKGYTGKQCEVDTHATCYKDQGVTYRGTWSTSESG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                101 AQCINWNSNLLTRRTYNGRRSDAITLGLGNHNYCRNPDNNSKPWCYVIKASKFILEFCSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      129 HDCADGKLKFQCG-QKTLRPRFKIIGGEFTTIENQPWFAAIYRRHRGGS-VTYVCGGSLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MTVVKLISHRECQQPHYYGSEVTTKMLCAADPQWKT-----DSCQGDSGGPLVCSLQGR
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A;Residues: 1-562 <DEG>
A;Cross-references: GB.K03021; NID:g339817; PIDN:AAA98809.1; PID:g339818
R;Itagaki, Y.; Yasuda, H.; Morinaga, T.; Mitsuda, S.; Higashio, K.
Agric. Biol. Chem. 55, 1225-1232, 1991
A;Title: Purification and characterization of tissue plasminogen activator
A;Reference number: JT0562; MUID:91291340; PMID:1368681
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SNCDCLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFYRGKASTDTMG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVGLKPLVQECMV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PVCS----KATCGLRKYKEPQLHSTGGLFTDITSHPWQAAIFAQNRRSSGERFLCGGILI
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 431;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Accession: A94004
A;Molecule type: DNA
A;Rolled: 1-562 cNyr>
A;Cross-references: GB:L00141
A;Note: the codon given for residue 93 (ACC) is inconsite
B;Friezner Degen, S.J.; Rajput, B.; Reich, E.
Biol. Chem. 251, 6972-6985, 1986
A;Title: The human tissue plasminogen activator gene.
A;Reference number: A23529; MUID: 96196143; PMID: 3009482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MILIGIVSWGRGCALKDKPGVYTRVSHFLPWIRSHTK 396
                                                                                                                                                                                                                                                                                                                                                                                                                                  38.2%; Score 862.5; DB 2;
44.1%; Pred. No. 2e-59;
iive 59; Mismatches 146;
                                                                                                                                                                                                                                                                                                                                                                F;345-361,378-406/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MILLGIISWGVGCGEKDIPGVYTKVINYLGWIRDNMR
                      F;1-21/Domain: signal sequence #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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les 175; Conserv
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C; Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
R; Gardell, S.J.; Duong, L.T.; Diehl, R.E.; York, J.D.; Hare, T.R.; Register, R.B.; Jacob J. Biol. Chem. 264, 17947-17952, 1989
A; Title: Isolation, characterization, and cDNA cloning of a vampire bat salivary plasmin A; Reference number: A34369; MUD:90036867; PMID:2509450
A; Accession: A434369
A; Status: preliminary
A; Accession: A434369
A; Residues: 1-477 cGAP
A; Residues: 1-477 cGAP
A; Residues: 1-477 cGAP
C; Superfamily: tissue plasminogen activator; EGF homology; fibronectin type I repeat hom C; Reywords: plasminogen activator #status predicted cSIG
C; Superfamily: tissue plasminogen activator #status predicted cSIG
F; 73/Domain: Eibronectin type I repeat homology cKRC>
F; 87-120/Domain: Eibronectin type I repeat homology cKRC>
F; 87-200main: Eibronectin type I repeat homology cKRC>
F; 87-200main: tibronectin type I repeat homology cKRC>
F; 87-200main: tibronectin type I repeat homology cKRC>
F; 226-471/Domain: trypsin homology cKRC>
F; 226-471/Domain: trypsin homology cKRC>
F; 222-472,70-79,87-98,92-109,111-120,128-209,149-191,180-204,214-345,257-273,256-334,359-4
F; 272,72,72,70-79,87-98,92-109,111-120,128-209,149-191,180-204,214-345,257-273,256-334,359-4
                                                                                    R.B.; Jacob
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L-plasminogen activator (EC 3.4.21.68) beta precursor - common vampire bat
N;Alternate names: tissue plasminogen activator
C;Species: Desmodus rotundus (common vampire bat)
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 16-Jul-1999
C;Accession: 305059
R;Kxaetzschmar, J; Haendler, B.; Langer, G.; Boidol, W.; Bringmann, P.; Alagon, A.; D
Gene 105, 229-237, 1991
A;Ritle: The plasminogen activator family from the salivary gland of the vampire bat D
A;Reference number: JS0597; MUID:92039036; PMID:1937019
A;Reference number: JS0599;
A;Residues: 1-431 <KRA>
A;Cross-references: GB:M63989; NID:g166076; PIDN:AAA31594.1; PID:g166077
C;Superfamily: tissue plasminogen activator; EGF homology; fibronectin type I repeat P
C;Reywords: fibrinolysis; glycoprotein; hydrolase; kringle; serine proteinase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     :: || :: || || || || || ::: | :| || || EFDDDT--YNNDIALLQLKSGSPQCAQESDSVRAICLPEANLQLPDWTECELSGYGKHKS 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VTYVCGGSLISPCWVISATHCFID-YPKKEDYIVYLGRSRLNSNTQGEMKFEVENLILHK 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DYSADTLAHHNDIALLKIRŞKEGRCAQPSRTIQTICLPSMYNDPQFGTSCEITGFGKENS 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TDYLYPEQLKMTVVKLISHRECQQPHYYGSEVTTKMLCAADPQWKT-----DSCQGDSG 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SSPFYSEQLKEGHVRLYPSSRCTSKFLFNKTVTKNMLCAGDTRSGEIHPNVHDACQGDSG 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QCHTVPVKSCSELRCFNGGTCWQAASFSDF-VCQCPKGYTGKQCEVDTHATCYKDQGVTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LKPLVQECMVHDCADGKLKFQCG-QKTLRPRFKIIGGEFTTIENQPWFAAIYRRRGGS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 ELHQVP----SNCDCLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFY
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43.7%; Pred. No. 9.4e-60;
tive 60; Mismatches 148;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 43.7
Matches 178, Conservative
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A;Title: Expression of human uterine tissue-type plasminogen activator in mouse cells a A;Reference number: 160110; MUID:88054470; PMID:2824147
A;Accession: 160110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cross-references: GB:M11890, NID:g339837, PIDN:AAAG1213.1; PID:g339839; Comment: Cleavage by plasmin or trypsin produces two chains held together by a single; Comment: t-PA converts plasminogen to plasmin by hydrolyzing a single Arg-Val bond. Icomment: t-PA binds chain A of fibrin by kringle 2 and the fibronectin type I repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A) Residues: 1562 (RES) Residues: 1562 (RES) Residues: 1562 (RES) Residues: 1582 (RES) RESIDER RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .311-556/Domain: trypsin homology <TRY>
.41-71,69-78,86-97,91-108,110-119,127-208,148-190,179-203,215-296,236-278,267-291,299-
.152,483/Binding site: carbohydrate (Asn) (covalent) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    F.219/Binding site: carbohydrate (Asn) (covalent) #status experimental F.219/Binding site: carbohydrate (Asn) (covalent) #status experimental F.310-311/Cleavage site: Arg-Ile (plasmin, trypsin) #status experimental F.357,406/Active site: His, Asp #status predicted F.557,406/Active site: His, Asp #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28
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                                                                                                                                                                    A;Cross-references: GB:M15518; NID:g190031; PIDN:AAA60111.1; PID:g190032
A;Note: parts of this sequence were confirmed by peptide sequencing
R;Reddy, V.B.; Garramone, A.J.; Sasak, H.; Wei, C.
DNA 6, 461-472, 1987
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                        A;Reference number: A54645; MUID:86284200; PMID:3090401
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37.5%; Pred. No. 5.6e-59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           iStatus: preliminary; translated from GB/EMBL/DDBJ
iMolecule type: DNA
iResidues: 1-36 <RE2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Genetics:
A;Gene: GDB:PLAT
A;Cross-references: GDB:119496; OMIM:173370
                                                                                                                                                                                                                                                                                                                                                                                                                              Status: translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LKPLVQECMVHDCADG
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Best Local Similarity
Matches 183; Conserva
                                                                                                A;Molecule type: mRNA
A;Residues: 1-562 <HAR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17
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A Molecule type: mRNA

A/Residues: 1-38, G', 46-433, E', 435-562 «KAG>

A/Residues: 1-38, G', 46-433, E', 435-562 «Els; ATCC 138

R/Edlund, T.; Ny, T.; Ranby, M.; Heden, L.O.; Palm, G.; Holmgren, E.; Josephson, S.

Proc. Natl. Acad. Sci. US. A. 80, 349-352, 1983

A/Title: Isolation of CDNA sequences coding-for a part of human tissue plasminogen activ

A/Reference number: A93951; MUID:83169656; PMID:6572897
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A; Residues: 33-45;311-320 < PDH>
A; Residues: 33-45;311-320 < PDH>
A; Residues: 33-45;311-320 < PDH>
A; Experimental source: uterus
A; Note: in the uterus, cleavage of the activation peptide may also occur after 38-Gln
R; van Zonneveld, A.J.; Veerman, H.; Pannekoek, H.
A; Daiol. Chem. 251, 14214-14218, 1986
A; Reference number: A37567; MUID:87033611; PMID:3021732
A; Contents: annotation; fibrin binding site
R; Vertheijen, J.H.; Cappers, M.P.M.; Chang, G.T.G.; de Munk, G.A.W.; Pouwels, P.H.; Enger
BMBO J. 5, 3525-3530, 1986
A; Title: Involvement of finger domain and kringle 2 domain of tissue-type plasminogen ad
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A;Reference number: A60902; MUID:89044681; PMID:3142086
A;Contents: annocation; novel forms of expressed recombinant t-PA
R;Harris, T.J.R.; Patel, T.; Marston, F.A.O.; Little, S.; Emtage, J.S.; Opdenakker, G.;
Mol. Biol. Med. 3, 279-292, 1986
A;Title: Cloning of cDNA coding for human tissue-type plasminogen activator and its expr
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A,Reference number: annotation; melanoma cells, partial sequence of residues 36-562, active and R; Pohl, G.; Kaplan, L.; Einarsson, M.; Wallen, P.; Jornvall, H.
FBBS Lett. 168, 29-32, 1984
FBRS Lett. 168, 29-32, 1984
A,Title: Differences between uterine and melanoma forms of tissue plasminogen activator. A,Reference number: A91322; MUID:84158956; PMID:6538514
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A;Contents: annotation; fibrin binding site
R;Dodd, I.; Nunn, B.; Robinson, J.H.
Thromb. Haemost. 59, 523-528, 1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Molecule type: mRNA
A;Residues: 251-358 exBL>
A;Experimental source: melanoma cells
R;Pohl, G.; Kallstrom, M.; Bergsdorf, N.; Wallen, P.; Jornvall, H.
Biochemistry 23, 3701-3707, 1984
A;Title: Tissue plasminogen activator: peptide analyses confirm an indirectly derived
differences.
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A.McTecardie trype: MRNA
A.Residues: 1-477 < KRA>
A.Cross=references: GB:M63987; NID:g166070; PIDN:AAA31591.1; PID:g166071
C; Superfamily: tissue plasminogen activator; EGF homology; fibronectin type I repeat hc
C; Keywords: fibrinolysis; glycoprotein; hydrolase; kringle; serine proteinase
C; Keywords: fibrinolysis; glycoprotein; hydrolase; kringle; serine proteinase
F: 22-36/Domain: signal sequence #status predicted < PRO-
F: 37-477/Product: plasminogen activator alpha-1 #status predicted < PLA>
F: 42-73/Domain: EGF homology < EGF>
F: 42-73/Domain: EGF homology < RRO>
F: 42-73/Domain: kringle homology < RRO>
F: 42-73/Domain: trypsin homology < RRO>
F: 42-73/Domain: trypsin homology < RRO>
F: 42-73/Domain: trypsin homology < RRO>
F: 42-73/Domain: grie: carbohydrate (Asn) (covalent) #status predicted
F: 255-226/Cleavage site: His-Ser (plasmin) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Accession: JS0597
R;Kraetzschmar, J.; Haendler, B.; Langer, G.; Boidol, W.; Bringmann, P.; Alagon, A.;
Gene 105, 229-237, 1991
A;Title: The plasminogen activator family from the salivary gland of the vampire bat
A;Reference number: JS0597; MUID:92039036; PMID:1937019
                                                                                                                                                                                                                             372
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 PLVQECMVHDCADGKLKFQCG-QKTLRPRFKIIGGEFTTIENQPWFAAIYRRHRGGS-VT 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       179 YVCGGSLISPCWVISATHCFIDYPKKEDYI-----VYLGRSRLNSNTQGEMKFEVENLIL 233
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N;Alternate names: tissue plasminogen activator
C;Species: Desmodus rotundus (common vampire bat)
C;Species: Desmodus rotundus (common vampire bat)
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 16-Jul-1999
                                                                                                                                                                                                                                                                                                                               QWKTDSCQGDSGGPLVCSLQGRMTLTGIVSWGRGCALKDKPGVYTRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             487 NMLCAGDTRTGGNQDVHDACQGDSGGPLVCMIDKRMTLLGIISWGLGCGQKDVPGIYTKV
   GKYTTEFCSTPACPKGPTEDCYVGKGVTYRGTHSFTTSKASCLPWNSMILIGKTYTAWRA
                                                                                                 253 NSQALGLGRHNYCRNPDGDAKPWCHVMKDRKLTWEYCDMSPCSTCGLRQYKQPQFRIKGG
                                                                                                                                                                          BETTIENOPWFAAIY-RRHRGGSVTYVCGGSLISPCWVISATHCFIDYPKKEDYIVYLGR
                                                                                                                                                                                                                                 313 LFTDITSHPWQAAIFVKNKRSPGERFLCGGVLISSCWVLSAAHCFVERFPPHHLKVVLGR
                                                                                                                                                                                                                                                                                          SRLNSNTQGEMKFEVENLILHKDYSADTLAHHNDIALLKIRSKEGRCAQPSRTIQTICLP
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llarity 43.0%; Pred. No. 1.2e-57;
Conservative 56; Mismatches 147;
                                                               -HDCADGKLKFQ-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TNYLWWIQDNWKQ 559
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Best Local Similarity
Matches 175; Conserv
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ASSO29

C. Species: Rattus norregicus (Norway rat)
C. Species: A31029, A31597
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                                                                                                                                                                                                                    434 ADLQLPDWTECELSGYGKHEALSPFYSERLKEAHVRLYPSSRCTSQHLLNRTVTDNMLCA 493
                                                                                                                                                                                                                                                                                          AD-----PQWKT-DSCQGDSGGPLVCSLQGRMTLTGIVSWGRGCALKDKPGVYTRVSHFL 388
                                                                                                                                                                                                                                                                                                                         CHSVPVRSCSEPRCFNGGTCQQALYFSDF-VCQCPDGFVGKRCDIDTRATCFEGGGTTY 132
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                                                                                              YRVVPGEEEQKFEVEKYIVHXEFDDDT--YDNDIALLQLKSDSSRCAQESSVVRTVCLPP 433
                                                                                                                                                                       MYNDPOFGTSCEITGFGKENSTDYLYPEOLKMTVVKLISHRECQQPHYYGSEVTTKMLCA 334
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                                                            RLNSNTQGEMKFEVENLILHKDYSADTLAHHNDIALLKIRSKEGRCAQPSRTIQTICLPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 ELHQVP----SNCDCLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----KPLVQECMV---
                                                                                                                                                                                                                                                                                                                                                                                                        PWIRSHIK 396
                                                                                                                                                                                                                                                                                                                                                                                                                                         ||| : :
DWIRDNMR 561
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                                                                                                                   376
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A; Molecule type: mRNA

A; Residues: 1-394 «KRAA

A; Cross-references: GB:M63990; NID:g166078; PIDN:AAA31595.1; PID:g166079

A; Mote: the authors translated the codon ATC for residue 75 as Thr

C; Superfamily; tissue plasminogen activator; EGF homology; fibronectin type I repeat h:

C; Superfamily; tissue plasminogen activator; EGF homology; fibronectin type I repeat h:

C; Superfamily; tissue plasminogen activator; EGF homology; fibronectin type I repeat h:

F; 1-21/Domain: signal sequence #status predicted <PRO>

F; 2-36/Domain: propeptide #status predicted <PRO>

F; 37-394/Product: plasminogen activator gamma #status predicted <PLA>

F; 45-126/Domain: trypsin homology <TRY>

F; 45-126, Chomain: trypsin homology <TRY>

F; 45-126, Chomain: trypsin homology <TRY>

F; 413-388/Domain: trypsin homology <TRY>

F; 413-388/Johavage site: His. Ser (plasmin) #status predicted

F; 182-143/Cleavage site: His, Asp, Ser #status predicted

F; 185, 185, 185, Active site: His, Asp, Ser #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Accession: JS0600
R;Kraetzschmar, J.; Haendler, B.; Langer, G.; Boidol, W.; Bringmann, P.; Alagon, A.; Gene 105, 229-237, 1991
A;Ttle: The plasminogen activator family from the salivary gland of the vampire bat A;Reference number: JS0597; MUID:92039036; PMID:1937019
A;Accession: JS0600
                                                                                                                                                                                                                                           273
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                                                                                                                                                                                                          213
                                                                                                154
                                                                                                                                                  253 NSQALGLARHNYCRNPDGDARPWCHVMKDRKLTWEYCDMSPCSTCGLRQYKRPQFRIKGG 312
                                                                                                                                                                                                                                                                                                                                                                                                                              SMYNDPOF----GTSCEITGFGKENSTDYLYPEQLKMTVVKLISHRECQOPHYYGSEVTT 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           486
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              45 DKSKTCYEGNGHFYRGKASTDIMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRN 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100 PDGASKPWCYVIKARKFISESCSVPVCS----KATCGLRKYKEPQLHSTGGLFTDITSHP 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              221
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N'Alternate names: tissue plasminogen activator
C;Species: Desmodus rotundus (common vampire bat)
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 16-Jul-1999
                                                                                                                                                                                                                                                                                                                                                    t-plasminogen activator (EC 3.4.21.68) gamma precursor - common vampire bat
                                   GKYTTEFCSTPACPKGKSEDCYVGKGVTYRGTHSLTTSQASCLPWNSIVLMGKSYTAWRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       487 NMLCAGDTRSGGNQDLHDACQGDSGGPLVCMINKQMTLTGIISWGLGCGGKDVPGVYTKV
                                                                                                                                                                                                       EFTTIENQPWFAAIY-RRHRGGSVTYVCGGSLISPCWVISATHCFIDYPKKEDYIVYLGR
                                                                                                                                                                                                                                                                                                                    SRINSNIQGEMKFEVENLILHKDYSADTLAHHNDIALLKIRSKEGRCAQPSRIIQTICLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KMLCAADP-----QWKTDSCQGDSGGPLVCSLQGRMTLTGIVSWGRGCALKDKPGVYTRV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GEMKFEVENLILHKDYSADTLAHHNDIALLKIRSKEGRCAQPSRTIQTICLPSMYNDPQF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TNYLDWIHDNMKQ 559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SHFLPWIRSHTKE 397
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Best Local Similarity
Matches 155; Conserv
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L-plasminogen activator (EC 3.4.21.68) precursor - mouse
C.Species Mss masculus (house mouse)
C.Species Mss masculus (house mouse)
C.Species in A29941 kag205, 84207, 84206
F.Rickles, R.J.; Darrow, A.L.; Strickland, S.
J. Biol. Chem. 263 1.563.1669 1869
R.Rickles, R.J.; Darrow, A.L.; Strickland, S.
J. Biol. Chem. 263 1.563.1669 1988
A.Fille: Molecular cloning of complementary DNA to mouse tissue plasminogen activator mR AAccession. A29941 MID: 88087303; PMID:2826484
A.Accession. A29941 MID: 88087303; PMID:2826484
A.Accession. A2994 MID: 88.18691303; PMID:2826484
A.Accession. A2994 MID: 88.1869 MID: 98010776; PMID:7821120
R.Lijnen, H.R.; van Hoef, B.; Beelan, 1994
A.Accession. S4205
A.Accession. S4206
A.Accession. S4206
A.Accession. S4207
A.Accession. S4208
A.Accession. S420
FLCGGILISSCWVLTAAHCF----QESYLPDQLKVVLGRTYRVKPGEEEQTFKVKKYIV 309
                                                                                                                     294 NSTDYLYPEQLKMTVVKLISHRECQQPHYYGSEVTTKMLCAADPQWKT-----DSCQGD 347
                                                                                                                                                                                                                                             368 KSSSPFYSEQLKEGHVRLYPSSRCAPKFLFNKTVTNNMLCAGDTRSGEIYPNVHDACQGD 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  118
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                                                                                     HKDYSADTLAHHNDIALLKIRSKEGRCAQPSRTIQTICLPSMYNDPQFGTSCEITGFGKE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GCHSVPVRSCSEPRCFNGGTCQQALYFSDF-VCQCPDGFVGKRCDIDTRATCFEEQGITY
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                                                                                                                                                                                                                                                                                                                                            SGGPLVCMNDNHMTLLGIISWGVGCGEXDVPGVYTKVTNYLGWIRDN 474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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larity 35.7%; Pred. No. 9.9e-57;
Conservative 63; Mismatches 149;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                119 LKPLVQECMVHDCADGKLK---
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les 176; Conserv
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Best Local S
Matches 176
                                                                                     234
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ζ ₀ α	282 GTSCEITGFGKENSTDYLYPEQLKYTVVKLISHRECQQPHYYGSEVTTKMLCAADPQWKT 341 273 WTECELGGYGKHKSSSPFYSEQLKEGHVRLYPSSRCTSKFLFNKTVTNNMLCAGDTRSGE 332	<i>≿</i> 8	212 GRSRLNSNIQGEMKFEVENLILHKDYSADTLAHHNDIALLKIRSKEGRCAQPSRTIQTIC 271
ò a	342DSCQQDSGDLVCSLQQRWTLTGIVSWGRGCALKDKPGVYTRVSHFLPWIRSHT 395	දු දු	272 LPSMYNDPQFGTSCEITGFGKENSTDYLYPEQLKMTVVKLISHRECQOPHYYGSEVTTKM 331
ò	×	%	LCAADEQWKTDSCQGDSGGPLVCSLQGRMTLTGIVSWGRGCALKDKPGVYTRVSHFLPWI
g G	יאין א יאין אין אין אין אין אין אין אין	අ _ධ ද	
RESULT 16 A46688 hepatocyte C;Species:	sor [validated] - human	3 8	592 NDRIR 646
C;Date: C;Acces: R;Miyaz; J; Biol;	tt_change 08-Dec-2000 Morimoto, Y.; Kitamura, N.	RESULT 1: S28941 Coagulati N,Alterna	on factor XIIa (EC 3.4.21.38) - guinea pig (fragment) te names: Hageman factor
d coagu A,Refert A,Access		C; Species C; Date: 2 C; Accessi R: Semba	
A; Moleci A; Residi A; Cross A; Experi	33113.1; PID:9219681	Biochim. A;Title: A;Referen	Okabe, leavage
A; Note:	1227, NCBIP:131228) of the heavy and light chains, d	A;Access: A;Status: A;Molecul	or: SZ8941 preliminary e type: mRNA
A, Gene: A, Map po		A; Residue A; Cross-r C; Superfa C; Keyword	s: 1-603 <sem> eferences: BMBL:X68615; NID:g49578; PIDN:CAA48600.1; PID:g49579 hily: coagulation factor I. EGF homology; fibronectin type I repeat homolog 8: hydrolase: serine profeinse</sem>
C; Funct. A; Descr. A; Pathwe C; Supert C; Keywor	tic cleavage I repeat homology;	F;46-87/1 F;134-16/1 F;177-208 F;216-294 F;359-597	F;46-87/Domain: fibronectin type II repeat homology <1F2> F;134-169/Domain: fibronectin type II repeat homology <fb1> F;177-208/Domain: EGF homology <egf> F;216-294/Domain: EGF homology <egf> F;259-597/Domain: tryesin homology <frq></frq></egf></egf></fb1>
F; 1 - 3.47 F; 1 - 3.47 F; 108 - 114 F; 164 - 115 F; 108 -	1F2> F1>	Query M Best Lo Matches	Y Match 31.0%; Score 700.5; DB 2; Length 603; Local Similarity 36.7%; Pred. No. 1.18-46; thes 160; Conservative 60; Mismatches 147; Indels 69: Gans 13:
平,2445-14 平,286-3(平,408-65 平,408-65	Portugath: Extractory sex. 57/Domain: Kringle homology «KRG» 57/Product: hepatocyte growth factor activator light chain #status experimental 55/Forduct: hepatocyte growth factor activator heavy chain #status experimental 11/Inomain: trynsin homology «TPV» «TPV»	Qy Dp	KYFSNIHWCNCPKKFGGQHCEIDKSKTCYBGNGHFYRGKASTDTWGRPCL 7 VEGHHLCDCPMGYTGPFCDLDTTASCYEGRGVSYRGWARTTVSGAKCQ 2
F; 40, 48, F; 164-17 F; 447, 49	.290,468,492,546/Binding site: carbohydrate (Asn) (covalent) #status predicted 55,169-186,188-197,202-230,228-237,245-256,250-267,269-278,286-367,307-349,338-36 37,598/Active site: His, Asp, Ser #status predicted	රු සු	
Query Best I Matche	Query Match Best Local Similarity 37.2%; Pred. No. 1.2e-48; Matches 158; Conservative 53; Mismatches 161; Indels 53; Gaps 9;	දු දු	132ADGKLKFQ
5 G	5 HQVPSNCDCLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGH 56	රු දි	
\$ 8 8	57 FYRGKASTDIMGRPCLPWNSATVLQQIYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYV- 115	· 6 원	
% a	116TURPREKI 151	<i>\$</i> 8	265 RIICTICLESMYNDPOFGTSCEITGECKENSTDYLYPEQLKMIVVKLISHRECQOPHY 322
, č	152 IGGEFTTIENQPWFAAIYRRHRGGSVTYVCGGSLISPCWVISATHCFIDYPKKEDYIVYL 211	ò	YGSEVTTKMLCAADPQWKTDSCQGDSGGPLVCSLQGRWTLTGIVSWGRGCALKDKPG 37

plasma

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A/Rethmay: blood coagulation; fibrinolysis
C;Superfamily: coagulation factor XII; EGF homology; fibronectin type I repeat homolog
C;Superfamily: coagulation factor XII; EGF homology; fibronectin type I repeat homolog
C;Kaywords: blood coagulation; fibrinolysis; glycoprotein; hydrolase; kringle; plasma;
F;119,Domain: signal sequence #status predicted <SIG>
F;20-372,373-615/Froduct: coagulation factor XIIa, alpha form #status experimental <AI
F;47-88/Domain: EGF homology <EG2>
F;138-130/Domain: EGF homology <EG2>
F;138-130/Domain: EGF homology <EG2>
F;178-209/Domain: kringle homology <EG2>
F;297-259/Domain: kringle homology <EG3>
F;297-259/Domain: kringle homology <EG3>
F;298-356/Region: proline-rich
F;354-362,373-615/Product: coagulation factor XIIa, beta form #status experimental <B;373-69/Domain: trypsin homology <ER2>
F;398-110,104-119,121-130,135-163,161-170,178-189,183-198, cooralent #status experimental
F;299,305,328,329,337/Binding site: carbohydrate (Fnr) (covalent) #status predicted
F;308/Binding site: carbohydrate (Ser) (covalent) #status predicted
F;308/Binding site: carbohydrate (Ser) (covalent) #status predicted
F;308/Binding site: carbohydrate (Ser) (covalent) #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           239
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           296 QTPTQAAPPTPVSPRLHVPLMPAQPAPPKPQPTTRTPPQSQTPGALPAKREQPPSLTRNG 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              137 KFQCGQ---KTLRPRFKIIGGEFTTIENQPWFAAIYRRHRGGSVTYVCGGSLISPCWVIS 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PLSCGORLRKSLSSMTRVVGGLVALRGAHPYIAALYWGHS-----FCAGSLIAPCWVLT 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          467
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SHRECQOPHYYGSEVITIMILCAADPOWKIDSCQGDSGGPLVCSLQG---RMILIGIVSWG 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PWNSATVLQQTY-HAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVGLKPLVQECMVHDC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13 CLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFYRGKASTDTMGRPCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       240 PWAS----EATYRNVTAEQARNWGLGGHAFCRNPDNDIRPWCFVLNRDRLSWEYCDLAQC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          254 R-SKEGRCAQPSRIIQTICLPSMYNDPQFGTSCEITGFGKENSTDYLYPEQLKMTVVKLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QEDADGSCALLSPYVQPVCLPSGAARPSETTLCQVAGWGHQFEGAEEYASFLQEAQVPFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30.2%; Score 681; DB 1; Length 615; 34.1%; Pred. No. 3.7e-45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. 3.7e-45;
3; Mismatches 158; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               58;
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A,Residues: 1-558 <HAS>
C,Comment: This protein acts as
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nes 152; Conserv
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                                                                                                                                                                                                                                                                Comparizion General Manera (EC 3.4.21.38) precureor [validated] - human comparizion General Manera (Maneral Control Manera) (Materiane manera Maneral 
coagulation factor XIIa (EC 3.4.21.38) precursor
                                                                                                              ||| |: :| ||: || VYTDVASYLTWIQKHT 601
                                                                                VYTRVSHFLPWIRSHT
                                526
                                                                                380
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Matches
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A;Residues: 1-560 <CHO>
A;Cross-references: GB:S83182; NID:g1836158; PIDN:AAB46909.1; PID:g1836159
A;Experimental source: plasma
A;Note: parts of this sequence, including the amino ends of the mature chains, were dete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A,Cross-references: GDE:4573962
C;Complex: a disulfide-bonded heterodimer of chains produced from the same precursor; th C;Complex: a disulfide-bonded heterodimer of chains produced from the same precursor; th C;Superfamily: plasma hyaluronan-binding protein; EGF homology, kringle homology, rrypsi C;Keywords: chondroitin sulfate protecglycan; glycoprotein; hyaluronic acid; hydrolase; F;1-23/Domain: signal sequence #status predicted <SIG>F;24-313/Product: plasma hyaluronan-binding protein, 50K chain #status predicted <50K>F;7-108/Domain: EGF homology <EG2>F;115-147/Domain: EGF homology <EG3>F;115-147/Domain: EGF homology <EG3>
C;Superfamily: plasma hyaluronan-binding protein; EGF homology; kringle homology; trypsi F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-311/Product: plasma hyaluronan-binding protein large chain #status predicted <MATD>
F;75-106/Domain: EGF homology <EG1>
F;15-116/Domain: EGF homology <EG3>
F;113-145/Domain: EGF homology <EG3>
F;152-185/Domain: EGF homology <EG3>
F;192-274/Domain: kringle homology <EG3>
F;312-558/Product: plasma hyaluronan-binding protein small chain #status predicted <MATS
F;312-558/Pomain: trypsin homology <TRY>
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A; Title: Purification and characterization of a novel hyaluronan-binding protein (PHBP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 389 RVEKILKYSQYNERDEIPHNDIALLKLKPVGGHCALESRYVKTVCLPS---DPFPSGTEC 445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            73 PWNSATVLOOTYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVGLKPL-----VQEC 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   215 YWNSHLLLQETYNMFMEDAETHGIAEHNFCRNPDGDHKPWCFVKVNSEKVKWEYCDVTVC 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              127 MVHDCADGKLKF------QCGQKTLRPRF--KIIGGEFTTIENQPWFAAIY---- 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        275 PVPDTPNPVESLLEPVMELPGFESCGKTEVAEHAVKRIYGGFKSTAGKHPWQVSLQTSLP 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         170 ---RRHRGGSVTYVCGGSLISPCWVISATHCFIDYPKKEDYIVYLGRSRLNSNTQGEMKF 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          227 EVENLILHKDYSADTLAHHNDIALLKIRSKEGRCAQPSRTIQTICLPSMYNDP-QFGTSC 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EITGFGKENSTDYLYPEQLKMTVVKLISHRECQQPHYYGSEVTTKMLCAADPQWK-TDSC 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      446 HISGWGVTETGE--GSROLLDAKVKLIANPLCNSROLYDHTIDDSMICAGNLOKPGSDTC 503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Species: Homo sapiens (man)
Date: 15-Oct-1995 #sequence_revision 16-Aug-1996 #text_change 19-Jul-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                345 QGDSGGPLVCSLQGRMTLTGIVSWGRGCALKDKPGVYTRVSHFLPWIRSHTKEENGL 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13 CLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFYRGKASTDTMGRPCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  157 CONGGVCSRHRRRSRF-TCACPDQYKGKFCEIGPD-DCYVGDGYSYRGKVSKTVNQNPCL
                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               plasma hyaluronan-binding protein precursor - human
N,Alternate names: hepatocyte growth factor activator-like protein; PHBP
N,Contains: serine proteinase (EC 3.4.21.-)
                                                                                                                                                                                                                                                                                                                                                                                 43;
                                                                                                                                                                                                                                                                                                                      Length 558;
                                                                                                                                                                                                                                                                                                                                                                             Indels
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A;Reference number: JC4795; MUID:96425001; PMID:8827452
                                                                                                                                                                                                                                                                                                                   29.4%; Score 664.5; DB 2; 36.9%; Pred. No. 6.4e-44; ive 57; Mismatches 163;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GDB:HABP2; HABP; PHBP; HGFAL
                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 36.9%
Matches 154; Conservative
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CyAccession: 845281, A61329
R;Shibuya, Y.; Semba, U.; Oxabe, H.; Kambara, T.; Yamamoto, T.
Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Bi
F.194-276/Domain: kringle homology <KRI>
F.314-550/Domain: trypsin homology <TRV>
F.314-550/Domain: trypsin homology <TRV>
F.314-516/Product: plasma hyaluronan-binding protein, catalytic chain #status predicte
F.34,207/Binding site: carbohydrate (Covalent) #status predicted
F.37-86,82-97,99-108,115-125,120-136,138-147,154-165,159-176,178-187,194-276,215-257,2
F.362,405,509/Active site: His, Asp, Ser #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A,Molecule type: protein
A,Relecule type: protein
A,Residues: 10-16, "X.', 18-19;525-550 cFUJ>
A,Residues: 10-16, "X.', 18-19;525-550 cFUJ>
C,Superfamily: coagulation factor XII; EGF homology; fibronectin type I repeat homolog C,Reywords: blood coagulation, fibrinolysis; glycoprotein; hydrolase; monomer; plasma; F;37-78 Domain: fibronectin type II repeat homology c1F2>
F;125-160/Domain: Eibronectin type I repeat homology cFB1>
F;207-281/Domain: kibronectin type I repeat homology cFB1>
F;207-281/Domain: trypsin homology cTRY>
F;350-881/Domain: trypsin homology cTRY>
F;541/Active site: Ser #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  284 SCEITGFGKENSTDYLYPEQLKMTVVKLISHRECQQPHYYGSEVTTKMLCAADPQWK-TD 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CONGATCSRHKRRSKF-TCACPDQFKGKFCEIG-SDDCYVGDGYSYRGKMNRTVNQHACL 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               132 ADGKLKF------QCGQKTLRPR--FKIIGGEFTTIENQPWFAAIYRRHR 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   277 SAQDVAYPEESPTEPSTKLPGFDSCGKTEIAERKIKRIYGGFKSTAGKHPWQASLQ---- 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             174 GGSVT------YVCGGSLISPCWVISATHCFIDYPKKEDYIVYLGRSRLNSNTQGEMK 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -SSLPLTISMPOGHFCGGALIHPCWVLTAAHC-TDI-KTRHLKVVLGDQDLKKEEFHEQS 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    226 FEVENLILHKDYSADTLAHHNDIALLKIRSKEGRCAQPSRTIQTICLPSMYNDPQF--GT 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                446 ECHISGWGVTETGK--GSRÖLLDAKVKLIANTLCNSROLYDHMIDDSMICAGNLQKPGQD 503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  343 SCOGDSGGPLVCSLOGRMTLTGIVSWGRGCALKDKPGVYTRVSHFLPWIRSHTKEENG 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     504 TCQGDSGGPLTCEKDGTYYVYGIVSWGLECG--KRPGVYTQVTKFLNWIKATIKSESG 559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Coagulation factor XIIa (EC 3.4.21.38) precursor - bovine (fragment)
Althernate names: Hageman factor (activated)
C;Species: Bos primigenius taurus (catte)
C;Date: 10-Apr-1995 #sequence_revision 22-Apr-1995 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            217 YWNSHLLLQENYNMFMEDAETHGIGEHNFCRNPDADERPWCFIKVTNDKVKWEYCDVSAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         390 FRVEKIFKYSHYNERDEIPHNDIALLKLKPVDGHCALESKYVKTVCLP----DGSFPSGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              73 PWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVGLKPLVQE-CMVHDC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13 CLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFYRGKASTDTMGRPCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            47;
                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1; Length 560;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            58; Mismatches 161; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                       28.9%; Score 651.5; DB 1 36.4%; Pred. No. 6.6e-43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              36.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   152;
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13

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plasmin (EC 3.4.21.7) precursor - sheep (fragments)
NiAlternate names: plasminogen
NiAlternate names: plasminogen
NiAlternate names: plasminogen
NiAlternate names: plasminogen
Cionation: miniplasminogen
Airtie: Structural aspects of the plasminogen of various species.
Airtie: Structural aspects of the plasminogen of various species.
Airtie: Structural aspects of the plasminogen of various species.
Airtie: protein B61545
Airtie: Molecule type: protein
Cionation: miniplasminogen
Cionation: miniplasminogen
Airtie: Complete amino acid sequence of ovine miniplasminogen.
Cionation: S28200; MUID: 93149995; PMID: 1492092
Airtie: Complete amino acid sequence of ovine miniplasminogen.
Cionation: S28200; MID: 93149995; PMID: 1492092
Airtie: Complete amino acid sequence of ovine miniplasminogen.
Cionation: S28200; MID: 93149995; PMID: 1492092
Airtie: Molecule type: protein
Airtie: Molecule type: prot
         F1-77/Domain: plasmingen related protein precursor homology (fragment) <PLPH>
F1-77/Domain: plasmingen related protein precursor homology (fragment) <PLPH>
F18-560/Product: plasmin chain A #status predicted <APT>
F18-560/Product: plasmin chain A #status predicted <ACH>
F18-560/Product: plasmin chain A #status predicted <ACH>
F166-243/Domain: kringle homology <KR1>
F156-333/Domain: kringle homology <KR2>
F156-333/Domain: kringle homology <KR3>
F156-790/Product: miniplasminogen #status experimental <MIN>
F161-540/Domain: kringle homology <KR5>
F161-540/Domain: kringle homology <KR5>
F161-790/Product: plasmin chain B #status experimental <BCH>
F161-790/Product: plasminogen #status experimental <BCH>
F161-790/Product: plasminogen #status experimental <BCH>
F161-790/Product: plasminogen #status experimental <BCH>
F161-790/Product plasminogen #status experimental 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 101 YCRNPD-NRRRPWCYVQVGLKPLVQECMVHDCADGKLKFQCGQKTLRPR----FKIIGGEF 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      277 NDPQF----GISCELIGEGKENSTDYLYPEQLKMTVVKLISHRECQQPHYYGSEVTTKML 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CAGHLAGGIDSCQGDSGGPLVCFEKDKYILQGVTSWGLGCALPNKPGVYVRVSRFVTWI 783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              217 NSNTQGEMKFEVENLILHKDYSADTLAHHNDIALLKIRSKEGRCAQPSRTIQTICLPSMY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                510 YCRNPDGDDNGPWCYT-TNPQKLFDYCDVPQCVTS--SFDCGKPKVEPKKCPARVVGGCV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               157 TTIENQPWFAAIYRRHRGGSVTYVCGGSLISPCWVISATHCFIDYPKKEDYIVYLGRSRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DKSKTCYEGNGHFYRGKASTDTMGRPCLPWNSATVLQQTYHAHR----SDALQLGLGKHN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     669 -- PNYVVADRIACYITGWGETKGT--YGAGLLKEARLPVIENKVCNRYEYLGGKVSPNEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CAADPQWKTDSCQGDSGGPLVCSLQGRMTLTGIVSWGRGCALKDKPGVYTRVSHFLPWI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 22.5%; Score 508.5; DB 1; Length Best Local Similarity 36.2%; Pred. No. 1.2e-31; Matches 130; Conservative 45; Mismatches 141; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      F;602,645,740/Active site: His, Asp, Ser #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    333
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Nicontains: miniplasminogen
Nicontains: miniplasminogen
Nicontains: miniplasminogen
Cispecies: Sus scrofa demestica (domestic pig)
Cispecies: Sus scrofa demestica (domestic pig)
Cibate: 07-Sep-1990 #sequence_revision.01-Nov-1996 #text_change 18-Jul-1997
Circession: S03737; A25834
Rischaller, J.; Marti, T.; Roesselet, S.J.; Kaempfer, U.; Rickli, E.E.
Rischaller, J.; Marti, T.; Roesselet, S.J.; Kaempfer, U.; Rickli, E.E.
A; Teterence number: S03733
A; Molecule type: protein
A; Residues: 1-560 -SCH>
R; Rruisholz, R.A.; Lerch, P.G.; Schaller, J.; Rickli, E.E.; Lergier, W.; Manneberg, M.;
R; Brunisholz, R.A.; Lerch, P.G.; Schaller, J.; Rickli, E.E.; Lergier, W.; Manneberg, M.;
A; Title: Comparison of the primary structure of the N-terminal CNBr fragments of human, A; Reference number: S03735; MUID: S1212097; PMID: 7238497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A.Molecule trye: protein
A.Residues: 1-57 - CBRU-
A.Residues: 1-57 - CBRU-
A.Residues: 1-57 - CBRU-
A.Residues: 1-57 - CBRU-
B.W.

B.W.

A.Title: Determination of the complete amino-acid sequence of porcine miniplasminogen.
A.Reference number: A25834; MUID: 85203907; PMID: 3846533
A.Molecule trye: protein
A.Residues: 450-790 - KMR-
C.Function:
A.Residues: 450-790 - KMR-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      S
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                                                                                                                                                                                                                                                              TILSGAPCQSWAS----EATYWNVTAEQVLNWGLGDHAFCRNPDNDTRPWCFIWKGDRLS 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TDIMGRPCLPWNSATVLQQIY-HAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVGLKPL 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ---KTLRPRFKIIGGEFTTIENOPWFAAIYRRHRGGSVTYVCGGSLISPCWVISATHCFI 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | | :::|| | :::|| | SLRKWLSSLNRVVGGLVALPGAHPYIAALYWDQ------HFCAGSLIAPCWVLTAAHCLQ 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    279 WNYCRLAPCQAAAGHEHFPLPSPSALQKPESTTQTPLPSLTSGWCSPTPLASGGPGGCGQ 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RCAQPSRTIQTICLPSMYNDPQFGTS--CEITGFGKENSTDYLYPEQLKMTVVKLISHRE 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COOPHYYGSEVITYMLCAADPQWKTDSCOGDSGGPLVC---SLQGRMTLIGIVSWGRGCA 373
                                                                                                                                                                                             QVPSNCDCLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYE--GNGHFYRGKAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DYPKKEDYIVYLGRSRLNSNTQGEMKFEVENLILHKDYSADTLAHHNDIALLKIR-SKEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                  68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VQECMVHDC--ADGKLKFQ-------
                   Length 593;
Score 638; DB 2; Length 59
Pred. No. 7.8e-42;
9; Mismatches 164; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LKDKPGVYTRVSHFLPWIRSHT 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : |||||| |:::| ||| ||
NRLKPGVYTDVANYLAWIREHT 591
         28.3%; Sco.
34.2%; Prec
tive 59; 1
                                                                                                        Conservative
                                                           Similarity
                                                                                                   151;
         Query Match
Best Local S:
Matches 151
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A. Necession: A Addition of the Action of the Action of the Accession: A Accession:
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A; Molecule type: DNA
A; Readues: 367-419 «MAL3»
A; Readues: 367-419 «MAL3»
A; Cross-references: GB:KC2921; NID:g190110; PIDN:AAA60123.1; PID:g190111
A; Brunisholz, R.A.; Lerch, P.G.; Schaller, J.; Rickli, E.E.; Lergier, W.; Manneberg, M. Eur. J. Biochem: 114, 465-470, 1981
Bur. J. Biochem: 114, 465-470, 1981
A; Title: Comparison of the primary structure of the N-terminal CNBr fragments of human, A; Reference number: S03735; MUID:81212097; PMID:7238497
                                                                                                                                        Title: Characterization of a complementary deoxyribonucleic acid coding for human and; Reference number: 145961; MUID:85023311; PMID:6148961
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A,Residues: 20-50,'Q',51-71,'E',73-85,87-100 <WI2>
R,Wiman, B.; Wallen, P.
Eur. J. Biochem. 58, 539-547, 1975
A,Title: Amino-acid sequence of the cyanogen-bromide fragment from human plasminogen 1
A,Reference number: A04626; MUID:76043692; PMID:126863
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A;Moleus: translated from GB/EMBL/DDBJ
A;Moleus: 292-471, 'D', 473-810 <WAL2>
A;Cross-references: GB:K02922; NID:g190112; PIDN:AAA60124.1; PID:g387031
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;Residues: 20-71,'E',73-85,87-106,'D',108-360,'E',362-810 <SOT>
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Bur. J. Biochem. 76, 129-137, 1977
A;Title: Primary structure of the B-chain of human plasmin.
A;Reference number: A04627; MUID:77225245; PMID:142009
A;Accession: A04627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Molecule type: protein
A;Residues: 581-810 <MI1>
R;Wiman, B.; Mallen, P.
Bur. J. Biochem. 50, 489-494, 1975
A;Title: Structural relationship between "glutamic acid"
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A/Residues: 20-71,'E',73-76 <BRU>
R/Sottrup-Jensen, L.; Petersen, T.E.; Magnusson,
ammitted to the Allas, July 1977
                                                      Malinowski, D.P.; Sadler, J.E.; Davie, E.W. ochemistry 23, 4243-4250, 1984
                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Accession: 184609
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PLHU

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NALerrate names: plasminogen precursor [walidated] - human
NyAlerrate names: plasminogen precursor [misnomer]
NyAlerrate names: plasminogen precursor [misnomer]
NyContains: angiostatin, microplasmin; plasminogen
C;Species: Homo saptens (man)
C;Species: Homo saptens (man)
C;Species: Homo saptens (man)
C;Accession: A35229; IS2242; A2646; IS2789; 184609; S03775; A00929; A04627; A0462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AH----RSDALQLGLGKHNYCRNPD-NRRRPWCYVQVGLKPLVQECMVHDCADGKLKFQC 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FIDYPKKEDYIVYLGRSRLNSNTQGEMKFEVENLILHKDYSADTLAHHNDIALLKIRSKE 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GQKTLRPR --- FKIIGGEFTTIENQPWFAAIYRRHRGGSVTYVCGGSLISPCWVISATHC 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          218 GKPKVEPKKCPARVVGGCVATPHSWPWQVSLRRRSR----EHFCGGTLISPEWVLTAAHC 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ---DIALLKLSSP- 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GRCAQPSRTIQTICLPSMYNDPQF----GISCEITGFGKENSTDYLYPEQLKMTVVKLIS 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ---AVITDEVIPACLPS----PNYVVADKTVCYITGWGETQGT--FGVGRLKEARLPVIE 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HRECQOPHYYGSEVTTKMLCAADPQWKTDSCQGDSGGPLVCSLQGRMTLTGIVSWGRGCA 373
                                                                                                                                                                                                                                                                                                                                                                                                                                      28 IHW--CNCPKKFGGQHCEIDKSKTCYEGNGHFYRGKASTDTMGRPCLPWNSATVLQQTYH 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VRWEFCNLKKAPQAPSVENPPEADCMLGIGKGYRGKKATTVAGVPCOEWAA----QEPH
                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                         46;
                                                                                                                                                                                                                                                              22.2%; Score 502; DB 2; Length 46 34.7%; Pred. No. 2.1e-31; Live 43; Mismatches 158; Indels
         miniplasminogen #status experimental <MIN>
P;118-460/Product: miniplasminogen #status experimental <MIN:
F;132-211/Domain: kringle homology <KR5>
F;226-460/Domain: plasmin chain B #status experimental <BCH>
F;231-453/Domain: trypsin homology <TRY>
F;231-453/Domain: trypsin homology <TRY>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       274 LDSILGPSFYTVILGAHYEMAREASVQEIPVSRLFLEPSRA--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    374 LKDKPGVYTRVSHFLPWI 391
                                                                                                                                                                                                                                                                                                       Best Local Similarry Matches 131; Conservative
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Cyperacription: dissolves the fibrin of blood clots; acts as a proteolytic factor in a vale the walls of the graafian follicle; also activates the urokinase-type plasminogen ac A; Pathway: fibrinolysis

A; Pathway: fibrinolysis

C; Superfamily: plasmin; kringle homology; plasminogen-related protein precursor homology

C; Keywords: anglogenesis inhibitor; blood; duplication; fibrinolysis; glycoprotein; hydright plasminogen-related protein precursor homology cptPh>

F; 1-96/Domain: plasminogen-related protein precursor homology cptPh>

F; 20-810/Product: plasminogen #status experimental cAPT>

F; 20-810/Product: nagiostatin #status experimental cAPT>

F; 20-810/Product: angiostatin #status experimental cAPT>

F; 37-580/Domain: plasmin chain # status experimental cAPA>

F; 37-580/Domain: kringle homology cXR2>

F; 20-50/Domain: kringle homology cXR2>

F; 37-550/Domain: kringle homology cXR3>

F; 37-550/Domain: kringle homology cXR3>

F; 37-550/Domain: kringle homology cXR5>

F; 37-560/Domain: kringle homology cXR5>

F; 350-580,581-810/Product: microplasmin #status experimental cMMT>
                 Microplasmin is formed by autolytic cleavage of plasmin under artificial cor Stromelysin 1 (see PIR:KCHUS1) acts on plasminogen to produce angiostatin. 7
                                                                                                                                                  A;Cross-references: GDB:119498; OMIM:1733S0
A;Map position: 6q26-6q27
A;Intropas: 17/1; 62/2; 98/1; 136/2; 183/1; 223/2; 263/1; 317/2; 366/1; 419/2; 480/1; 52
G;Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               plasmin (EC 3.4.21.7) precursor - rhesus macaque
C;Species: Macaca mulatta (rhesus macaque)
C;Date: 31-Mar-1989 Bequence_revision 31-Mar-1989 #text_change 22-Jun-1999
C;Accession: B32869; B30848
B;Tomlinson, J.E.; McLean, J.W.; Lawn, R.M.
J. Biol. Chem. 264, 5957-5965, 1989
A;Title: Rhesus monkey apolipoprotein(a). Sequence, evolution, and sites of synthesis. A;Reference number: A32869; MUID:89174660; PMID:2925643
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          112 WCYVQVGLKPLVQECMVHDCADGKLKFQCGQKTLRPR----FKIIGGEFTTIENOPWFAAI 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     428 NPDADKGPWCFTTDPSVRWEYCNLKKCSGTEASVVAPPPVVLLPNVETPSEEDCMFGNGK 487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            542 WCYT-TNPRKLYDYCDVPQCA--APSFDCGKPQVEPKKCPGRVVGGCVAHPHSWPWQVSL 598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        655 SRLFLEPT-----RKDIALLKLSSP----AVITDKVIPACLPS-----PNYVVADRTE 698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      169 YRRHRGGSVTYVCGGSLISPCWVISATHCFIDYPKKEDYIVYLGRSRLNSNTQGEMKFEV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     488 GYRGKRATTVTGTPCQDWAA----QEPHRHSIFTPETNPRAGLEK-NYCRNPDGDVGGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                229 ENLILHKDYSADTLAHHNDIALLKIRSKEGRCAQPSRTIQTICLPSMYNDPQF----GTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    699 CFITGWGETQGT--FGAGLLKEAQLPVIENKVCNRYEFLNGRVQSTELCAGHLAGGTDSC
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22.2%; Score 501; DB 1; Le
Best Local Similarity 33.7%; Pred. No. 4.7e-31;
Matches 137; Conservative 45; Mismatches 169;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10 NCDCLNGGTCVSNKYFSNIHWCNCPKKFGGQ-----
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                    C,Comment: Microple
C,Comment: Stromely
ting solid tumors.
C,Genetics:
                                                                                                                                 A;Gene: GDB:PLG
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A; Reference number: AbsyBo; Pub:inkn
A; Contents: annotation; X-ray crystallography, 1.67 angstroms, residues 376-454
R;Rajante, M.; Lilnas, M.
A; Contents: annotation; Conformation by (1)H-NMR, residues 103-181
A; Contents: annotation; conformation by (1)H-NMR, residues 96-184
A; Contents: annotation; conformation by (1)H-NMR, residues 96-184
A; Contents: annotation; conformation by (1)H-NMR, residues 96-184
A; Reference number: S43645; MUID:94237189; PMID:8181475
A; Contents: annotation; conformation by (1)H-NMR, residues 96-184
A; Reference number: S48817; MUID:94237189; PMID:8181476
A; Contents: annotation; conformation by (1)H-NMR, residues 96-184
A; Reference number: S48817; MUID:94237189; PMID:8181476
A; Contents: annotation; conformation by (1)H-NMR
Eur. J. Blochem. 221, 939-949, 1994
A; Title: Solution structure of the epsilon-aminohexanoic acid complex of human plasminogen is converted to plasmin by plasminogen activators (see PIR:UKHU a A; Comment: Plasminogen is converted to plasmin by plasminogen activators (see PIR:UKHU a D; RIR: Reflucis)
C; Comment: Plasminogen is converted by alpha-2-antiplasmin (see PIR:ITHUA2) immediately af Fg-580, resulting in two chains connected by two disulfide bonds. Without the inhibitor,
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C)Comment: Plasminogen is synthesized by the kidney and is present in plasma and many c C)Comment: Plasminogen is converted into plasmin by plasminogen activators, both plasminediately after dissociation from the old. In the presence of the inhibitor, the activation involves also removal of the activation peptide.

C;Comment: Stromelysin 1 (see PIR:KCMSS1) acts on plasminogen to produce angiostatin. 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  128 NPDGDKGPWCYTTDPSVRWEYCNLKRCSETGGSVVELPTVSQEPSGPSDSETDCMYGNGK 487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       488 DYRGKTAVTAAGTPCQGWAA----QEPHRHSIFTPQTNPRADL-----EKNYCRNPDG 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            107 NRRRPWCYVQVGLKPLVQECMVHDCADGKLKFQCGQKTLRPR---FKIIGGEFTTIENQP 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       224 MKFEVENLILHKDYSADTLAHHNDIALLKIRSKEGRCAQPSRTIQTICLPSMYNDPQF-- 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       --GTSCEITGFGKENSTDYLYPEQLKMTVVKLISHRECQQPHYYGSEVTTKMLCAADPQW 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              F;78-79/Cleavage site: Glu-Asn (stromelysin 1) #status predicted
F;136.300|Binding site: Carbohydrate (Asn) (covalent) #status predicted
F;466-467/Cleavage site: Thr-Val (stromelysin 1) #status predicted
F;581-582/Cleavage site: Arg-Val (plasminogen activator) #status experimental
F;624,667,762/Active site: Arg-Val (plasminogen activator)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10 NCDCLNGGTCVSNKYFSNIHWCNCPK--KFGGQHCEI------DKSKTCYEGNGH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -- RSDALQLGLGKHNYCRNPD-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 164 WFAAIYRRHRGGSVTYVCGGSLISPCWVISATHCFIDYPKKEDYIVYLGRSRLNSNTQGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        652 QEISVAKLILE------PNNRDIALLKL----SRPATITDKVIPACLPS----PNYMV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22.2%; Score 501; DB 1; Length 812; ilarity 32.3%; Pred. No. 4.8e-31; Conservative 50; Mismatches 165; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      57 FYRGKASTDTMGRPCLPWNSATVLQQTYHAH-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          plasmin (EC 3.4.21.7) precursor - bovine N;Alternate names: plasminogen
                                                                                                                                                                                                     eful in treating solid tumors.
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Best Local (
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A; Molecule type: mRNA
A; Residues: 1-810 <-TOM>
A; Residues: 1-810 <-TOM
A; Residues: GB:J04697; NID:g342272; PIDN:AAA36901.1; PID:g342273
C; Superfamily: plasmin; kringle homology; plasminogen-related protein precursor homology
C; Keywords: fibrinolysis; glycoprotein; hydrolase; kringle; serine proteinase
F; 1-96 Domain: signal sequence #status predicted <SIG>
F; 1-96 Domain: kringle homology <KR1>
F; 103-181/Domain: kringle homology <KR2>
F; 227/Domain: kringle homology <KR3>
F; 377-454/Domain: kringle homology <KR3>
F; 377-454/Domain: trypsin homology <KR3>
F; 811-80/Domain: trypsin homology <RR3>
F; 822,665,760/Active site: His, Asp, Ser #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nicontains: angiostatin; plasminogen
Nicontains: angiostatin; plasminogen
Nicontains: angiostatin; plasminogen
Cispecies: Mus musculus (house mouse)
Cispecies: Mus musculus (house mouse)
Cispecies: 20-Sep-1991 #sequence revision 01-Nov-1996 #text_change 18-Jun-1999
Ciscession: A38514; S48202; S48203
Ribegen, S.J.F.; Bell, S.M.; Schaefer, L.A.; Elliott, R.W.
Canomics 8, 49-61, 1990
A;Title: Characterization of the cDNA coding for mouse plasminogen and localization of A; Testerence number: A38514
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 1-812 cbgA
A; Cross-references: GB: J04766; NID: 9200402; PIDN: AAB50168.1; PID: 9200403
R; Lijnen, H.R.; van Hoef, B.; Beelen, V.; Collen, D.
Bur. J: Biochem. 224, 86:3-871, 1994
A; Title: Characterization of the murine plasma fibrinolytic system.
A; Reference number: $48202; MUD: 95010076; PMID: 7523120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            596
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     169 YRRHRGGSVTYVCGGSLISPCWVISATHCFIDYPKKEDYIVYLGRSRLNSNTQGEMKFEV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    22.2%; Score 501; DB 2; Length 810; 34.4%; Pred. No. 4.7e-31;
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ive 46; Mismatches 165; Indels
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A,Residues: 20-25 <LIJ>
A,Accession: $48203
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us-09-880-503-6.rpr

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apoprotein(a) (EC 3.4.21..) precursor [validated] - human NyAlternate names: apolipoprotein(a); lipoprotein(a) chain apo(a) (Specias: Homo saplens (man) is lipoprotein(a) chain apo(a) (Specias: Homo saplens (man) (C) Specias: Homo (man) (M. 1) (M. 1
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R/Malgaretti, N.; Acquati, F.; Magnaghi, P.; Bruno, L.; Pontoglio, M.; Rocchi, M.; Sacc. Natl. Acad. Sci. U.S.A. 89, 11584-11588

A/Title: Characterization by yeast artificial chromosome cloning of the linked apolipof A/Reference number: A47233; MUID:93087573; PMID:1454851

A/Accession: 160906

A/Accession: preliminary, translated from GB/EMBL/DDBJ

A/Accession: Preliminary

A/Accession: A47233

A/Accession: A47234

A/Accession: A4723

          166 AAIYRRHRGGSVTYVCGGSLISPCWVISATHCFIDYPKKEDYIVYLGRSRLNSNTQGEMK 225
                                                                                                                                                                                                                                                                                                   654 IPVSRLFREPSQA-----DIALLKL----SRPAIITKEVIPACLPPPNYMVAARTEC 701
                                                                                                                                                                                                                                                                                                                                                                                                       286 BITGFGKENSTDYLYPE-QLKMTVVKLISHRECQQPHYYGSEVTTKMLCAADPQWKTDSC 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 702 YITGWGETQGT---FGEGLLKEAHLPVIENKVCNRNEYLDGRVKPTELCAGHLIGGTDSC 758
                                                                          S99 VSLRRSSR-----HFCGGTLISPKWVLTAAHCLDNILALSFYKVILGAHNEKVREQSVQE
                                                                                                                                                                                                         226 PEVENLILHKDYSADTLAHHNDIALLKIRSKEGRCAQPSRTIQTICLPSMYNDPQFGTSC
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A,Residues: 1-16 <RE3>
A,Cross-references: GB:M86877; NID:9178780; PIDN:AAB49909.1; PID:9553185
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Cispecies: Bos prinigentus teurus (matte)
Concession: Grescole & Explaination teurus (matte)
Concession: Grescole & Explaination (matte)
Ribertolind, L.; Andersen, Mb. 1995 [16391]
Ribertolind, L.; Andersen, Mb. 1997
Appearation: Cloning and characterizatin of the bovine plasminogen cDNA.
Appearation: Cloning and characterizatin of the bovine plasminogen cDNA.
Appearation: State & Explaination (matter)
Appearation: Matter & Explaination (matter)
Appearation: Matter & Explaination (matter)
Appearation (mat
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35.4%; Pred. No. 9.1e-30;
tive 42; Mismatches 151; Indels 31; Gaps 11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     F;315/Binding site: carbohydrate (Asn) (covalent) #status experimental F;315/Binding site: carbohydrate (Ser) (covalent) #status experimental F;624,667,762/Active site: His, Asp, Ser #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 35.4%
Matches 123; Conservative
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apolipoprotein(a) (EC 3.4.21.-) - rhesus macaque (fragment)
C.Species: Macaca mulatta (rhesus macaque)
C.Species: Macaca mulatta (rhesus macaque)
C.Date: 22-Nov-1989 #squence_revision 22-Nov-1989 #text_change 22-Jun-1999
C.Accession: A32869; A30848
R.Tomlinson, J.E.; McLean, J.W.; Lawn, R.M.
R.Tomlinson, J.E.; McLean, J.W.; Lawn, R.M.
A:fittle: Rhesus monkey apolipoprotein(a) . Sequence, evolution, and sites of synthesis.
A:Reference number: A32869; MUID:89174660; PMID:2925643
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Accession: A12869
A; Molecule type: mRNA
A; Residues: 1.1420 < TOM
A; Cross-references: GB:UJ4635; NID; G342072; PIDN:AAA36833.1; PID:G342073
C; Superfamily: apolipoprotein(a); kringle homology; trypsin homology
C; Keywords: hydrolase; kringle; lipid binding; lipoprotein; serine proteinase
F; 50-127/Domain: kringle homology < KR1>
F; 50-127/Domain: kringle homology < KR2>
F; 278-355/Domain: kringle homology < KR4>
F; 520-697/Domain: kringle homology < KR6>
F; 526-697/Domain: kringle homology < KR6>
F; 526-697/Domain: kringle homology < KR7>
F; 840-917/Domain: kringle homology < KR8>
F; 840-917/Domain: kringle homology < KR9>
F; 840-1031/Domain: kringle homology < KR9>
F; 1191-1413/Domain: kringle homology < KR9>
F; 1191-1413/Domain: trypsin homology < TRY>
                        4436 -PDYMVTARTECYITGWGETQGT--FGTGLLKEAQLLVIENEVCN--HY------KYIC 4483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1123 DIGPWCFT----MDPSVRREYCNLTRCSDIEGTVVTPPTVIPVPSLEAPSEQASSSFDCGK 1179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1394
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     278 DPQF----GTSCEITGFGKENSTDYLYPEQLXMTVVKLISHRECQQPHYYGSEVTTKMLC 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 313 SHRECOOPHYYGSEVITKMLCAADPOWKTDSCOGDSGGPLVCSLQGRMTLTGIVSWGRGC 372
                                                                                                                                                                                                                                                             4484 AEHLARGIDSCQGDSGGPLVCFEKDKYILQGVISHGLGCARPNKPGVYARVSRFVIWI 4541
                                                                                                                                                                                                                         334 AADPQWKTDSCQGDSGGPLVCSLQGRMTLTGIVSWGRGCALKDKPGVYTRVSHFLPWI 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           50 CYEGNGHFYRGKASTDTMGRPCLPWNSATVLQ--QTYHAHRSDALQLGLGKHNYCRNPDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       108 RRRPWCYVQVGLKPLVQE--CMVHDCAD------GKLKFQCGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DYPKKEDYIVYLGRSR---LNSNTQGEMKFEVENLILHKDYSADTLAHHNDIALLKIRSK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EGRCAQPSRTIQTICLPSMYNDPQF----GTSCEITGFGKENSTDYLYPEQLKMTVVKLI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21.1%; Score 477; DB 2; Length 14; 34.0%; Pred. No. 6.4e-29; ive 43; Mismatches 137; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ALKDKPGVYTRVSHFLPWI 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 34.0%
Matches 129; Conservative
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A.Note: apo(a) gene i (nomenclature of reference 122415)
A.Rocesson i f6286
A.Status preliminary; translated from GB/BMBL/DB3
A.Rocesson i f6286
A.Gomenica preliminary; translated from GB/BMBL/DB3
A.Rocesson GB/BB678; NID:g178782; PIDN:AAA51749.1; PID:g553186
A.Gomenica craces GB/BB6678; NID:g178782; PIDN:AAA51749.1; PID:g553186
A.Gomenica craces GB/BB678; NID:g178782; PIDN:AAA51749.1; PID:g553186
CS/Byperfamin (a) proported in GB/BB7878; PIDS:AAA51749; PID:g553186
F1.39Commin (a) proported in GB/BB7878; PIDS:AAA51749; PID:g553186
F1.30Commin (a) proported in GB/BB7878; PID:G4-13170; PID:G4-131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PDGDINGPWCYT-MNPRKLFDYCDIPLCASS--SFDCGKPQVEPKKCPGSIVGCVAHPH 4337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SWPWQVSL--RTRFGK--HFCCGTLISPEWVLTAAHCLKKSSRPSSYKVILGAHQEVNLE 4393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     50 CYEGNGHFYRGKASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGK-----HNYCRN 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SNTQGEMKFEVENLILHKDYSADTLAHHNDIALLKIRSKEGRCAQPSRTIQTICLPSMYN 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PD-NRRRPWCYVQVGLKPLVQECMVHDCADGKLKFQCGQKTLRPR---FKIIGGEFTTIE
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kringle homology
trypsin homology
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C.Superfamily: plasmin, kringle homology, plasminogen-related protein precursor homology C.Keywords: fibrinolysis, glycoprotein, hydrolase, kringle, plasma; serine proteinase, z F;1-33,34-117,118-455/Product: plasminogen (fragments) #status experimental <PRO> F;1-33/Domain: activation peptide (fragment) #status experimental <APT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         F.1-37/Domain: activation peptide (fragment) #status experimental fapts.
F.34-117,118-225,226-455/Product: plasmin (fragments) #status experimental «MAT>
F.34-117,118-225,226-455/Product: plasmin (fragments) #status experimental «MIN>
F.31-14/Domain: kringle homology «KR5>
F.31-8-455/Domain: kringle homology «KR5>
F.226-4455/Domain: plasmin chain B #status experimental «BCH>
F.226-448/Domain: trypsin homology «TRY>
F.226-448/Domain: trypsin homology «TRY>
F.226-448/Domain: trypsin homology «TRY>
F.226-448/Domain: trypsin homology «TRY>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              87 H---RSDALQLGLGKHNYCRNPD-NRRRPWCYVQVGLKPLVQECMVHDCADGKLKFQCGQ 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  158 HSIFTPEANPWANLEKNYCKNPDGDVNGPWCYT-MNPQKLFDYCDVPQCESS--PFDCGK 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              143 KTLRPR---FKIIGGEFTTIENOPWFAAIYRRHRGGSVTYVCGGSLISPCWVISATHCFI 199
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MyAlternate names: plasminogen
NyAlternate names: plasminogen
NyContains: miniplasminogen
NyContains: miniplasminogen
NyContains: miniplasminogen
CySpecies: Equus caballus (domestic horse)
CySpecies: Equus caballus (domestic horse)
CySpecies: 28-Oct-1994 #sequence_revision 01-Nov-1996 #text_change 18-Jul-1997
CySpecies: Naicki, E.E.
Enzyme 40, 63-69, 1988
AyTitle: Structural aspects of the plasminogen of various species.
AyReference number: A61545, MUID:89005015; PMID:3168975
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A; Readules: 1-33:34-117 <SCH>
A; Readules: 1-33:34-117 <SCH>
R; Schaller, J.; Straub, C.; Kaempfer, U.; Rickli, E.E.
Protein Seq. Data Anal. 4, 69-74, 1991
A; Title: Complete amino acid sequence of equine miniplasminogen.
A; Reference number: S17527; MUID:92052077; PMID:1946332
A; Accession: S17527
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A;Residues: 118-455 <SC2>
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Search completed: December 3, 2003, 14:44:18 Job time: 23.8448 secs

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Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-880-503-6 2257 1 SNELHQVPSNCDCLNGGTCV.....VSHFLPWIRSHTKEENGLAL 403 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

127863 Total number of hits satisfying chosen parameters: 127863 segs, 47026705 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_41:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

RESULT 1

A CT	HUMAN UROK HUMAN STANDARD; P00749; Q15844; Q16618; Q96 21-2101-1986 (Rel. 01, Creat
	<pre>20-WAR-1987 (Rel. 04, Last sequence update) 15-SEP-2003 (Rel. 42, Last annotation update) Urokinase-type plasminogen activator precursor (EC 3.4.21.73) (uPA) (U-plasminogen activator).</pre>
80000	Hono sapiens (Human) Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. NCBI_TaxID=9606;
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MEDLINE=83055099; PubMed=6754572;
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MEDLINE-833003608; PubMed=6749491;
Schaller J., Nick H., Rickli E.E., Gillessen D., Lergier W.,
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SEQUENCE OF 21-177.
MFDI.INE=83055084; PubMed=6754569;
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MEDLINE=93003110, PubMed=1327118,
Li X., Smith R.A.G., Dobson C.M.;
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EMBL; K03226; AAC97138.1; -.
EMBL; K02286; AAC81552.1; -.
EMBL; A21571; CAA01559.1; -.
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433 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                  HSSP; P00749; 1LM
MEROPS; S01.231;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 375;
                                                                                                                                                                                                                                        Kringle; I
SIGNAL
CHAIN
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ACT_SITE
ACT_SITE
CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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                                                                                     172
                                                                                                                                200
                                                                                                                                              RGGSVTYVCGGSLISPCWVISATHCFIDYPKKEDYIVYLGRSRLNSNTQGEMKFEVENLI 232
                                                                                                                                                                                             ENSTDYLYPEQLKMTVVKLISHRECQQPHYYGSEVTTRMLCAADPQWKTDSCQGDSGGPL 380
                                           9
                                                           80
                                      SNELHQVPSNCDCLNGGTCVSNKYFSNIHWCNCPKKFGQQHCEIDKSKTCYEGNGHFYRG
                                                 21 SNELHQVPSNCDCLNGGTCVSNKYFSNIHWCNCPKKFGGQHCBIDKSKTCYEGNGHFYRG
                                                                           KASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVGLK
                                                                                                                          141 PLVQECMVHDCADGKKPSSPPEELKFQCGQKTLRPRFKIIGGEFTTIENQPWFAAIYRRH
                                                                                                                                                         LHKDYSADTLAHHNDIALLKIRSKEGRCAQPSRTIQTICLPSMYNDPQFGTSCEITGFGK
                                                                                                                                                                                                                  ENSTDYLYPEQLKMTVVKLISHRECQQPHYYGSEVTTKMLCAADPQWKTDSCQGDSGGPL
                                                                                                            PLVQECMVHDCADGK-----LKFQCGQKTLRPRFKIIGGEFTTIENQPWFAAIYRRH
                         Gaps
                                                                                                                                                                                                                                                                                                                                01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
01-APR-1903 (Rel. 41, Last annotation update)
Urokinase-type plasminogen activator precursor (EC 3.4.21.73) (uPA)
(U-plasminogen activator).
                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa; Chordata; Craniata, Vertebrata, Euteleostomi,
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Papio.
                                                                                                                                                                                                                                                     VCSLQGRMTLTGIVSWGRGCALKDKPGVYTRVSHFLPWIRSHTKEENGLAL 403
                                                                                                                                                                                                                                                                 VCSLQGRMTLTGIVSWGRGCALKDKPGVYTRVSHFLPWIRSHTKEENGLAL 431
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8
        Length 431;
     Score 2240; DB 1; Length 4:
Pred. No. 7.4e-171;
1; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                   433
                                                                                                                                                                                                                                                                                                                                                                                      Papio cynocephalus (Yellow baboon).
      99.2%;
                       402; Conservative
                                                                                                                                                                                                                                                                                                                  STANDARD;
               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9556;
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ID UROK PAPCY
AC P16227;
     Query Match
Best Local S
Matches 402
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61 KASTDIMGRPCLPWNSAIVLQQTYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVGLK 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 PLVQECMVHDCADGK-----LKFQCGQKTLRPRFKIIGGEFTTIENOPWFAAIVRRH 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 233 LHKDYSADTLAHHNDIALLKIRSKEGRCAQPSRTIQTICLPSMYNDPQ---FGTSCEITG 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SREL-QVPSDCGCLNGGTCMSNKYFSSIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFYRG 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 SNELHQVPSNCDCLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFYRG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RGGSVTYVCGGSLISPCWVISATHCFIDYPKKEDYIVYLGRSRLNSNTQGEMKFEVENLI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              UROKINASE-TYPE PLASMINOGEN ACTIVATOR.
CHAIN A (BY SIMILARITY).
SHORT A CHAIN (A1) (BY SIMILARITY).
CCHAIN B (BY SIMILARITY).
EGF-LIKE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Serine protease; Glycoprotein; Signal.
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BY SIMILARITY.
BY SIMILARITY.
INTERCHAIN (BY SIMILARITY).
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
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90.6%; Pred. No. 6.2e-159;
iive 17; Mismatches 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KRINGLE.
CONNECTING PEPTIDE.
SERINE PROTEASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-LINKED (GLCNAC
InterPro; IPR001314; Chymotrypsin.
InterPro; IPR005209; EGF like.
InterPro; IPR006210; IEGF
InterPro; IPR001254; Ser Protease_Try.
Fam; PF000051; Kringle; I.
Fam; PF000051; Kringle; I.
Fam; PF000051; Kringle; I.
FRINTS; PR001051; KRINGLE.
PRODOM; PR001052; CHYMOTRYPSIN.
PRINTS; PR001051; KRINGLE.
PRODOM; PR001051; KRINGLE.
SWART; SW00130; KRINGLE.
SWART; SW00130; KRINGLE.
SWART; SW00130; KRINGLE.
PROSITE; PS01025; EGF 1; I.
PROSITE; PS01025; EGF 1; I.
PROSITE; PS01021; KRINGLE 1; I.
PROSITE; PS01031; KRINGLE 2; I.
PROSITE; PS01031; TRYPSIN JER; I.
PROSITE; PS01134; TRYPSIN JER; I.
PROSITE; PS01135; TRYPSIN JER;
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RESULT 4
UROK_BOVIN ST
ID UROK BOVIN ST
AC Q05589; Q28209;
DT 01-FEB-1994 (Rel.)
DT 01-FEB-1994 (Rel.)
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ACT SITE
ACT SITE
CONFLICT
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FGKENSTDYLYPEQLKMTVVKLISHRECQQPHYYGSEVTTKMLCAADPQWKTDSCQGDSG 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Kidney;
MEDLINE=85087954; PubMed=6096832;
Nagamine Y., Pearson D., Altus M.S., Reich E.;
"CDNA and gene nucleotide sequence of porcine plasminogen activator.";
Nucleic Acids Res. 12:9525-9541(1984)
                                                                                                                                                        403
                                                                                                                                                                                                                                                                                                                                      20-MAR-1987 (Rel. 04, Created)
13-AUG-1987 (Rel. 05, Last sequence update)
18-AUG-1987 (Rel. 41, Last annotation update)
Urokinase-type plasminogen activator precursor (EC 3.4.21.73) (uPA)
(U-plasminogen activator).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae, Sus.
NCBI_TaxID=9823,
                                                                                                                                                                          GPLVCSIQGHMTLTGIVSWGRGCALKDKPGVYTRVSRFLPWIHSHTREQNGLAL
                                                                                                                                                  GPLVCSLQGRMTLTGIVSWGRGCALKDKPGVYTRVSHFLPWIRSHTKEENGLAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nagamine Y.;
Submitted (DEC-1986) to the PIR data bank.
-!- CATALVTIC ACTIVITY: Specific cleavage of Arg-|-Val bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            plasminogen to form plasmin.
-- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1
-- SIMILARITY: Contains 1 kringle domain.
-- SIMILARITY: Contains 1 EGF-like domain.
                                                                                                                                                                                                                                                                                                    442 AA
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InterPro; IPR001114; Chymotrypsin.
InterPro; IPR001014; Chymotrypsin.
InterPro; IPR0010154; Ser_Inke.
InterPro; IPR001054; Ser_Drotease_Try.
Pfam; PF000051; Kringle; 1.
Pfam; PF000051; Kringle; 1.
PRINTS; PR00012; CHYMOTRYPSIN.
PRODOM; PD0000395; KRINGLE.
PRODOM; PD000395; KRINGLE.
PRODOM; PD000395; KRINGLE.
PROSTIE; PS00022; EGF_1; 1.
PROSTIE; PS00021; KRINGLE 1; 1.
PROSTIE; PS00024; KRINGLE 2; 1.
PROSTIE; PS00024; KRINGLE 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; X02724; CAA26511.1; -.
                                                                                                                                                                                                                                                                                                    STANDARD;
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PIR; A00932; UKPG.
HSSP; P00749; 1KDU.
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P04185;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  162 QPWFAAIYRRHRGGSVTYVCGGSLISPCWVISATHCFIDYPKKEDYIVYLGRSRLNSNTQ 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               401
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              201 QPWFAAIYRRHRGGSVTYVCGGSLISPCWVVSATHCFINYQQKEDYIVYLGRQTLHSSTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                261 GEMKFEVEKLILHEDYSADSLAHHNDIALLKIRTDKGQCAQPSRSIQTICLPPVNGDAHF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             282 GTSCEITGFGKENSTDYLYPEQLKMTVVKLISHRECQQPHYYGSEVTTKMLCAADPQWKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           342 DSCQGDSGGPLVCSLQGRMTLTGIVSWGRGCALKDKPGVYTRVSHFLPWIRSHTKEENGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 SNELHQV -- PSNCDCLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                222 GEMKFEVENLILHKDYSADTLAHHNDIALLKIRSKEGRCAQPSRTIQTICLPSMYNDPQF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               381 DSCQGDSGGPLVCSTQGRLTLTGIVSWGRECAMKDKPGVYTRVSRFLTWIHTHVGGENGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19; Gaps
PROSITE; PS00135, TRYPSIN_SER; 1.
Plasminogen activation; Hydrolase; Serine protease; Glycoprotein; Kringle; EGF-like domain; Zymogen; Signal.
SIGNAL 1 20 BY SIMILARITA.
CHAIN 21 442 UROKINASE-TYPE PLASMINOGEN ACTIVATOR.
CHAIN 21 188 CHAIN A (BY SIMILARITY).
CHAIN 190 442 CHAIN B (BY SIMILARITY).
CHAIN 29 65 EGF-LIKE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1; Length 442;
                                                                                                                                                                                     CONNECTING PEPTIDE.
SERINE PROTEASE.
N-LINKED (GLCNAC. ..).
BY SIMILARITY.
BY SIMILARITY.
INTERCHAIN (BY SIMILARITY).
BY SIMILARITY.
CHARGE RELAY SYSTEM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -> H (IN REF. 1; CAA25806).
-> H (IN REF. 1; CAA26511).
-> GS (IN REF. 1; CAA25806)
EE32FCEFS01321EE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      41; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          81.0%; Score 1827.5; DB 1
78.1%; Pred. No. 4.7e-138;
live 32; Mismatches 41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (Rel. 28, Created)
(Rel. 28, Last sequence update)
(Rel. 41, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        49116 MW;
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Best Local Similarity 78.1%
Matches 329; Conservative
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                                                                                          4442
1888
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64
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Conservative
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                                                                                                                                                                                                                       Local Similarity
hes 305; Conserv
                                                                                                                                                                           433 AA;
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SEQUENCE FROM N.A.
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ACT SITE
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CONFLICT
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                                                                                                                                                                           SEQUENCE
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                                                                                                                                                                                                                                                                                        Ravn P., Berglund L., Petersen T.E.; "Cloning and characterization of the bovine plasminogen activators uPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; L03546; AA5141991.

R EMBL; M05560; CAA59796.1; -

R EMBL; M05501.

R RSPP; NON560; JN0556.

R HSSP; NON560; JN0556.

R HSSP; NON560; JN0560.

R HSSP; NON500; JN0560.

R InterPro; IPR000114; Chymotrypsin.

R InterPro; IPR000001; Kringle.

R InterPro; IPR000001; Kringle.

R Pfam; PF000039; Kringle; I.

R PRNTG; PR00018; KRINGLE.

R PRODOM; PR000019; KRINGLE.

R RMART; SM00010; KRINGLE.

R RMART; SM00010; KRINGLE.

R RMART; SM00010; KRINGLE.

R RMART; SM00010; KRINGLE.

R RNOSITE; PS00020; EGF 1; 1.

R RNOSITE; PS00021; KRINGLE 2; I.

R RNOSITE; PS00014; TRYPSIN JNS; 1.

R RNOSITE; PS00014; TRYPSIN JNS; 1.

R PROSITE; PS000134; TRYPSIN JNS; 1.

R RNOSITE; PS000134; TRYPSIN JNS; 1.

R RNOSITE; PS000134; TRYPSIN JNS; 1.

R RNOSITE; PS000134; TRYPSIN JNSR; 1.
Urokinase-type plasminogen activator precursor (EC 3.4.21.73) (upa)
(U-plasminogen activator).
                                                 Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PLASMINOGEN ACTIVATOR
                                                                                                                                                                                                                                                                                                                                  Int. Dairy J. 5:605-617(1995).
-!- CATALYTIC ACTIVITY: Specific cleavage of Arg-|-Val bond in plasminogen to form plasmin.
-!- INDUCTION: By retinoic acid.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
-!- SIMILARITY: Contains 1 kringle domain.
-!- SIMILARITY: Contains 1 BGF-like domain.
                                                                                                                                                                                                "Bovine urokinase-type plasminogen activator and its receptor:
cloning and induction by retinoic acid.";
Gene 125:177-183(1993).
                                                                                                                                           TISSUE-Aortic endothelium;
MEDLINE-93216119; PubMed-8385052;
Kraetzschmar J., Haendler B., Kojima S., Rifkin D.B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CHAIN A (BY SIMILARITY)
CHAIN B (BY SIMILARITY)
EGF-LIKE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KEINGLE,
CONNECTING PEPTIDE.
SERINE PROTEASE.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         UROKINASE-TYPE
                                                                                                                                                                                                                                                             SEQUENCE OF 12-433 FROM N.A.
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433
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                                         taurus (Bovine).
                                                                                                                                                                                        Schleuning W.-D.;
                                                                                                                              SEQUENCE FROM N.A
                                                                                                   NCBI_TaxID=9913;
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181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RGKASTDIMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVG 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 380
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  171 RHRGGSVTYVCGGSLISPCWVISATHCFIDYPKKEDYIVYLGRSRLNSNTQGEMKFEVEN
                                                                                                                                                                                                                                                                                                                                                                                                                                             1 SNELHQV -- PSNCDCLNGGTCVSNKYPSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21 SNEVHKESGESNCGCLNGGKCVTYKYFSNIQRCSCPKKFQGEHCEIDTSKTCYQGNGHSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      119 LKPLVQECMVHDCADGKL------KFQCGQKTLRPRFKIIGGEFTTIENQPWFAAIYR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            321 GKENPSDYRYSDELKMIFVSLVSHEVCQQPHYYGAEVTDKMLCAADPQWETDSCQGDSGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LILHKDYSADTLAHHNDIALLKIRSKEGRCAQPSRTIQTICLPSMYNDPQFGTSCEITGF
                                                                                                                                                                                                                                                                                                                                                                                                  10; Gaps
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
  BY SIMILARITY.
BY SIMILARITY.
INTERCHAIN (BY SIMILARITY).
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
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BY SIMILARITY.
CHARGE RELAY SYSTEM (BY SIMILARITY).
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01-APR-1993 (Rel. 25, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
Urokinase-type plasminogen activator precursor (EC 3.4.21.73) (uPA)
(U-plasminogen activator).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       351 PLVCSLQGRMTLTGIVSWGRGCALKDKPGVYTRVSHFLPWIRSHTKEENGLAL 403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Transcriptional and posttranscriptional activation of urokinase plasminogen activator gene expression in metastatic tumor cells."; Cancer Res. 52:2489-2496(1992).
                                                                                                                                                                                                                                                                                                                                               76.6%; Score 1728; DB 1; Length 433; 73.8%; Pred. No. 3.8e-130; iive 44; Mismatches 54; Indels 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=Fischer 344;
MEDLINE=92233409; PubMed=1568219;
Hendderson B.R., Tansey W.P., Phillips S.M., Ramshaw I.A.,
Kefford R.F.;
                                                                                                                                                                                                                                                                          A -> T (IN REF. 2).
4DE1B8D4DA47027A CRC64;
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                                          plasminogen to form plasmin.
SUBUNIT: FOUND IN HIGH AND LOW MOLECULAR MASS FORMS. BACH
CONSISTS OF TWO CHAINS, A AND B. THE HIGH MOLECULAR MASS FORM
CONTAINS A LONG CHAIN A. CLEAVAGE OCCURS AFFER RESIDUE 156 IN THE
LOW MOLECULAR MASS FORM TO YIELD A SHORT AI CHAIN (BY SIMILARITY)
SIMILARITY: BELONGS TO PERPITABRE FAMILY S1.
SIMILARITY: Contains 1 Kringle domain.
                                                                                                                                                                                                                                                                                                                                                                                         R InterPro; IPR001314; Chymotrypsin.
R InterPro; IPR006210; IEGF like.
R InterPro; IPR006210; IEGF like.
R InterPro; IPR006210; IEGF.
R InterPro; IPR000210; IEGF.
R InterPro; IPR000101; Kringle.
R Pfam; PF00018; Kringle; 1.
R PRINTS; PR001918; Kringle; 1.
R PRINTS; PR001018; Kringle; 1.
R PRART; SM00118; EGF; 1.
R SMART; SM00120; Tryp SPC; 1.
R PROSTIE; PS01020; Tryp SPC; 1.
R PROSTIE; PS01020; Tryp SPC; 1.
R PROSTIE; PS01020; Tryp SPC; 1.
R PROSTIE; PS01021; KRINGLE; 1.
R PROSTIE; PS01021; KRINGLE; 1.
R PROSTIE; PS01034; TRYPSIN LIKE; FALSE NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                UROKINASE-TYPE PLASMINOGEN ACTIVATOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CHAIN A (BY SIMILARITY).
SHORT A CHAIN (A1) (BY SIMILARITY).
CHAIN B (BY SIMILARITY).
               nitted (APR-1992) to the EMBL/GenBank/DDBJ databases.
CATALYTIC ACTIVITY: Specific cleavage of Arg-|-Val bond in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SERINE PROTEASE.
BY SIMILARITY.
CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
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4EBIB96C716244C8 CRC64;
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(IN REF. 2).
(IN REF. 2).
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EMBL; X65651; CAA4601.1; --
PIN; S24604; S18932.

MESCP; P00149; 1KUU.
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432 AA;
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Rabbani S.A.
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                                                                                                                                                                                                                                                                        129 HDCADGKLK-----FQCGQKTLRPRFKIIGGEFTTIENQPWFAAIYRRHRGGS-VTY 179
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"The murine urckinase-type plasminogen activator gene.";

"The murine urckinase-type plasminogen activator gene.";

Biochemistry 25:8270-8279(1987).

-!- CATALYTIC ACTIVITY: Specific cleavage of Arg-|-Val bond in plasminogen to form plasmin.

-!- GATALYTIC ACTIVITY: Specific cleavage of Arg-|-Val bond in plasminogen to form plasmin.

-!- SUBDUNT: FOUND IN HIGH AND LOW MOLECULAR MASS FORMS. EACH CONSISTS OF TWO CHAINS, A AND B. THE HIGH MOLECULAR MASS FORM CONTAINS A LONG CHAIN A. CLEAVAGE OCCURS AFTER RESIDUE 156 IN THE LOW MOLECULAR MASS FORM TO YIELD A SHORT AI CHAIN (BY SIMILARITY).

-!- SIMILARITY: Contains 1 Kringle domain.

-!- SIMILARITY: Contains 1 EGF-like domain.
                                                                                                                      SNCGCQNGGVCVSYKYFSSIRRCSCPKKFKGEHCEIDTSKTCYHGNGQSYRGKANTDTKG
                                                                                       9 SNCDCLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFYRGKASTDTMG
                                                                                                                                                                                                      99 RPCLAWNSPAVLQQTYNAHRSDALSLGLGKHYCRNPDNQRRPWCYVQIGLKQFVQECMV
                                                                                                                                                                                                                                                                                                   300 YPEQLKMTVVKLISHRECQQPHYYGSEVTTKMLCAADPQWKTDSCQGDSGGPLVCSLQGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  329 YPKDLKMSVVKIISHEQCKQPHYYGSEINYKMLCAADPEWKTDSCSGDSGGPLICNIDGR
                                                                                                                                                                                                                                                                                                                                                               180 VCGGSLISPCWVISATHCFIDYPKKEDYIVYLGRSRLNSNTQGEMKFEVENLILHKDYSA
                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
Urokinase-type plasminogen activator precursor (EC 3.4.21.73) (uPA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-BEITH 19474; PubMed-2985383; Belin D., Vassalli J.-D., Combepine C., Godeau F., Nagamine Y., Reich E., Kocher H.P., Duvoisin R.M.; "Cloning, nucleotide sequencing and expression of cDNAs encoding mouse urokinase-type plasminogen activator."; Eur. J. Biochem. 148:225-232(1985).
                                              ο
••
  DB 1; Length 432;
73.4%; Score 1656.5; DB 1; Length
72.2%; Pred. No. 1.8e-124;
.ive 45; Mismatches 58; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       389 PTLSGIVSWGSGCAEKNKPGVYTRVSYFLNWIQSHIGEENGLA 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             360 MILIGIVSWGRGCALKDKPGVYTRVSHFLPWIRSHTKEENGLA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE=88163489; PubMed=2831940;
                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse)
Query Match
Best Local Similarity
Matches 291; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   UROK MOUSE
P06869;
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                        210 KCGGSLISPCWVASAAHCFIQLPKKENYVVYLGQSKESSYNPGEMKFEVEQLILHEYYRE 269
   180 VCGGSLISPCWVISATHCFIDYPKKEDYIVYLGRSRLNSNTQGEMKFEVENLILHKDYSA 239
                                                                                      270 DSLAYHNDIALLKIRTSTGQCAQPSRSIQTICLPPRFTDAPFGSDCEITGFGKESESDYL
                                                                  DILAHHNDIALLKIRSKEGRCAOPSRTIOTICLPSMYNDPOFGTSCEITGFGKENSTDYL
                                                                                                                                   YPEQLIMITVIKLISHRECQQPHYYGSEVITIMICAADPQWKTDSCQGDSGGPLVCSLQGR
                                                                                                                                                                 330 YPKNLKMSVVKLVSHEQCMQPHYYGSEINYKMLCAADPEWKTDSCKGDSGGPLICNIEGR
                                                                                                                                                                                                                                                                                                                 UROK CHICK STANDARD; PRT; 434 AA.

P15120;
01-APR-1990 (Rel. 14, Last sequence update)
20-FEB-2003 (Rel. 41, Last sequence update)
20-FEB-2003 (Rel. 41, Last sequence update)
Urokinase-type plasminogen activator precursor (EC 3.4.21.73) (uPA)
(U-plasminogen activator).
Gallus gallus (Chicken).
Eukaryota; Metazoa Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE=90110185; PubMed=2295632;
MEDLINE=90110185; PubMed=2295632;
MEDLINE=90110185; PubMed=2295632;
The chicken urokinase-type plasminogen activator gene.";
J. Biol. Chem. 265:1339-1344(1990).
-!- CAPALYTIC ACTIVITY: Specific cleavage of Arg-|-Val bond in plasminogen to form plasmin.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
-!- SIMILARITY: Contains 1 kringle domain.
-!- SIMILARITY: Contains 1 EGF-like domain.
                                                                                                                                                                                                                      390 PTLSGIVSWGRGCAEKNKPGVYTRVSHFLDWIQSHIGEEKGLA 432
                                                                                                                                                                                                    360 MTLTGIVSWGRGCALKDKPGVYTRVSHFLPWIRSHTKEENGLA 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEROPS, SOL.231, --.
INTERPORT IPROGATIL4; Chymotrypsin.
INTERPORT IPROGA1314; Chymotrypsin.
INTERPORT IPROGA210; EGF_like.
INTERPORT IPROGA210; IEGF.
INTERPORT IPROGA214; SAT_protease_Try.
Pfam; PF00009; kringle; 1.
Pfam; PF00009; trypsin; 1.
PRINTS; PR00122; CHYMOTRYPSIN.
PRODAM, PD000395; Kringle; 1.
SWART; SM0018; KRINGLE.
SWART; SM0018; KRINGLE.
SWART; SM00180; KRINGLE.
PROSITE; PS00022; EGF_1; 1.
PROSITE; PS01021; KRINGLE_1; 1.
PROSITE; PS01021; KRINGLE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL, JO5187, AA49131.1; -.
EMBL, JO5188; AA49130.1; -.
PIR, A35005; A35005.
HSSP, P00763; IDPO.
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the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        89
                                                                                                                                                     30 SNCGCQNGGVCVSYKYFSRIRRCSCPRKFQGEHCEIDASKTCYHGNGDSYRGKANTDTKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9 SNCDCLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFYRGKASTDTMG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      69 RPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVGLKPLVQECMV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    90 RPCLAWNAPAVLQKPYNAHRPDAISLGLGKHNYCRNPDNQKRPWCYVQIGLRQFVQECMV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL.
UROKINASE-TYPE PLASMINOGEN ACTIVATOR.
CHAIN A (BY SIMILARITY).
SHORT A CHAIN (A1).
CHAIN B (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
INTERCHAIN (BY SIMILARITY).
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A99C35F6250443F9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Pred. No. 4.4e-122; 50; Mismatches 61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CONNECTING PEPTIDE. SERINE PROTEASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     72.1%; Score 1626.5; 70.2%; Pred. No. 4.4e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EGF-LIKE
                                                                                EMBL; X02389; CAA26231.1; --
EMBL; M17922; AAA40539.1; --
BIR; A29420; UGMS.
HSSP; P00749; IKDU.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      48268 MW;
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Best Local Similarity 70.2'
Matches 283, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      433 AA;
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Desmodus
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SMART; SM00181; EGF; 1.
SMART; SM00058; FN1; 1.
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                                                          FROM N.A.
                                                                                                                                                                                                                                                                                                                                               CHARACTERIZATION.
                            NCBI_TaxID=9430;
                Desmodontinae;
                                                                                                                                                                                                                                                                                                                                                                                                               Donner P.;
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             7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLPWNSATVLQ-QTYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVGLKPLVQE--CM 127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-APR-1990 (Rel. 14, Created)
01-FBE-1996 (Rel. 33, Last sequence update)
28-FBE-2003 (Rel. 41, Last annotation update)
Salivary plasminogen activator alpha 2 precursor (EC 3.4.21.68) (DSPA alpha-2) (BAT-PA) (T-plasminogen activator).
Desmodus rotundus (Vampire bat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                             KRINGLE.
CONNECTING PEPTIDE.
SERINE PROTEASE.
BY SIMILARITY.
CHARGE RELAY SYSTEM (BY SIMILARITY).
UROKINASE-TYPE PLASMINOGEN ACTIVATOR.
CHAIN A (BY SIMILARITY).
CHAIN B (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Chiroptera, Microchiroptera, Phyllostomidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Score 997; DB 1; Length 434;
; Pred. No. 4.9e-72;
64; Mismatches 122; Indels 18;
                                                                                                                                                                                                                                                                                                                                                                                                                    BD881048DD666A55 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GIVSWGRGCALKDKPGVYTRVSHFLPWIRSH 394
                                                                                                                                                   EGF-LIKE.
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Best Local Similarity 47.8'
Matches 187; Conservative
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                                                                                                      434
171
158
158
172
434
488
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2298
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373
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434 AA;
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CARBOHYD
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           NAME OF THE PETT O
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NORELTRANDS 4310;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RGKASTDIMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVG 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LKPLVQECMVHDCADGKLKFQCG-QKTLRPRFKIIGGEFTTIENQPWFAAIYRRHRGGS- 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                197 SKPILEFCSVPVCS----KATCGLRKYKEPQLHSTGGLFTDITSHPWQAAIFAQNRRSSG 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VTYVCGGSLISPCWVISATHCFID-YPKKEDYIVYLGRSRLNSNIQGEMKFEVENLILHK 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           311
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     369
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         SMAKI; SMO0020; TYP_SPC; 1.

PROSITE; PS00022; BGF_1; 1.

PROSITE; PS01022; BGF_2; 1.

PROSITE; PS01021; KRINGLE_1; 1.

PROSITE; PS00021; KRINGLE_1; 1.

PROSITE; PS000134; TRYPSIN_HIS; 1.

PROSITE; PS00134; TRYPSIN_HIS; 1.
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-> H (IN REF. 2).
-> R (IN REF. 2).
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Ann. N.Y. Acad. Sci. 667:395-403 (1992).

-i. FUNCTION: PROBABLY ESSENTIAL TO SUPPORT THE FEEDING HABITS OF THIE EXCLUSIVELY HAEMATOFHAGOUS ANIMAL. PROBABLE POTENT THROMBOLYTIC
                                                                                                                                                              (EC 3.4.21.68) (DSPA
                                                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Chiroptera, Microchiroptera, Phyllostomidae,
Desmodontinae, Desmodus
                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Salivary gland;
MEDLINE=92039036; PubMed=1937019;
Retetzschmar J., Haendler B., Langer G., Boidol W., Bringmann P.,
Alagon A., Donner P., Schleuning W.D.;
"The plasminogen activator family from the salivary gland of the
vampire bat Desmodus rotundus: cloning and expression.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Schleuning W.-D., Alagon A., Boidol W., Bringmann P., Petri T.,
Kraetzschmar J., Haendler B., Langer G., Baldus B., Witt W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- CATALYTIC ACTIVITY: Specific cleavage of Arg-|-Val bond in plasminogen to form plasmin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -i- SIMILARITY: BELONGS TO PEPTIDASE FAMILY SI.
-i- SIMILARITY: Contains 1 kringle domain.
-i- SIMILARITY: Contains 1 EGF-like domain.
                                                         01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
08-FEB-2003 (Rel. 41, Last annotation update)
Salivary plasminogen activator beta precursor
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InterPro; IPR006209; EGP_like.
InterPro; IPR006210; EGF_like.
InterPro; IPR000021; Kringle.
InterPro; IPR001254; Sar_protease_Try.
Pfam; PF000081; Kringle; 1.
Pfam; PF000081; Kringle; 1.
PRINTS; PR00125; CHYMOTRYPSIN.
PRINTS; PR00129; KRINGIE.
ProDom; PD000395; KRINGIE.
ProDom; PD000395; KRINGIE.
ProDom; PD000181; EGF; 1.
SWART; SM00130; KR; 1.
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MEDLINE=93393059; PubMed=1309059;
                                                                                                                                                                                                                 Desmodus rotundus (Vampire bat)
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E; PS00022; EGF_1; 1.
E; PS01186; EGF_2; 1.
E; PS00021; KRINGLE_1; 1.
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STANDARD;
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HSSP; P98119; 1A51.
MEROPS; S01.239;
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DESRO
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us-09-880-503-6.rsp

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KRINGLE.

KRINGLE.

CHARGE RELAY SYSTEM (BY SIMILARITY).

CHARGE RELAY SYSTEM (BY SIMILARITY).

CHARGE RELAY SYSTEM (BY SIMILARITY).

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                                                                                                                                                                                                                                   SALIVARY PLASMINOGEN ACTIVATOR
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P00750; Q15103;
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation 
15-SEP-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LINKED (GLCNAC. . .) (PC 699B5E675B162CBF CRC64;
PROSITE; PS50070; KRINGLE 2; 1.
PROSITE; PS50240; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_HIS; 1.
PROSITE; PS00135; TRYPSIN_SER; 1.
Plasminogen activation; Hydrolase; Serine procease; Kringle; EGF-like domain; Signal; Multigene family.

SIGNIBLE STENIAL STENIA
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38.2%; Score 862.5; DB 1;
Best Local Similarity 44.1%; Pred. No. 2.4e-61;
Matches 175; Conservative 59; Mismatches 146;
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
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TISSUE=Umbilical vein;
MEDLINE=90192129; PubMed=2107528;
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IISSUE=Brain;
MEDLINE=22388257; PubMed=12477932;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     recombinant kringle 2 domain
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 OF CATALYTIC DOMAIN.
                                                                                                                                  X-RAY CRYSTALLOGRAPHY (3.1 ANGSTROMS) OF CATALYTIC DOMAIN
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56; Mismatches 152; Indels
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                                                           O-chain human tissue-type plasminogen activator. Mol. Biol. 258:117-135 (1996).
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X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS)
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Matches 183; Conservative
                                               Bode W.;
"The 2.3 A crystal
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RESULT 11 TPA_RAT

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PROSITE; PS01253; FIBRONECTIN 1, PROSITE; PS01253; FIBRONECTIN 2, PROSITE; PS00021; KRINGLE 1; Z. PROSITE; PS00021; KRINGLE 2; Z. PROSITE; PS00034; TRYPSIN DOM; 1. PROSITE; PS00134; TRYPSIN HIS; 1. PROSITE; PS00134; TRYPSIN HIS; 1. PROSITE; PS00135; TRYPSIN SER; 1. PROSITE; PS00135; TRYPSIN SER; 1. PROSITE; PS00135; TRYPSIN SER; 1. Plasminogen activation; Hydrolase, Serine protease; Glycoprotein; Plasminogen activation; PROBABLE.
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TISSUE-TYPE PLASMINOGEN ACTIVATOR A
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InterPro; 1900.231, Chymotrypsin.
InterPro; 1900.0029; EGF 11ke.
InterPro; 1900.003; Fibractal.
InterPro; 1900.003; Fibractal.
InterPro; 1900.0001; Kringle.
InterPro; 1900.0001; Kringle.
InterPro; 1900.0001; Kringle.
Ffam; PF00.003; Ff1; 1.
Pfam; PF00.003; Ff1; 1.
Pfam; PF00.003; Kringle; 2.
Pfam; PF00.003; Kringle; 2.
PRINTS; PR0.0125; KRINGLE.
PRODOM; PD00.0395, KRINGLE.
PRODOM; PD00.0395, KRINGLE.
SWART; SW0.0181; EGF; 1.
SWART; SW0.0181; KRINGLE.
PROSITE; PS0.0022; EGF=1; 1.
PROSITE; PS0.022; EGF=1; 1.
PROSITE; PS0.022; FIBF.DE.
PDD.PROSITE; PS0.023; FIBF.DE.
PD.PROSITE; PS0.023; FIBF.DE.
PD.PROSI
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EMBL; A19618; CAA01482.1;
PIR; A35029; A35029.
                                                                                                                            AAA42261.1;
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                                                                                                      M31188;
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       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                    335 AD----PQWKT-DSCQGDSGGPLVCSLQGRMTLTGIVSWGRGCALKDKPGVYTRVSHFL 388
                                                                                                                                                                  494 GDTRSGGPQANLHDACQGDSGGPLVCLNDGRMTLVGIISWGLGCGQXDVPGVYTKVTNYL 553
376 YRVVPGEEEQKFEVEKYIVHKEFDDDT--YDNDIALLQLKSDSSRCAQESSVVRTVCLPP 433
                                            275 MYNDPQFGTSCEITGFGKENSTDYLYPEQLKMTVVKLISHRECQQPHYYGSEVTTKMLCA 334
                                                                                         434 ADLQLPDWTECELSGYGKHEALSPFYSERLKEAHVRLYPSSRCTSQHLLNRTVTDNMLCA 493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-90130448; PubMed=2105315;
MEDLINE-90130448; PubMed=2105315;
MEDLINE-90130448; PubMed=2105315;
MEDLINE-90130448; PubMed=2105315;
MEDLINE-90130448; PubMed=2105315;
MEDLINE-90130448; PubMed=2105315;
MEDLINE Specific sequence divergences in the promoter predict differences in regulation of gene expression.";
MEDLINE 10 regulation of gene expression.";
MEDLINE 10 PLASMIN BY HYDROLYZING A SINGLE ARG-VAL BOND IN PLASMINOGEN TO PLASMIN MEDLING PLASMIN-MEDIATED PROTEOLYSIS; IT PLAYS AN IMPORTANT ROLE IN TISSUE REMODELING AND DEGRADATION, IN CELL MIGRATION AND MANY OTHER PHYSIOPATHOLOGICAL EVENTS.

-:-CATALYTIC ACTIVITY: Specific cleavage of Arg-|-Val bond in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PUBLICATION SCALED FOR STRANGED LAW.

PIN: THE SINGLE CHAIN ALMOST FULLY ACTIVE ENZYME, CAN BE FURTHER PROCESSED INTO A TWO-CHAIN FULLY ACTIVE FORM BY A CLEAVAGE AFTER ACG-308 CATALYZED BY PLASHIN, TISSUE KALLIKKEIN OR FACTOR XA.

MISCELLANEOUS: BINDS TO THE KINGLE STRUCTURE OF THE FIBRIN A CHAIN. BINDING TO FIBRIN ENHANCES ITS CATALYTIC ACTIVITY.

SIMILARITY: CELONIS TO PEPTIDASE FAMILY SI.

SIMILARITY: CONTAINS I EGF-TIKE domain.

SIMILARITY: Contains I fibronectin type I domain.

SIMILARITY: Contains 2 kringle domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rattus norvegicus (Rat).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi; Muridae, Murinae, Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               plasminogen to form plasmin.
SUBUNIT: HETERODIMER OF CHAIN A AND CHAIN B HELD BY A DISULFIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                             01-FEB-1991 (Rel. 17, Created)
01-NOV-1991 (Rel. 20, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Tissue-type plasminogen activator precursor (EC 3.4.21.68) (tPA)
(t-ph) (t-plasminogen activator).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE=89170114; PubMed=3148445;
NY T., Leonardsson G., Hsueh A.J.W.;
"Cloning and characterization of a cDNA for rat tissue-type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBCELLULAR LOCATION: SECRETED; EXTRACELLULAR
                                                                                                                                                                                                                                                                                                                                                                                                     559 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; M23697; AAA41812.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     plasminogen activator.";
DNA 7:671-677(1988).
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554 DWIRDNMR 561
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SIMILARITY).

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65; Mismatches 143; Indels 105; Gaps 12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           487 NMLCAGDTRIGGNQDVHDACQGDSGGPLVCMIDKRMILLGIISWGLGCGQKDVPGIYIKV 546
                                                                                                                                                                                                                                                                                      74 QCHSVPVRSCSEPRCFNGGTCQQALYFSDF-VCQCPDGFVGKRCDIDTRATCFEGQGITY 132
                                                                                                                                                                                                                                                                                                                             59 RGKASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYV-QV 117
                                                                                                                                                                                                                                                                                                                                                   118 GL------KPLVQECMV-----128
                                                                                                                                                                                                                                                                                                                                                                                                                                               193 GKYTTEFCSTPACPKGPTEDCYVGKGVTYRGTHSFTTSKASCLPWNSMILIGKTYTAWRA 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         129 ------CGQKTLR-PRFKIIGG 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 253 NSQALGLGRHNYCRNPDGDAKFWCHVMKDRKLTWEYCDMSPCSTCGLRQXXQPQFRIKGG 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          155 EFTTIENOPWFAAIY-RRHRGGSVTYVCGGSLISPCWVISATHCFIDYPKKEDYIVYLGR 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               313 LFTDÍTSHÞWQAAIFVKOKKRSPGERFLÖGGVLÍSSÖMVLSAAHÖFVERFPPHHLKVVLGR 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         214 SRINSNTQGEMKFEVENLILHKDYSADTLAHHNDIALLKIRSKEGRCAQPSRTIQTICLP 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          274 SMYNDPQF----GTSCEITGFGKENSTDYLYPEQLKMTVVKLISHRECQQPHYYGSEVTT 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                330 KMLCAADP-----QWKTDSCQGDSGGPLVCSLQGRMTLTGIVSWGRGCALKDKPGVYTRV 384
                                                                                                                                                                                                                                            3 ELHQVP----SNCDCLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFY 58
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01-FBB-1996 (Rel. 33, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
Salivary plasminogen activator alpha 1 precursor (EC 3.4.21.68) (DSPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Salivary gland;
MEDLINE=92039036; PubMed=1937019;
Kraetzschmar J., Hendler B., Langer G., Boidol W., Bringmann P.,
Alagon A., Donner P., Schleuning W.D.;
"The plasminogen activator family from the salivary gland of the
vamplire bat Desmodus rotundus: cloning and expression.";
[2]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Desmodus rotundus (Vampire bat).
Eukaryota; Meteazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Chiroptera; Microchiroptera; Phyllostomidae;
Desmodontinae; Desmodus.
BY SIMILARITY.
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BY SIMILARITY.
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
E -> K (IN REF. 1).
TDBD3809C1DIC921 CRC64;
                                                                                                                                                                DB 1; Length 559;
                                                                                                                                                                37.3%; Score 841.5; DB 1
36.5%; Pred. No. 1.5e-59;
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                                                                                                                          62903 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                547 TNYLNWIQDNMKQ 559
                                                                                                                                                                                                         Matches 180; Conservative
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380
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559 AA;
                                                                                                                                                                                        Similarity
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80 HTVPVNSCSEPRCFNGGTCWQAVYFSDF-VCQCPAGYTGKRCEVDTRATCYEGQGVTYRG 138
                                                                                           61 KASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVGLK 120
                                                                                                                                                                           199 FTSESCSVPVCS----KATCGLRKYKEPQLHSTGGLFTDITSHPWQAAIFAQNRRSSGER 254
                                                                                                                                                                                                                              121 PLVQECMVHDCADGKLKFQCG-QKTLRPRFKIIGGEFTTIENQPWFAAIYRRHRGGS-VT 178
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MCDINE-22388257; PubMed=12477932;

MCDINE-22388257; PubMed=12477932;

MCDINE-22388257; PubMed=12477932;

MCDINE-22388257; PubMed=12477932;

MCDINE-22388257; PubMed=12477932;

MCDINE-22388257; PubMed=12477932;

MCDINES R.D., Colling P.E., McGree L., Shemmen C.M., Schuler G.D.,

MCDINES R.D., Colling P.E., McGree T., Max S.I., Wang J., Hatch N.K.,

MCDINES M. M. Moore T., Max S.I., Wang J., Hatch F.,

MCDINES M. M. M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

MCDINES M. M. Woldin T.B., Toshhyuki S., Carninci P., Prange C.,

MCDOMSTein M.J., Woldin T.B., Toshhyuki S., Carninci P., Prange C.,

MCDINES M. Wolden P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

MCDINES M. Morley M., Sodergree E.J., Lu X., Gibbs R.A.,

MILANG M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

MILLING M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

MCDING M., McGreen E.D., Dickson M.C.,

MCDING M., McGreen E.D., McKern M.,

MCDING M., MCGREEN M.,

MCDING M., MCC,

                                                                                                             179 YVCGGSLISPCWVISATHCFIDYPKKEDYI-----VYLGRSRLNSNTQGEMKFEVENLIL
                                  HQVPSN-CD---CLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFYRG
                                                                                                                                                                                                                                                                        234 HKDYSADTLAHHNDIALLKIRSKEGRCAQPSRTIQTICLPSMYNDPQFGTSCEITGFGKE
                                                                                                                                                                                                                                                                                          368 KSSSPFYSEQLKEGHVRLYPSSRCAPKFLFNKTVTNNMLCAGDTRSGELYPNVHDACQGD
                                                                                                                                                                                                                                                                                                                                294 NSTDYLYPEQLKMTVVKLISHRECQOPHYYGSEVTTKMLCAADPQWKT-----DSCQGD
      29; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE=88087303; PubMed=2826484;
Rickles R.J., Darrow A.L., Strickland S.;
Molecular cloning of complementary DNA to mouse tissue plasminogen activator mRNA and its expression during F9 teratocarcinoma cell differentiation ";
J. Biol. Chem. 263:1563-1569(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TPA_MOUSE STANDARD; PRT; 559 AA.
P11214, Q91vp2,
01-dUL-1999 (Rel. 11, Created)
15-SEP-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Tissue-type plasminogen activator precursor (EC 3.4.21.68) (tPA)
(t-PA) (t-plasminogen activator)
                                                                                                                                                                                                                                                                                                                                                                                             348 SGGPLVCSLQGRMTLTGIVSWGRGCALKDKPGVYTRVSHFLPWIRSH 394
                                                                                                                                                                                                                                                                                                                                                                                                             428 SGGPLVCMNDNHMTLLGIISWGVGCGEKDVPGVYTKVTNYLGWIRDN 474
       56; Mismatches 147; Indels
      175; Conservative
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      Matches
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                 SALIVARY PLASMINOGEN ACTIVATOR ALPHA 1. FIBRONECTIN TYPE-I.
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N-LINKED (GLCNAC. .).
/FTId=CAR_000028.
                                                                                        RELAY SYSTEM.
RELAY SYSTEM.
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                                                                        SERINE PROTEASE.
CHARGE RELAY SYST
CHARGE RELAY SYST
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BY SIMILARITY.
                                                           KRINGLE
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477 AA;
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477;

Score 840.5; DB 1; Length Pred. No. 1.5e-59;

37.2%;

Query Match Best Local Similarity

427

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Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S., 99:16899-16903 (2002).
-!- FUNCTION: CONVERTS THE ABUNDANT, BUT INACTIVE, ZYMOGEN PLASMINOGEN TO PLASMIN BY HYPROLYZING A SINGLE RAG-VL BOND IN PLASMINOCEN. BY CONTROLLING PLASMIN-MEDIATED PROTECLYSIS, IT PLAYS AN IMPORTANT ROLE IN TISSUE REMODELING AND DEGRADATION, IN CELL MIGRATION AND MANY OTHER PHYSIOPRAPHOLOGICAL EVENTS.
-!- CATALYTIC ACTIVITY: Specific cleavage of Arg-|-Val bond in plasminogen to form plasmin.
-!- SIBMINIT: HETERODIMER OF CHAIN A AND CHAIN B HELD BY A DISULFIDE
                                                                                                                                              BUBCELLULAR LOCATION: SECRETED; EXTRACELLULAR.

FUND: THE SINGLE CHAIN, ALMOST FULLY ACTIVE ENZYME, CAN BE FURTHER PROCESSED INTO A TWO-CHAIN FULLY ACTIVE FORM BY A CLEAVAGE AFTER ARC-308 CATALYZED BY PLASMIN, TISSUE KALLIKREIN OR FACTOR XA.

MISCELLANEGUS: BINDS TO THE KRINGLE STRUCTURE OF THE FIBRIN A SIMILARITY: DELONGS TO PERTINASE FAMILY SI.

SIMILARITY: CONTAINS I EGR-11ke domain.

SIMILARITY: Contains 1 fibronectin type I domain.

SIMILARITY: Contains 2 kringle domains.
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PLASMINOGEN ACTIVATOR
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FIBRONECTIN TYPE-I.
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TISSUE-TYPE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      193 GKYTTEFÖSTPACPKGKSEDCYVGKGVTYRGTHSLTTSQASCLPANSIVLMGKSYTAWRT 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            213
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SMYNDPQF----GISCELIGEGKENSTDYLYPEQLKMTVVKLISHRECQQPHYYGSEVTT 329
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            74 QCHSVPVRSCSEPRCFNGGTCQQALYFSDF-VCQCPDGFVGKRCDIDTRATCFEEQGITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ELHQVP----SNCDCLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                119 LKPLVQECMVHDCADGKLK-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----FQCG-QKTLRPRFKIIGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 155 BFTTIENQPWFAAIY-RRHRGGSVTYVCGGSLISPCWVISATHCFIDYPKKEDYIVYLGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    214 SRLNSNTQGEMKFEVENLILHKDYSADTLAHHNDIALLKIRSKEGRCAQPSRTIQTICLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      373 TYRVVPGEEEQTFEIEKXIVHEEFDDDT--YDNDIALLQLRSQSKQCAQESSSVGTACLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               431 ----DPNLQLPDWİECELSGYGKHEASSPFFSDRLKEAHVRLYPSSRCTSQHLFNKTVTN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          330 MALCAADP-----QWKTDSCQGDSGGPLVCSLQGRMTLTGIVSWGRGCALKDKPGVYTRV
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-> A (IN REF. 1)
  EGF-LIKE.
KRINGLE 1.
KRINGLE 2.
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260
325
63122 MW,
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Matches 175; Conservative
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RESULT 14 TPA_BOVIN

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                                                                                                                                                                                                                                                                                                                                                        Int. Dairy J. S:605-617(1995).

-!- FUNCTION: CONVERTS THE ABUNDANT, BUT INACTIVE, ZYMOGEN PLASMINOGEN

-!- FUNCTION: CONVERTS THE ABUNDANT, BUT INACTIVE, ZYMOGEN PLASMINOGEN

TO PLASMIN BY HYDROLYZING A SINGLE ARG-VAL BOND IN PLASMINOGEN. BY
CONTROLLING PLASMIN-MEDIATED PROTECLYSIS, IT PLAYS AN IMPORTANT

ROLE IN TISSUE REMODELING AND DEGRADATION, IN CELL MIGRATION AND
MANY OTHER PHYSIOPATHOLOGICAL EVENTS.

-!- CATALYTIC ACTIVITY: Specific cleavage of Arg-|-Val bond in
plasminogen to form plasmin.

-!- SUBUNIT: HETERODIMER OF CHAIN A AND CHAIN B HELD BY A DISULFIDE
                                                                                                                                                                                                                                                                                                     Ravn P., Berglund L., Petersen T.E.;
"Cloning and characterization of the bovine plasminogen activators uPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BURNEL.

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PULI ACTIVE ENZYME, CAN BE FURTHER

RECESSED INTO.

A TWO-CHAIN FULLY ACTIVE FORM BY A CLEAVAGE AFTER

ARG-314 CATALYZED BY PLASHIN, TISSUE KALLIKREIN OR FACTOR XA.

MISCELLANEOUS BINDS TO THE KRINGLE STRUCTURE OF THE FIBRIN A

SIMILARITY: BELONGS TO PEPTIONSE FAMILY S1.

SIMILARITY: COntains I EGF-like domain.

SIMILARITY: Contains I fibronectin type I domain.

SIMILARITY: Contains 2 kringle domains.
                                                                                                                                                 Bos taurus (Bovine).
Sukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
      01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Tissue-type plasminogen activator precursor (EC 3.4.21.68) (tPA)
(t-PA) (t-plasminogen activator).
  566 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR001314, Chymotrypsin.
InterPro; IPR001314, Chymotrypsin.
InterPro; IPR00003; Fibrnctnl.
InterPro; IPR006510; IEGF.
InterPro; IPR00001; Kringle.
InterPro; IPR00001; Kringle.
Pfam; PF00008; EGF; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ä
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PEAM, PRO0069; KTYDSID, 1.
PRINTS; PRO0122; CHYMOTRYPSIN.
PRINTS; PRO0129; KRINGLE.
PRODOM; PD000395; KRINGLE.
SWART; SM00181; EGF; 1.
SWART; SM00181; EGF; 1.
SWART; SM00180; KR; 2.
SWART; SM00130; KR; 2.
PROSITE; PS01186; EGF 1; 1.
PROSITE; PS01186; EGF 2; 1.
PROSITE; PS01186; EGF 2; 1.
PROSITE; PS01186; EGF 2; 1.
PROSITE; PS01186; EGF 2; 1.
PROSITE; PS01186; EGF 2; 1.
PROSITE; PS01186; EGF 2; 1.
PROSITE; PS01186; EGF 2; 1.
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STANDARD;
                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
TISSUE=Kidney;
                                                                                                                                                                                                                          NCBI_TaxID=9913;
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TPA_BOVIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ------DGKLKFQ-----CG-QKTLRPRFKII 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGLFADITSHPWQAAIFVKNRRSPGERFLCGGILISSCWVLSAAHCFQERYPPHHLKVFL 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GRSRLNSNTQGEMKFEVENLILHKDYSADTLAHNDIALLKIRSKEGRCAQPSRTIQTIC 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LPSMYNDPQFGTSCEITGFGKENSTDYLYPEQLKMTVVKLISHRECQQPHYYGSEVTTKM 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            435 LPDASLQLPDWTECELSGYGKHESSSPFFSERLKEAHVRLYPSSRCTSQHLFNRTVTNNM 494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QCHSVPVRSCSEPWCFNGGTCRQALYSSDF-VCQCPEGFMGKLCEIDATATCYKDQGVAY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ELHQVP-SNCD----CLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          197 GKYISEFCSTPACAKVAEEDGDCYTGNGLAYRGTRSHTKSGASCLPWNSVFLTSKIYTAW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGEFITIENQPWFAAIY-RRHRGGSVTYVCGGSLISPCWVISATHCFIDYPKKEDYIVYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 36.1%; Score 814; DB 1; Length 566;
35.8%; Pred. No. 2.4e-57;
iive 60; Mismatches 155; Indels 100; Gaps
PROSITE; PS50240; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN HIS; 1.
PROSITE; PS00135; TRYPSIN SER; 1.
Plasminogen activation; Hydrolase; Serine protease; Glycoprotein; Plasma; Kringle; EGF-like domain; Repeat; Signal.
SIGNAL
PROPER
2 33 BY SIMILARITY.
PROPER
2 33 BY SIMILARITY.
                                                                                                   TISSUE-TYPE PLASMINOGEN ACTIVATOR.
TISSUE-TYPE PLASMINOGEN ACTIVATOR A
                                                                                                                                           TISSUE-TYPE PLASMINOGEN ACTIVATOR B CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
                                                                                                                                                                                                                                                             CHARGE RELAY SYSTEM.

GRANGE RELAY SYSTEM.

BY SIMILARITY.

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CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
                                                                                                                                                                      FIBRONECTIN TYPE-I
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BY SIMILARITY.
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KRINGLE 1.
KRINGLE 2.
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Best Local Similarity 35.8<sup>1</sup>
Matches 176; Conservative
                                                                                       33
566
314
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153
487
566 AA;
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LCAADPQW-----KTDSCQGDSGGPLVCSLQGRMTLTGIVSWGRGCALKDKPGVYTRVS 385
                   495 LCAGDTRSGGDHTNLHDACQGDSGGPLVCMKDNHMTLVGIISWGLGCGRKDVPGVYTKVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Donner P.;
"Plasminogen activators from the saliva of Desmodus rotundus (common vample bat): unique fibrin specificity.";
Ann. N.Y. Acad. Sci. 67:305-403(1992)
-i- FUNCTION: PROBABLY ESSENTIAL TO SUPPORT THE FEEDING HABITS OF TH
                                                                                                                                                                       01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Salivary plasminogen activator gamma precursor (EC 3.4.21.68) (DSPA
                                                                                                                                                                                                                                                                                                                                   TISSUE=Salivary gland;
MEDLINE=92039036; PubMed=1937019;
Kretzschmar J., Haendler B., Langer G., Boidol W., Bringmann P., Alagon A., Donter P., Schleuning W.D.;
"The plasminogen activator family from the salivary gland of the vampire bat Desmodus rotundus: cloning and expression.";
                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Chiroptera, Microchiroptera, Phyllostomidae,
Desmodontinae, Desmodus.
                                                                                                                                                                                                                                                                                                                                                                                                                                            CHARACTERIZATION.
MEDLINE-93393059; PubMed=1309059;
Schleuning W.-D., Alagon A., Boidol W., Bringmann P., Petri T.,
Kraetzschmar J., Haendler B., Langer G., Baldus B., Witt W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CATALYTIC ACTIVITY: Specific cleavage of Arg-|-Val bond in plasminogen to form plasmin. SUBUNIT: Monomer. SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. SIMILARITY: Contains 1 kringle domain.
                                                                                                                                                  394 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR01314; Chymotrypsin.
InterPro; IPR000001; Kringle.
InterPro; IPR01254; Ser_protease_Try.
Pfam; PF00051; Kringle; I.
Pfam; PF00089; trypsin; I.
                                                                                                                                                 PRT;
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PRINTS; PR00018; KRINGLE.
ProDom, PD000395; Kringle; 1.
SWART; SM00130; KR; 1.
SWART; SM00020; Tryp SPC; 1.
PROSITE; PS00021; KRINGLE_1; 1.
                                                                                                                                                                                                                                            Desmodus rotundus (Vampire bat).
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                                                                        NYLDWIRDNTR 565
                                                    HFLPWIRSHTK 396
                                                                                                                                                 STANDARD;
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HSSP; P98119; 1A5I.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     282 GISCEITGFGKENSTDYLYPEQLKMTVVKLISHRECQQPHYYGSEVTTKMLCAADPQWKT 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      342 -----DSCOGDSGGPLVCSLOGRMTLTGIVSWGRGCALKDKPGVYTRVSHFLPWIRSHT 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          333 IYPNVHDACQGDSGGPLVCMNDNHMTLLGIISWGVGCGEKDIPGVYTKVTNYLGWIRDNM 392
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   222 GEMKFEVENLILHKDYSADTLAHHNDIALLKIRSKEGRCAQPSRTIQTICLFSMYNDPQF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DPHATCYKDOGVTYRGTWSTSESGAQCINWNSNLLIRRTYNGRMPEAVKLGLGNHNYCRN
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CHARGE RELAY SYSTEM (BY SIMILARITY).
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N-LINKED (GICNAC...) (POTENTIAL).
                                                                                                                   SALIVARY PLASMINOGEN ACTIVATOR GAMMA
                                                                  Plasminogen activation; Hydrolase; Serine protease; Glycoprotein;
Kringle; Signal; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryoca, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606,
                                                                                                                                                                                                                                                                                                                                                                                                                                                         16;
                                                                                                                                                                                                                                                                                                                                                                                                                        Length 394;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HGPA_HUMAN STANDARD; PRT; 655 AA.
004756; 014726;
01-UNN-1994 (Rel. 29, Created)
01-UNN-1994 (Rel. 29, Last sequence update)
48 FFBE-2003 (Rel. 41, Last annotation update)
Hepatocyte growth factor activator precursor (EC 3.4.21.-)
                                                                                                                                                                                                                                                                                                                                                                                                                   Score 756; DB 1; Length 39
Pred. No. 6.4e-53;
6; Mismatches 134; Indels
                                                                                                                                                                                                                                                                                                                                                                     -LINKED (GLCNAC. . .) (POSCEDEFSZER)
                                                                                                     POTENTIAL.
                                                                                                                                     KRINGLE
PSS0070; KRINGLE 2; 1.
PSS0240; TRYPSIN_DOM; 1
PS00134; TRYPSIN_HIS; 1
PS00135; TRYPSIN_SER; 1
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190
251
351
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1126
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                                                                                                                                                                                                                                                                                                                                                                   315 ;
394 AA;
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                                               PROSITE;
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DOMAIN
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                                                                                                                                                CLEAVED IN ACTIVE FORM. HEPATOCYTE GROWTH FACTOR ACTIVATOR SHORT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               293 GYRGVASTSASGLSCLAWNSDLLYQELHVDSVGAAALLGLGPHAYCRNPDNDERPWCYVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5 HQVPSNCDCLNGGTCVSNKYFSNIHW------CNCPKKFGGQHCEIDKSKTCYEGNGH
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PROSITE; PS50070; KRINGLE 2; 1.

PROSITE; PS50240; TRYPSIN_DOM; 1.

PROSITE; PS00134; TRYPSIN_HIS; 1.

PROSITE; PS00135; TRYPSIN SE; 1.

Hydrolase; Glycoprocein; Flasma; Serine protease; Kringle; Signal; EGF-like domain; Repeat; Zymogen.

EGF-like domain; Repeat; Zymogen.

I 30 CLEAVED IN ACTIVE FORM.

CHAIN 373 407 HEPATOCYTE GROWTH FACTOR ACTIVATOR SHG
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SIMILARITY).
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EGF-LIKE 1.
FIBRONECTIN TYPE-I.
EGF-LIKE 2.
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LCAADPQWKTDSCQGDSGGPLVCSLQGRMTLTGIVSWGRGCALKDKPGVYTRVSHFLPWI 391
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Van Adelsberg J.S., Sehgal S., Kukes A., Brady C., Barasch J.,
Van Adelsberg J.S., Sehgal S., Kukes A., Brady C., Barasch J.,
Van J., Huan v.;

"Activation of HGF by endogenesis in vitro.";

"Activation of HGF by endogenesis in vitro.";

Submitted (JAN-2000) to the EMBL/Genebank/DDBJ databases.

-: FUNCTION: ACTIVATES HEAPTOCYTE GROWTH FACTOR (HGF) BY CONVERTING.

-: FUNCTION: ACTIVATES HEAPTOCYTE GROWTH FACTOR (HGF) BY CONVERTING.

-: SUBUNIT: DIMER OF A SHORT CHAIN AND A LONG CHAIN LINKED BY A DISULFIDE BOND (BY SIMILARITY).

-: SUBCELLULAR LOCATION: SECRETED AS AN INACTIVE SINGLE-CHAIN PRECURSOR AND IS THEN ACTIVATED TO A HETERODIMERIC FORM (BY PRECURSOR AND IS THEN ACTIVATED TO A HETERODIMERIC FORM (BY PRECURSOR AND IS THEN ACTIVATED TO A HETERODIMERIC FORM (BY PROCESSED).
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                          HGFA MOUSE STANDARD, PRT, 653 AA.
Q9R088; Q9XKV4;
16-0CT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
4 Hepatocyte growth factor activator precursor (EC 3.4.21.-) (HGF HGFAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=BALB/c;
ltoh H., Kataoka H., Koono H.;
"Mouse hepatroyte growth factor activator.";
Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
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SIMILARITY: Contains 2 EGF-11ke domains.
SIMILARITY: Contains 1 fibronectin type I domain.
SIMILARITY: Contains 1 fibronectin type II domain.
SIMILARITY: Contains 1 kringle domain.
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InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001314; Chymotrypsin.
InterPro; IPR006209; EGF_1:e.
InterPro; IPR000683; Fibrnch1.
InterPro; IPR000662; FYTye_II.
InterPro; IPR006210; IEGF.
InterPro; IPR00101; Kringle.
InterPro; IPR01254; Ser_Drotease_Try.
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PROSITE; PS00021; KRINGLE 1; I.
PROSITE; PS00021; KRINGLE 2; 1.
PROSITE; PS50240; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN HIS; 1.
PROSITE; PS00134; TRYPSIN HIS; 1.
PROSITE; PS00135; TRYPSIN HIS; 1.
PROSITE; PS00136; TRYPSIN HIS; 1.
EGF-Like domain; Repeat; Zymogen.
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FIBRONECTIN TYPE-I.
EGF-LIKE 2.
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SMART; SM01019; EGF; 2.
SMART; SM0019; EN2; 1.
SMART; SM00130; KR; 1.
SMART; SM00130; Tryp SPc; 1.
PROSITE; PS01022; EGF[1, 2.
PROSITE; PS01025; FIBRONECTIN_1; 1.
PROSITE; PS01025; FIBRONECTIN_1; 1.
PROSITE; PS00023; FIBRONECTIN_1; 1.
PROSITE; PS00023; KRINGLE 1; 1.
PROSITE; PS00013; KRINGLE 1; 1.
Pfam; PF00008; EGF; 2.
Pfam; PF00039; fin; 1.
Pfam; PF00040; fin2; 1.
Pfam; PF00051; kringle; 1.
Pfam; PF00089; trypsin; 1.
PRINTS; PR00122; CHYMCTRYPSIN.
PRINTS; PR0013; FNTYPEII.
PRINTS; PR0013; FNTYPEII.
PRODOM; PD000995; FN TRINGE.
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     MEDLINE=93003567; PubMed=1390917;
Semba U., Yamamoto T., Kunisada T., Shibuya Y., Tanase S.,
Nambara T., Okabe H.;
Nambara T., Okabe H.;
Trimary structure of guinea-pig Hageman factor: sequence around the cleavage site differs from the human molecule.";
Blochim: Blochim: Blochim: Blochim: Blochim: Blochim: Blochim: Blochim: Blochim: Blochim: Blochim: Blochim: Blochim: Blochim: Blochim: Blochim: Blochim: Blochim: Blochim: Blochim: Blochim: Blochim: Blochim: Blochim: Blochim: Blochim: Blochim: Blochim: Blochim: Blochim: Blochim: Blochim: Blochim: Blochim: Blochim: Blochim: Blochim: Blochim: Blochim: Blochim: Blochim: Blochim: Blochim: Blochim: Blochim: Blochim: Blochim: Blochim: Blochim: Blochim: Blochim: Blochim: Blochim: Blochim: Blochim: Blochim: Blochim: Blochim: Blochim: Blochim: Blochim: Blochim: Blochim: Blochim: Blochim: Blochim: Blochim: Blochim: Blochim: Blochim: Blochim: Blochim: Blochim: Blochim: Blochim: Blochim: Blochim: Blochim: Blochim: Blochim: Blochim: Blochim: Blochim: Blochim: Blochim: Blochim: Blochim: Blochim: Blochim: Blochim: Blochim: Blochim: Blochim: Blochim: Blochim: Blochim: Blochim: Blochim: Blochim: Blochim: Blochim: Blochim: Blochim: Blochim: Blochim: Blochim: Blochim: Blochim: Blochim: Blochim: Blochim: Blochim: Blochim: Blochim: Blochim: Blochim: Blochim: Blochim: Blochim: Blochim: Blochim: Blochim: Blochim: Blochim: Blochim: Blochim: Blochim: Blochim: Blochim: Blochim: Blochim: Blochim: Blochim: Blochim: Blochim: Blochim: Blochim: Blochim: Blochim: Blochim: Blochim: Blochim: Blochim: Blochim: Blochim: Blochim: Blochim: Blochim: Blochim: Blochim: Blochim: Blochim: Blochim: Blochim: Blochim: Blochim: Blochim: Blochim: Blochim: Blochim: Blochim: Blochim: Blochim: Blochim: Blochim: Blochim: Blochim: Blochim: Blochim: Blochim: Blochim: Blochim: Blochim: Blochim: Blochim: Blochim: Blochim: Blochim: Blochim: Blochim: Blochim: Blochim: Blochim: Blochim: Blochim: Blochim: Blochim: Blochim: Blochim: Blochim: Blochim: Blochim: Blochim: Blochim: Blochim: Blochim: Blochim: Blochim: Blochim: B
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HTACLSSPCLNGGTC-----HLIVGTGTSVCTCPLGYAGRFCNIVPTEHCFLGNGT 289
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                                               FYRGKASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQ 116
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Sukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Hystricognathi, Caviidae, Cavia.
NCBI_TaxID=10141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Coaquiation factor XII precursor (EC 3.4.21.38) (Hageman factor)
(HAF) (Fragment).
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the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Glycoprotein; Blood coagulation; Plasma; Kringle; Serine protease; Hydrolase; Fibrinolygis; EGF-like domain; Repeat; Zymogen; Signal. Non TER 1 18 ALPHA-PACTOR XIIA HENNY CHAIN CHAIN
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ALPHA-FACTOR XIIA LIGHT
FIBRONECTIN TYPE-II.
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InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001881; EGF_Ca.
InterPro; IPR001881; EGF_Ca.
InterPro; IPR000083; Fib_nctn1.
InterPro; IPR000083; Fib_nctn1.
InterPro; IPR000082; Fib_nctn1.
InterPro; IPR0001254; Fib_nctn1.
InterPro; IPR001254; Ser_protease_Try.
Pfam; PF00008; EGF; 2.
Pfam; PF00008; fn1; 1.
Pfam; PF00008; fn1; 1.
Pfam; PF00089; fn1; 1.
Pfam; PF00089; trypsin; 1.
PRINTS; PR00013; KRINGLE.
PRODOM; PD000995; KRINGLE.
PRODOM; PD000995; KRINGLE.
PRODOM; PD000995; KRINGLE.
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PRO-RICH.
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SWART; SM00181; EGF; 2;
SWART; SM00180; RN; 1;
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SWART; SM00180; RN; 1;
PROSITE; PRO1186; EGF 2; 1;
PROSITE; PRO10186; EGF 2; 1;
PROSITE; PRO10186; EGF 2; 1;
PROSITE; PRO0021; KRINGLE: 1; 1;
PROSITE; PRO10186; EGF 2; 1;
PROSITE; PRO0013; FIRROLE: 2; 1;
PROSITE; PRO10186; EGF 2; 1;
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N-LINKED (GLORAC. ..) (POTENTIAL).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
111. TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=88007593; PubMed=2888762;
Cool D.E., McGillivray R.T.A.;
"Characterization of the human blood coagulation factor XII gene.
Intron/exon gene organization and analysis of the 5'-flanking
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FA12_HUMAN STANDARD; PRT; 615 AA.
P00748 P78339;
21_UUL-1966 (Rel. 01, Created)
01-OCT-1989 (Rel. 12, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
(Coagulation factor XII precursor (EC 3.4.21.38) (Hageman factor)
(HAF).
                                                                                                                                                                                                   69;
                                                                                                                                                             31.0%; Score 700.5; DB 1; Length 603; 36.7%; Pred. No. 2.7e-48;
                                                                                                                                                                                               60; Mismatches 147; Indels
                                                                                                                             48DC6B946FB9ED59 CRC64;
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structure of beta-factor XIIa.";
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MEDLINE=94325559; PubMed=8049433;
Hovinga J.K., Schaller J., Stricker H., Wuillemin W.A., Furlan
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Cool D.E., Edgell C.-J.S., Louie G.V., Zoller M.J., Brayer G.
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MEDLINE=90046788; PubMed=2510163;
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MEDLINE=99290785; PubMed=10361128;
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SEQUENCE OF 146-615 FROM N.A.
MEDLINE=86216049; PubMed=3011063; Que B.G., Davie E.W.;
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SEQUENCE OF 4-615 FROM N.A.
MEDLINE=86176794; PubMed=3754331;
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McGillivray R.T.A.;
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The sector XII Tenri, a novel cross-reacting material negative factor XII

deficiency, occurs through a proteasome-mediated degradation.";

Blood 93:4300-4308(1999)

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THE INITIATION OF BLOOD COAGULATION, FIBRINOLYSIS, AND THE CHARATION OF BRADYKININ AND ANGIOTENNIN.

CHARALYTIC ACTIVITY: Cleaves selectively Actor Xia.

VII to form factor VIIa and factor XI to form factor XIa.

CHARALYTIC ACTIVITY: CLEAVES Selectively Actor Xia.

CHARALYTERS IN F12 DO NOT CAUSE ANY CLINICAL SYMPTOMS. THE SOLE EFFECT IS THAT WHOLE-BLOOD CLOTTING TIME IS PROLINGED.

CHOPPIES BOUND TO AN ANIONIC SURFACE. PREMALIKERIN IS CLEAVED BY FACTOR XII TO FORM KALLIKERIN, WHICH THEN CLEAVES FACTOR XII FIRST TO ALPHA-FACTOR XIIA. AND THEN TO BETA-FACTOR XIIA. ALPHA-FACTOR XIA.

CHARALYTY: CONTAINS I GIDEODECTIN TYPE II domain.

CHARALYTY: Contains I fibronectin type II domain.

CHARALYTY: Contains I Kingle domain.
                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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PROSITE; PS50070; KRINGLE 2; 1.
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CHAIN 373 615 ALPHA-FACTOR XIIA HEAVY CHAIN.
CHAIN 354 362 BETA-FACTOR XIIA PART 1.
CHAIN 373 615 BETA-FACTOR XIIA PART 2.
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C-LINKED RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
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ALPHA-FACTOR XIIA LIGHT CHAIN.
BETA-FACTOR XIIA PART 1.
FIBRONECTIN TYPE-II.
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tive 58; Mismatches 158; Indels
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                                                                                                                                                                                                     TISSUE-Liver;
MEDLINE-9424702; PubMed-8186251;
Shibuya Y., Semba U., Okabe H., Kambara T., Yamamoto T.;
Shibuya Y., Semba U., Okabe H., Kambara T., Yamamoto T.;
Shibuya Y., Semba U., Okabe H., Kambara T., Yamamoto T.;
XII): comparison with human and guinea pig molecules.";
Blochim. Blophys. Acta 1206:63-70(1994).
                                                                         Bos taurus (Bovine).
Sukaryota: Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
28-FEB-2003 (Rel. 41, Last annotation update)
Coagulation factor XII precursor (EC 3.4.21.38) (Hageman factor)
(HAF) (Fragment).
                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 10-21; 350-364 AND 525-550.
MEDIINE=77182112; Pubmed=861210;
Fujikawa K., Walsh A.K., Davie W.E.;
"Isolation and characterization of bovine factor XII (Hageman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MILEATER'S IDRO01314; Chymotrypsin.
InterPro; IPR001314; Chymotrypsin.
InterPro; IPR00003; EGF like.
InterPro; IPR000063; FIDFnctn1.
InterPro; IPR000063; FN Type_II.
InterPro; IPR000001; Kringle.
InterPro; IPR000001; Kringle.
InterPro; IPR000001; Ser_Protease_Try.
Pfam; PF00009; EGF; 2.
Pfam; PF00009; EGF; 2.
Pfam; PF00009; fn1; 1.
Pfam; PF00009; Kringle; 1.
Pfam; PF00009; Kringle; 1.
Pfam; PF00009; Kringle; 1.
Pfam; PF00009; Kringle; 1.
PRINTS; PR0012; CHYMOTRYPSIN.
PRINTS; PR0013; FNTYPEII.
PRODOM; PD0000995; FN Type_II; 1.
ProDOM; PD0000995; KINGLE.
ProDOM; PD0000995; KINGLE.
ProDOM; PD0000995; KINGLE.
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HSSP; P00763; 1DPO.
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                                                                                                                                               NCBI TaxID=9913;
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R SWART; SM00058; FN1; 1.

R SMART; SM00130; FN2; 1.

SMART; SM00130; FN2; 1.

R SMART; SM00020; Tryp_SPc; 1.

R PROSITE; PS01022; EGF_1; 2.

R PROSITE; PS01023; FIBRONECTIN 1; 1.

R PROSITE; PS00021; KRINGLE_1; 1.

R PROSITE; PS00013; KRINGLE_2; 1.

R PROSITE; PS00014; TRYPSIN DOM; 1.

R PROSITE; PS01134; TRYPSIN DOM; 1.

R PROSITE; PS01134; TRYPSIN SER; 1.

R PROSITE; PS01135; TRYPSIN SER; 1.

R PROSITE; PS01135; TRYPSIN SER; 1.

R PROSITE; PS01135; TRYPSIN SER; 1.

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34.2%; Pred. No. 2.4e-43;
ive 59; Mismatches 164; Indels
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ALPHA-FACTOR XIIA LIGHT
FIBRONECTIN TYPE-II.
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Best Local Similarity 34.2'
Matches 151; Conservative
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790 AA; 88592 MW;
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Best Local Similarity 36.2'
Matches 130; Conservative
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                                                                       MEROPS; S01.233;
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X MEDLINE-8818529; Pubmed=3356193;
A Marti T., Schaller J., Rickli E.E., Schmid K., Kamerling J.P.,
Marti T., Schaller J., Rickli E.E., Schmid K., Kamerling J.P.,
Marti T., Schaller J., Rickli E.E., Schmid K., Kamerling J.P.,
The N- and O-linked carbohydrate chains of human, bovine and porcine
The N- and O-linked carbohydrate chains of human, bovine and porcine
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                           ENZYME REGULATION: CONVERTED INTO PLASMIN BY PLASMINOGEN
ACTIVATORS, BOTH PLASMINOGEN AND ITS ACTIVATOR BEING BOUND TO
BERIN. CANNOT BE ACTIVATED WITH STREPTOKINASE.
PTW: N-LINKED GLYCAN CONTAINS N-ACETYLLACTOSAVINE, SIALIC ACID AND
IS CORE FUCOSYLATED. O-LINKED GLYCANS CONSIST OF GAL-GALNAC
DISACCHARIDE WITH IS MODIFIED WITH UP TO 2 SIALIC ACID RESIDUES
MICCOLETEROGENEITY).
MICCOLETEROGENEITY).
MICCOLLANGOUS: PLASMIN IS INACTIVATED BY ALPHA-2-ANTIPLASMIN
IMMEDIATELY AFTER DISSOCIATION FROM THE CLOT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Schaller J., Marti T., Roesselet S.J., Kaempfer U., Rickli E.E., "Amino acid sequence of the heavy chain of porcine plasmin. Comparison of the carbohydrate attachment sites with the human and bovine
                                                                                               451 CCAHPSPFVQPVCLPSTAARPAESEAAVCEVAGWGHQFEGGE-YSSFLQEAQVPLIDPQR
                                                                                                                                                                       DYPKKEDYIVYLGRSRLNSNTQGEMKFEVENLILHKDYSADTLAHHNDIALLKIR-SKEG
                                                                           RCAQPSRTIQTICLPSMYNDPQFGTS--CEITGFGKENSTDYLYPEQLKMTVVKLISHRE
                                                                                                                                                 COOPHYYGSEVITIMICAADPOWKTDSCOGDSGGPLVC---SLOGRMTLTGIVSWGRGCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Euteleostomi;
Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIINE=85203907; PubMed=3846533;
Marti T., Schaller J., Rickli E.E.;
"Determination of the complete amino-acid sequence of porcine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Mecazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae;
NCBI TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                      01-JAN-1988 (Rel. 06, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Plasminogen (EC 3.4.21.7).
                                                                                                                                                                                                                                                                                                                                                         790 AA.
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                                                                                                                                                                                                                                                                                                                                                             PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              species.";
Fibrinolysis 1:91-102(1987).
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Schaller J., Marti
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-i- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. PLASMINOGEN SUBFAMILY.
-!- SIMILARITY: Contains 5 Kringle domains.
PIR; $03733; PLPG.
HSSP, P00747; 5HPG.
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R PRINTS; PRO0722; CHYMCTREIN.
R PRINTS; PRO018; KRINGLE.
R PRINTS; PRO0180; KRINGLE.
R PROD000395; KRINGLE.
R SMART; SM00130; KR; 5.
R SMART; SM00130; KR; 5.
R SMART; SM00130; KR; 5.
R SMART; SM00120; TYPE SPC: 1.
R PROSITE; PS00121; KRINGLE.1; 5.
R PROSITE; PS0014; TRYPSIN LDG; 1.
R PROSITE; PS0014; TRYPSIN LDG; 1.
R PROSITE; PS0014; TRYPSIN LDG; 1.
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R PROSITE; PS0014; TRYPSIN LDG; 1.
R PROSITE; PS001
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KRINGLE 2.
KRINGLE 3.
KRINGLE 5.
CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
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O-LINKED (GALNAC.
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Interpro; IPR003609; Pan app.
Interpro; IPR003966; Prothrombin.
Interpro; IPR001254; Ser Protease_Try.
Pfam; PF00051; Kringle; 5.
Pfam; PF00054; PAN; 1.
Pfam; PF00089; trypsin; 1.
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                                                                                                                                                                                                                                                 GlycoSuiteDB; P66867; -.
InterPro, IPR001314; Chymotrypsin.
InterPro, IPR000001; Kringle.
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TISSUE-Liver,

Whedel1247932;

Whedel1247932;

PubMedel1247932;

Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

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A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hsieh F.,

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Fahey J., Helton B., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

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R Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

B Schain J.S., Warra M.A.,

R Schain J.S., Jones S.J.M., Marra M.A.;

R Generation and initial analysis of more than 15,000 full-length human
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MEDLINE=59647288; PubMed=7225077;

MEDLINE=59647288; PubMed=7225077;

MOSES M., Lane W.S., Cao Y., Sage E.H., Folkman J.;

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                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=129/Sv;
Brathwaite M., Waeltz P., Qian Y., Dudekula D., Schlessinger D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bannach F.G., Gutierrez A., Fowler B.J., Bugge T.H., Degen J.L.,
Parmer R.J., Miles L.A.;
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P20918; Q8CIS2; Q9IWJ5;
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15-SEP-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
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STRAIN=129/SvJ; TISSUE=Liver;
PubMed=12149246;
                                                                                                                                                                musculus (Mouse)
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FYRGKASTDIMGRPCLPWNSAIVLQQIYHAHRSDALQ----LGLGKHNYCRNPD-NRRRP 111
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its way non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- ENZYME REGULATION: CONVERTED INTO PLASMIN BY PLASMINOGEN
ACTIVATORS, BOTH PLASMINOGEN AND ITS ACTIVATOR BEING BOUND TO
FIRBIN. ACTIVATED WITH CATALYTIC AMOUNTS OF STREPTOKINASE.
-!- MISCELLANBOUS: PLASMIN IS INACTIVATED BY ALPHA-2-ANTIPLASMIN
IMMEDIATELY AFTER DISSOCIATION FROM THE CLOT.
-!- MISCELLANBOUS: IN THE PRESENCE OF THE INHIBITOR, THE ACTIVATION
INVOLVES ONLY CLEAVAGE AFTER ARG-580, RESULTING IN 2 CHAINS HELD
TOGETHER BY 2 DISULFIDE BONDS. WITHOUT THE INHIBITOR, THE
ACTIVATION INVOLVES ALSO REMOVAL OF THE ACTIVATION PEPTIDE.
-!- SIMILARITY: COLCAINS 5 Kringle domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JUBICAL CHEM. 264:5957-5965(1989).

-1. FUNCTION: PLASMIN DISSOLVES THE FIBRIN OF BLOOD CLOTS AND ACTS AS A PROTEOLYTIC FACTOR IN A VARIETY OF OTHER PROCESSES INCLUDING BRERYOMIC DEVELORMENT. TISSUE REMODELING, TUMOR INVASION, AND INFLAMMATION; IN OVULATION IT WEAKENS THE WALLS OF THE GRAAFIAN FOLLICLE. IT ACTIVATES THE UROKINASE-TYPE PLASMINOGEN ACTIVATOR, COLLAGERASES AND SEVERAL COMPLEMENT ZYMOGENS, SUCH AS CI AND CO. II CLEAVES FIBRIN, FIBRONECTIN, THROMEOSPONDIN, LAMININ AND VON WILLEBRAND FACTOR.

-1. CATALYTIC ACTIVITY: Preferential cleavage: Lys-|-xaa > Arg-|-xaa; higher selectivity than trypsin. Converts fibrin into soluble
                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
PubMed=2925643;
Tonlinson J.E., McLean J.W., Lawn R.M.;
"Rhesus monkey apolipoprotein(a). Sequence, evolution, and sites of
                                                                                                                                                                                   Macaca mulatta (Rhesus macaque).

Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,

Mammalia, Butheria, Primates, Catarrhini, Cercopithecidae,

Cercopithecinae, Macaca.
                                Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IRR001314, Chymotrypsin.
InterPro; IRR001001, Kringle.
InterPro; IRR003014; PAN.
InterPro; IRR003609; Pan. app.
InterPro; IRR00366; Prothrombin.
InterPro; IRR001254; Par. protease_Try.
Pfam; Pr00051; Kringle; 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Print; Pro0009; trypsin; 1.
PRINTS; PR00122; CHYMOTRYPSIN.
PRINTS; PR001018; KRINGLE.
PRINTS; PR001395; KRINGLE.
SNOAT; SM00139; KR; 4.
SMART; SM00139; KR; 4.
SMART; SM00130; KR; 4.
SMART; SM00120; Tryp_SPc; 1.
PROSITE; PS00021; KRINGLE 1; 5.
PROSITE; PS50070; KRINGLE 2; 5.
PROSITE; PS50070; TRYPSIN DOM; 1.
PROSITE; PS500134; TRYPSIN DOM; 1.
P12545;
01-0CT-1989 (Rel. 12, Created)
10-0CT-1989 (Rel. 12, Last sequence
28-FEB-2003 (Rel. 41, Last annotati
Plasminogen precursor (EC 3.4.21.7)
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PIR, B32869; B30848.
HSSP; P00747; 1PMK.
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CFITGWGETQGT--YGAGLLKEARLPVIENKVCNRYEFLNGTVKTTELCAGHLAGGTDSC 756
                                                            QEIEVSKMFSEPARA---DIALLKLSSP----AIITDKVIPACLPS----PNYVVADRTE 698
        ENLILHKDYSADTLAHHNDIALLKIRSKEGRCAQPSRTIQTICLPSMYNDPQF----GTS
                                                                                                                CEITGFGKENSTDYLYPEQLKMTVVKLISHRECQQPHYYGSEVTTKMLCAADPQWKTDSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=85023311; PubMed=6148961;
MEDLINE=85023311; PubMed=6148961;
Malinowski D.P., Sadler J.E., Davie E.W.;
"Characterization of a complementary deoxyribonucleic acid coding for
Human and bovine plasminogen.";
Biochemistry 23:4243-4250(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 95-580; 581-626; 657-700 AND 732-810.
Sottrup-Jensen L., Claeys H., Zajdel M., Petersen T.E., Magnusson S.; (In) Davidson J.F., Rowan R.M., Samama M.M., Desnoyers P.C. (eds.); Progress in chemical finolysis and thrombolysis, pp.3:191-209; Raven Press, New York (1978).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE=90202879; PubMed=2318848;
Petersen T.E., Martzen M.R., Ichinose A., Davie E.W.;
"Characterization of the gene for human plasminogen, a key proenzyme in the fibrinolytic system.";
J. Biol. Chem. 265:6104-6111(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
FOLSON M., RAdon B., Israelsson M., Larsson K., Heden L.-O.;
Molecular cloning and characterization of a full-length cDNA clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 483-604.
MIDDINE-7604592; PubMed=126863;
Miman B., Wallen P.;
"Amino-acid sequence of the cyanogen-bromide fragment from human plasminogen that forms the linkage between the plasmin chains.";
Eur. J. Biochem. 58:539-547(1975).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIJNE=5093329; PubMed=122932; Wiman B., Wallen P.; PubMed=122932; Wiman B., Wallen P.; PubMed=122932; Structural relationship between 'glutamic acid' and 'lysine' foof human plasminogen and their interaction with the NH2-terminal activation peptide as studied by affinity chromatography."; Eur. J. Biochem. 50:489-494(1975).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-JUL-1986 (Rel. 01, Created)
1-JMAR-1989 (Rel. 10, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Plasminogen precursor (EC 3.4.21.7) [Contains: Angiostatin]
                                                                                                                                                                                                                                                        QGDSGGPLVCFEKDKYILQGVTSWGLGCARPNKPGVYVRVSRFVTWI
                                                                                                                                                                                                                        QGDSGGPLVCSLQGRMTLTGIVSWGRGCALKDKPGVYTRVSHFLPWI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Magnusson S.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sottrup-Jensen L., Petersen T.E., Magnussk
Submitted (JUL-1977) to the PIR data bank
                                                                                                                                                                                                                                                                                                                                                                                                                    810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   human plasminogen.";
; Lett. 213:254-260(1987)
                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
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Blochemietry 37:3258-3271(1998).
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                                                                                                                                                                                                                                                                                                                                                    MEDLINE=92031503; PubMed=1657149; Wu T.-P., Padmanabhan K., Tulinsky A., Mulichak A.M.; Wither effined structure of the epsilon-aminocaproic acid complex of human plasminogen kringle 4."; Biochemistry 30:10589-10594(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRUCTURE BY NMR OF 183-154.
BUDILINE=56194156; PubMed=8652577;
Soehndel S., Hu C.-K., Marti D., Affolter M., Schaller J., Llinas
Rickli E.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rejante M.R., Llinas M.;
"IH-NMR assignments and secondary structure of human plasminogen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      X-TAX CRYSTALLOGRAPHY (1.67 ANGSTROMS) OF 376-454.
Stec B., Yamano A., Whitlow M., Teerer M.M.;
Structure of human plasminogen kringle 4 at 1.68 Angstrom and A possible structural role of disordered residues.";
Acta Crystallogr. D 53:169-178(1997).
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                                                                                                                                                                                   human plasminogen kringle
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MEDLINE-98198034; PubMed-9521645;
Chang Y., Mochalkin I., McCance S.G., Cheng B., Tulinsky A.,
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Best Local Similarity 33.7%; Pred. No. 3.9e-32;
Matches 137; Conservative 44; Mismatches 170;
                                                                        OF 374-461.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF 102-181.
                                                                                                       MEDLINE=92031502, PubMed=1657148;
Mulichak A.M., Tulinsky A., Ravichandran K.G.
"Crystal and molecular structure of human pla
refined at 1.9-A resolution.";
Biochemistry 30:10576-10588(1991).
                                                                        (1.9 ANGSTROMS)
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57:1329-1334(1997).
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                                                                            K-RAY CRYSTALLOGRAPHY
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                                                                                                       CFITGWGETQGT--FGAGLLKEAQLPVIENKVCNRYBFLNGRVQSTELCAGHLAGGTDSC 756
                                                                                                                                                                          229 ENLILHKDYSADTLAHHNDIALLKIRSKEGRCAQPSRTIQTICLPSMYNDPQF----GTS 284
                             NPDADKGPWCFTTDPSVRWEYCNLKKCSGTEASVVAPPPVVLLPDVETPSEEDCMFGNGK 487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- ENZYME REGULATION: CONVERTED INTO PLASMIN BY PLASMINOGEN
ACTIVATORS, BOTH PLASMINOGEN AND ITS ACTIVATOR BEING BOUND TO
FIBRIN. ACTIVATED WITH UROKINASE AND HIGH CONCENTRATIONS OF
STREPTOKINASE.
-!- MISCELLANDOUS: PLASMIN IS INACTIVATED BY ALPHA-2-ANTIPLASMIN
IMPRIPATELY AFFER DISSOCIATION FROM THE CLOT.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY SI. PLASMINOGEN SUBFAMILY:
-!- SIMILARITY: Contains at least 1 kringle domain.
           ----HCEIDKSKTCYEGNGH
                                                  57 FYRGKASTDTMGRPCLPWNSATVLQQTYHAHR----SDALQLGLGKHNYCRNPD-NRRRP
                                                                WCYVQVGLKPLVQECMVHDCADGKLKFQCGQKTLRPR---FKIIGGEFTTIENQPWFAAI
                                                                                                                                  YRRHRGGSVTYVCGGSLISPCWVISATHCFIDYPKKEDYIVYLGRSRLNSNTQGEMKFEV
                                                                                                                                                     --RTRFG--MHFCGGTLISPEWVLTAAHCLEKSPRPSSYKVILGAHOEVNLEPHVQEIEV
                                                                                                                                                                                             SRIFIEPT-----RKDIALLKLSSP----AVITDKVIPACLPS----PNYVVADRTE
                                                                                                                                                                                                                   CELTGFGKENSTDYLYPEQLKMTVVKLISHRECQQPHYYGSEVTTKMLCAADPQWKTDSC
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Mammalia, Eutheria, Carnivora, Fissipedia, Canidae, Canis.
NCBI_TaxID=9615,
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                                                                                                                                                                                                                                                                              OGDSGGPLVCFEKDKYILQGVTSWGLGCARPNKPGVYVRVSRFVTWI 803
                                                                                                                                                                                                                                                                                                                                                     01-NOV-1991 (Rel. 20, Created)
01-NOV-1991 (Rel. 20, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Plasminogen (EC 3.4.21.7) (Fragment).
                                                                                                                                                                                                                                                                                                                                 333 AA
           NCDCLNGGTCVSNKYFSNIHWCNCPKKFGGQ---
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InterPro, IPR000001; Kringle.
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35.6%; Pred. No. 1.6e-32;
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Matches 126; Conservative
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                                                                  68
                                                                                                                                                                                                           69 DGDVNGPWCYT-TNPRKLFDYCDIPQC---ESSFDCGKPKVEPKKCPARVVGGCVATPHS
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MEDDINE-8503311; PubMed-6148961;
Malinowski D.P., Sadler J.E., Davis E.W.;
"Characterization of a complementary deoxyribonucleic acid coding for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         porcine
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CYEGNGHFYRGKASTDTMGRPCLPWNSATVLQQTYHAH----RSDALQLGLGKHNYCRNP
                                                                  CMLGIGKGYRGKKATTVAGVPCQEWAA-----QEPHRHGIFTPETNPRAGLEK-NYCRNP
                                                                                                                                            D-NRRRPWCYVQVGLKPLVQECMVHDCADGKLKFQCGQKTLRPR----FKIIGGEFTTIBN
                                                                                                                                                                                                                                                                                         162 QPWFAAIYRRHRGGSVTYVCGGSLISPCWVISATHCFIDYPKKEDYIVYLGRSRLNSNTQ
                                                                                                                                                                                                                                                                                                                                                                                                                                         222 GEMKFEVENLILHKDYSADTLAHHNDIALLKIRSKEGRCAQPSRTIQTICLPSMYNDPQF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181 SVQEIPVSRLFLEPSRA-----DIALLKLSSP----AVITDEVIPACLPS----PNY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CARBOHYDRATE-LINKAGE SITES.

MEDLINE=88185329; PubMed=3136193;

Marti T., Schaller J., Rickli E.E., Schmid K., Kamerling J.P.,

Marti T., Schaller J., Rickli E.E., Schmid K., Kamerling J.P.,

Marti T., Schaller J., Rickli E.E., Schmid K., Kamerling J.P.,

Martingen J., van Halbeek H., Vliegenthart J.F.,

"The N- and O-linked carbohydrate chains of human, bovine and porcing plasminogen. Species specificity in relation to sialylation and fluosylation patterns."

Biochem. 173:57-63(1988).

-!- FUNCTION: PLASMIN DISSOLVES THE FIBRIN OF BLOOD CLOTS AND ACTS PAROTEOLYTIC PROTEOLYTIC                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              283 AGGTDSCQGDSGGPLVCFEKDKYILQGVTSWGLGCARPNKPGVYVRVSTYVPWI 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       338 QWKTDSCOGDSGGPLVCSLOGRMTLTGIVSWGRGCALKDKPGVYTRVSHFLPWI 391
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Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
Bovidae, Bovinae, Bos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Berglund L., Andersen M.D., Petersen T.E.; "Cloning and characterization of the bovine plasminogen cDNA."; Int. Dairy J. 5:593-603(1995).
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MEDLINE=85203906; PubMed=3846532;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PLMN BOVIN STANDARD; PRT; 812 AA. P06868; Q28162; 01-JAN-1988 (Rel. 06, Created) 01-NOV-1997 (Rel. 35, Last sequence update) PREB-2003 (Rel. 41, Last annotation update) Plasminogen precursor (EC 3.4.21.7).
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Biochemistry 23:4243-4250(1984).
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TISSUE=Liver;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=91149995; PubMed=1492092; Schaller J., Straub C., Kampfer U., Rickli E.E.; Schaller J., Straub C., Kampfer U., Rickli E.E.; Schaller J., Straub C., Kampfer U., Rickli E.E.; Schaller J., Straub C., Kampfer U., Rickli E.E.; Prometer amino acid sequence of ovine miniplasminogen."; Protein Seq. Data Anal 5:21-25(1992).

-i. FUNCTION: PLASMIN DISSOLVES THE FIBRIN OF BLOOD CLOTS AND ACTS A PROTECLYTIC FACTOR IN A VARIETY OF COTHER PROCESSES INCLUDING REMANATION: IN OVULATION IT WEAKENS THE WALLS OF THE GRAAFTAN FOLLICLE. IT ACTIVATES THE UROKINASE-TYPE PLASNINOGEN ACTIVATOR, COLLAGENASES AND SEVERAL COMPLEMENT ZYMOGENS, SUCH AS CI AND CS. IT CLEAVES FIBRIN, FIBRONECTIN, THROMBOSPONDIN, LAMININ AND VON WILLEBRAND FACTOR.
                                                                                                                                                                                                                              Ovis aries (Sheep).

Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Caprine; Ovis.
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SMART; SMOOLOS, Tryp_SPc; 1.
SMOOLOS, Tryp_SPc; 1.
PROSITE; PSSOOLO; KRINGLE_1, 1.
PROSITE; PSSOOLO; KRINGLE_2, 1.
PROSITE; PSOOLOS; TRYPSIN_DOM; 1.
PROSITE; PSOOLOS; TRYPSIN_SER; 1.
Hydrolase; Serine procease; Plasma; Glycoprotein; Fibrinolysis; 1.
Tissue_remodeling; Blood coagulation; Kringle; Zymogen; Repeat.
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LIGHT CHAIN A.
KRINGLE 4.
KRINGLE 5.
SERINE PROTEASE
CHARGE RELAY SYST
CHARGE RELAY SYST
CHARGE RELAY SYST
                                          15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
28-PEB-2003 (Rel. 41, Last annotation update)
Plasminogen (EC 3.4.21.7) (Fragment).
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InterPro: IPR001001; Kiringle.
InterPro: IPR00154; Prothrombin.
InterPro: IPR00154; Ser_protease_Try.
Fram; PP00051; Kiringle; 1.
Fram; PR00129; trypsin; 1.
PRINTS; PR00129; CHYMOTRYPSIN.
PRINTS; PR00129; KRINGLE.
PRINTS; PR01505; PR01505; PR01505; PR01505; PR01505; PR01505; PR01505; PR01505; PR01505; PR01505; PR01505; PR01505; PR01505; PR01505; PR01505; PR01505; PR01505; PR01505; PR01505; PR01505; PR01505; PR01505; PR01505; PR01505; PR01505; PR01505; PR01505; PR01505; PR01505; PR01505; PR01505; PR01505; PR01505; PR01505; PR01505; PR01505; PR01505; PR01505; PR01505; PR01505; PR01505; PR01505; PR01505; PR01505; PR01505; PR01505; PR01505; PR01505; PR01505; PR01505; PR01505; PR01505; PR01505; PR01505; PR01505; PR01505; PR01505; PR01505; PR01505; PR01505; PR01505; PR01505; PR01505; PR01505; PR01505; PR01505; PR01505; PR01505; PR01505; PR01505; PR01505; PR01505; PR01505; PR01505; PR01505; PR01505; PR01505; PR01505; PR01505; PR01505; PR01505; PR01505; PR01505; PR01505; PR01505; PR01505; PR01505; PR01505; PR01505; PR01505; PR01505; PR01505; PR01505; PR01505; PR01505; PR01505; PR01505; PR01505; PR01505; PR01505; PR01505; PR01505; PR01505; PR01505; PR01505; PR01505; PR01505; PR01505; PR01505; PR01505; PR01505; PR01505; PR01505; PR01505; PR01505; PR01505; PR01505; PR01505; PR01505; PR01505; PR01505; PR01505; PR01505; PR01505; PR01505; PR01505; PR01505; PR01505; PR01505; PR01505; PR01505; PR01505; PR01505; PR01505; PR01505; PR01505; PR01505; PR01505; PR01505; PR01505; PR01505; PR01505; PR01505; PR01505; PR01505; PR01505; PR01505; PR01505; PR01505; PR01505; PR01505; PR01505; PR01505; PR01505; PR01505; PR01505; PR01505; PR01505; PR01505; PR01505; PR01505; PR01505; PR01505; PR01505; PR01505; PR01505; PR01505; PR01505; PR01505; PR01505; PR01505; PR01505; PR01505; PR01505; PR01505; PR01505; PR01505; PR01505; PR01505; PR01505; PR01505; PR01505; PR01505; PR01505; PR01505; PR01505; PR01505; PR01505; PR01505; PR01505; PR01505; PR01505; PR01505; PR01505; PR01505; PR01505; PR01505; PR01505; PR01505
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P -> L (IN REF. 2).
T -> R (IN REF. 3).

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Science 246:904-910(1989).
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812 AA;
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                                                                                                                                                                   ENZYME REGULATION: CONVERTED INTO PLASMIN BY PLASMINOGEN
CATIVATORS, BOTH PLASMINOGEN AND ITS ACTIVATOR BEING BOUND TO
FIERIN. CANNOT BE ACTIVATED WITH STREPTOKINASE.

PTM: N-LINKED GLYCAN CONTAIN N-ACETYLLACTOSAMINE AND SIALIC ACID.
C-LINKED GLYCAN CONSIST OF GAL-CARNAC DISACCHARIDE WITH IS
MODIFIED WITH UP TO 2 SIALIC ACID RESIDUES (MICROHETEROGENEITY).
MISCELLANGOUS: PLASMIN IS INACTIVATED BY ALPHA-2-ANTIPLASMIN
SIMILARITY: BELONGS TO PEPTIDASE FAMILY SI. PLASMINOGEN SUBFAMILY.
SIMILARITY: CONTAINS 5 KTINGJE domains.
    GRAAFIAN FOLLICLE. IT ACTIVATES THE UROXINASE-TYPE PLASMINOGEN ACTIVATOR, COLLAGENASES AND SEVERAL COMPLEMENT ZYMOGENS, SUCH AS CI AND CS. IT CLEAVES FIBRIN, FIBRONECTIN, THROMBOSPONDIN, LAMININ AND VON WILLEBRAND FACTOR.
CATANYTIC ACTIVITY: Preferential cleavage: Lys-|-Xaa; higher selectivity than trypsin. Converts fibrin into soluble
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Interpro; IPR00366; Pan app.

Interpro; IPR00366; Prochrombin.

Interpro; IPR003966; Prochrombin.

Interpro; IPR003966; Prochrombin.

Interpro; IPR003166; Prochrombin.

Interpro; IPR00316; Ser_procease_Try.

IPR00316; IPR00316; Ser_procease_Try.

IPR00316; IPR00316; Ser_procease_Try.

IPR00316; IPR00316; IPR0316; Ser_procease_Try.

IPR00316; IPR00316; IPR0316; IPR0316; Ser_procease; IPR0316; IPR0316; IPR0316; IPR0316; IPR0316; IPR0316; IPR0316; IPR0316; IPR0316; IPR0316; IPR0316; IPR0316; IPR0316; IPR0316; IPR0316; IPR0316; IPR0316; IPR0316; IPR0316; IPR0316; IPR0316; IPR0316; IPR0316; IPR0316; IPR0316; IPR0316; IPR0316; IPR0316; IPR0316; IPR0316; IPR0316; IPR0316; IPR0316; IPR0316; IPR0316; IPR0316; IPR0316; IPR0316; IPR0316; IPR0316; IPR0316; IPR0316; IPR0316; IPR0316; IPR0316; IPR0316; IPR0316; IPR0316; IPR0316; IPR0316; IPR0316; IPR0316; IPR0316; IPR0316; IPR0316; IPR0316; IPR0316; IPR0316; IPR0316; IPR0316; IPR0316; IPR0316; IPR0316; IPR0316; IPR0316; IPR0316; IPR0316; IPR0316; IPR0316; IPR0316; IPR0316; IPR0316; IPR0316; IPR0316; IPR0316; IPR0316; IPR0316; IPR0316; IPR0316; IPR0316; IPR0316; IPR0316; IPR0316; IPR0316; IPR0316; IPR0316; IPR0316; IPR0316; IPR0316; IPR0316; IPR0316; IPR0316; IPR0316; IPR0316; IPR0316; IPR0316; IPR0316; IPR0316; IPR0316; IPR0316; IPR0316; IPR0316; IPR0316; IPR0316; IPR0316; IPR0316; IPR0316; IPR0316; IPR0316; IPR0316; IPR0316; IPR0316; IPR0316; IPR0316; IPR0316; IPR0316; IPR0316; IPR0316; IPR0316; IPR0316; IPR0316; IPR0316; IPR0316; IPR0316; IPR0316; IPR0316; IPR0316; IPR0316; IPR0316; IPR0316; IPR0316; IPR0316; IPR0316; IPR0316; IPR0316; IPR0316; IPR0316; IPR0316; IPR0316; IPR0316; IPR0316; IPR0316; IPR0316; IPR0316; IPR0316; IPR0316; IPR0316; IPR0316; IPR0316; IPR0316; IPR0316; IPR0316; IPR0316; IPR0316; IPR0316; IPR0316; IPR0316; IPR0316; IPR0316; IPR0316; IPR0316; IPR0316; IPR0316; IPR0316; IPR0316; IPR0316; IPR0316; IPR0316; IPR0316; IPR0316; IPR0316; IPR0316; IPR0316; IPR0316; IPR0316; IPR0316; IPR0316; IPR0316; IPR0316; IPR0316; IPR0316; IPR0316; IPR0316; IPR0316; IPR0
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/FTId=CAR 000014.
O-LINKED (GALNAC. ..).
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CHARGE RELAY SYSTEM.
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PLASMIN LIGHT CHAIN
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KRINGLE 3.
KRINGLE 4.
KRINGLE 5.
SERINE PROTEASE.
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EMBL, X02935; AAA30714.1; --
PIR, S45046; PLBO.

MRSOP, P00747; 2PK4.

MRROPS; S01.233; --
GlycosuiteDB; P06868; --
InterPro; IPR00001314; Chymotrypsin.
InterPro; IPR000001; Kringle.
InterPro; IPR000001; Kringle.
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                                                                                                                             CYEGNGHFYRGKASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPD-NR
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                                                             31; Gaps
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MEDLINE=21303595; PubMed=11294842;
Ganner B., Merry A.H., Royle L., Harvey D.J., Rudd P.M., Thillet J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Euteleostomi;
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MEDLINES-88039109; PubMed=3670400;
MCLean J.W., Tomlison J.E., Kuang W.-J., Eaton D.L., Chen E.Y.,
Fless G.M., Scanu A.M., Lawn R.M.;
Floss G.M., Scanu apolipoprotein(a) is homologous to
plasminogen.";
Nature 330:132-137(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=90076123; PubMed=2531657; Salonen E.-M., Jauhlainen M., Zardi L., Vaheri A., Ehnholm C.; Salonen E.-M., Jauhlainen M., Zardi L., Vaheri A., Ehnholm C.; "Lipoproteàind binds to fibronectin and has serine proteinase activity capable of cleaving it."; EMBO J. 8:4035-4040(1989).
   DB 1; Length 812;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      345 QGDSGGPLVCSLQGRMTLTGIVSWGRGCALKDKRGVYTRVSHFLPWI 391
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01-MUG-1988 (Rel. 08, Created)
12-MUG-1988 (Rel. 08, Last sequence update)
15-SRP-2003 (Rel. 42, Last annotation update)
Apolipoprotein(a) precursor (EC 3.4.21.-) (Apo(a)) (Lp(a)).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Eutelo
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
21.5%; Score 484.5; DB 1; Length 35.4%; Pred. No. 5.6e-31; ive 42; Mismatches 151; Indels
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SMART; SM00130; KR; 38
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            DISEASE: Elevated plasma concentrations of apo(a) and its naturally occurring proteolytic fragments are correlated with exherosclerosis. Homology with plasminogen kringles IV and V is thought to underlie the atherogenicity of the protein, because the fragments are competing with plasminogen for fibrin(ogen) binding. MISCELLANEOUS. Apo(a) is known to be proteolytically cleaved, leading to the formation of the so called mini-Lp(a). Apo(a) fragments accumulate in atherosclerotic lesions, where they may promote thrombogenesis. O-glycosylation may limit the extent of
                                                                                                                                                                                                                                                                                                                                                                        PTM: N- and O-glycosylated. The N-glycans are complex biantennary structures present in either a mono- or distalylated state. The O-glycans are mostly (80%) represented by the monosialylated core type I structure, NeuMacalpha2-3Galbeta1-3GalNAc, with smaller amounts of disialylated and non-sialylated O-glycans also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     proteolytic fragmentation.
SIMILARITY: BELONGS TO PEPTIDASE FAMILY SI. PLASMINOGEN SUBFAMILY
SIMILARITY: Contains 38 kringle domains.
                                                                                                                                                                                         MEDLINE=95002201; PubNed=7918682;
MEDLINE=95002201; PubNed=7918682;
Scanu A.M., Pfaffinger D., Lee J.C., Hinman J.;
Scanu A.M., Pfaffinger D. (Trp72-->Arg) in human apo(a) kringle 4-37 associated with a lysine binding defect in Lp(a).";
Blochim. Blochim. Blophys. Acta 1227-41-45(1994).
-1- FUNCTION: Apo(a) is the main constituent of lipoprotein(a) (Lp(a)). It has serine proteinase activity and is able of autoproceolypas. Inhibits tissue-type plasminogen activator 1. Lp(a) may be a ligand for megalin/Gp 330.
-1- SUBUNIT: Disulfide-linked to apo-B100. Binds to fibronectin and
                                                                 X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 4121-4208.
MEDLINE=96217891; PubMed=8642595;
Mixol V., Lograsso P.V., Boettcher B.R.;
Mixol V., Lograsso P.V., Boettcher B.R.;
complexed structures of apolipoprocein(a) kringle IV37 free and
complexed with 6-aminohexanoic acid and with p-aminomethylbenzoic
acid: existence of novel and expected binding modes.";
J. Mol. Biol. 256:751-761(1996).
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RGO; GO:0004866; F:endopeptidase inhibitor activity; TAS.

RGO; GO:0004015; P:circulation; TAS.

RGO; GO:0009405; P:pathogenesis; TAS.

RILEAPPO; IPRO01314; Chymotrypsin.

R InterPro; IPRO01314; Chymotrypsin.

R Pfam; PF00061; Kringle; 38.

R Pfam; PF00089; trypsin; 1.

R PRINTS; PR00018; KRINGIR:

R PRINTS; RR00018; KRINGIR:

R PRODOM; PD000395; KRINGIR: 38.
"Structural elucidation of the N- and O-glycans of human apolipoprotein(a): role of o-glycans in conferring protease
                                            Biol. Chem. 276:22200-22208(2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; X06290; CAA29618.1; -. PIR; S00657; S00657. PDB; 1171; 13-UNN-01. PDB; 1JFN; 28-UNN-02. PDB; 1KIV; 18-MAY-99. PDB; 3KIV; 18-MAY-99. MEMOPS; S01.226; -. Genew; HGNC:6667; LPA.
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SWPWQVSL--RTRFGK--HFCGGTLISPEWVLTAAHCLKKSSRPSSYKVILGAHQEVNLE 4393
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PROSITE; PS00021; TYP_SPC; 1.
PROSITE; PS00021; KRINGLE 1; 38.
PROSITE; PS00070; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN HIS; 1.
PROSITE; PS00135; TRYPSIN SI 1.
PROSITE; PS00135; TRYPSIN SI 1.
PROSITE; PS00135; TRYPSIN SI 1.
PROSITE; PS00135; TRYPSIN SI 1.
Kringle; Repeat; Atherosclerosis; Signal; Polymorphism; 3D-structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OF LYSINE-SEPHAROSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /FTId=VAR_006633.
4548 AA; 501313 MW; 96921BE96A465CSF CRC64;
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Best Local Similarity
Matches 129; Conserv
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                                                              -PDYMVTARTECYITGWGETQGT--FGTGLLKEAQLLVIENEVCN--HY-----KYIC 4483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   syntheses:

1. Chem. 264:5957-5965(1989).

2. Bidl. Chem.

2. FUNCTION: Apo(a) is the main constituent of lipoprotein(a) (Lp(a)). It has serine proteinses activity and is able of autoproteolysis. Inhibite tissue-type plasminogen activator 1. Lp(a) may be a ligand for megalin/Gp 330.

2. SUBLUNIT: Disublidel-linked to apo-B100. Binds to fibronectin and decorin (By similarity).

3. PTM: N- and 0-glycosylated (By similarity).

3. DISEASE: Elevated plasma concentrations of apo(a) and its naturally occurring proteolytic fragments are correlated with atherosclerosis. Homology with plasminogen kringles IV and V is thought to underlie the atherogenicity of the protein, because the fragments are competing with plasminogen for fibrin (ogen) binding.

4. Hought to underlie the atherogenicity of the protein, because the fragments are competing with plasminogen for fibrin (ogen) binding.

4. Hought to the formation of the so called mini-Lp(a). Apo(a) fragments are competing with plasminosis, where they may promote thrombogenesis. O-glycosylation may limit the extent of proteolytic fragmentation (By similarity).

5. SIMILARITY: BOLDING TO PERTIDASE FAMILY SI. PLASMINOGEN SUBFAMILY.

5. SIMILARITY: Contains at least 10 kringle domains.
                         SNIQGEMKFEVENLILHKDYSADTLAHHNDIALLKIRSKEGRCAQPSRIIQTICLPSMYN 277
                                                                                                                                  DPOF----GISCEITGFGKENSTDYLYPEQLKMTVVKLISHRECQOPHYYGSEVTTKMLC 333
                                                                                                                                                                                                                                                                     334 AADPQWKTDSCQGDSGGPLVCSLQGRMTLTGIVSWGRGCALKDKPGVYTRVSHFLPWI 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=89174660; PubMed=2925643;
Tomlinson J.E., McLean J.W., Lawn R.M.;
"Rhesus monkey apolipoprotein(a). Sequence, evolution, and sites of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Macaca mulatta (Rhesus macaque).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-07N'-1990 (Rel. 13, Created)
01-07N'-1990 (Rel. 13, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Apolipoprotein(a) (EC 3.4.21.-) (Apo(a)) (Lp(a)) (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                               1420 AA
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InterPro; IPR000001; Kringle.
InterPro; IPR010254; Ser protease_Try.
Pfam; PF00051; Kringle; I1.
Pfam; PF00089; trypsin; I1.
PRINTS; PR00722; CHYMOTRYPSIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; J04635; AAA36833.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cercopithecinae; Macaca
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HSSP; P00747; 2PK4.
MEROPS; S01.226; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9544;
                                                                                                                                                                                                                                                                                                                                                                                                                               APOA MACMU
P14417;
                                                                                                                                     278
                               218
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1123 DTGPWCFT----MDPSVRREYCNLTRCSDTEGTVVTPPTVIPVPSLEAPSEQASSSFDCGK 1179
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DR PRINTS; PRO0018; KRINGLE.
DR RAART; SM00130; KR; 10.
DR SMART; SM00130; KR; 10.
DR PROSTE; PS00021; KRINGLE 1; 10.
DR PROSTE; PS50070; KRINGLE 2; 10.
DR PROSTE; PS500134; TRYPSIN_LOW; 1.
DR PROSTE; PS00134; TRYPSIN_LOW; 1.
DR PROSTE; PS00135; TRYPSIN_SER; FALSE NEG.
W HYDROJAS; PROSTE; PS00135; TRYPSIN_SER; FALSE NEG.
W Kringle; Serine protease; Lipid transport; Plasma; Glycoprotein; TRYPSIN_TER.
DR TER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      50 CYEGNGHFYRGKASTDTMGRPCLPWNSATVLQ--QTYHAHRSDALQLGLGKHNYCRNPDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CYHGNGOSYRGTFSTTVTGRTCQSWSSMTPHQHKRTPENHPNDDLTM-----NYCRNPDA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1236 TFSRPSFYKVILGAHOEVNLESHVO---EIEVSRLFLEPIGA-----DIALLKL---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        143 KTLRPR---FKIIGGEFTTIENQPWFAAIYRRHRGGSVTYVCGGSLISPCWVISATHCFI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              282 -SRPAIITDKVIPACLPS----PNYVITAWTECYITGWGETQGT--FGAGLLKEAQLHVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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Mammalia, Eutheria, Perissodactyla, Equidae, Equus.
NCBI_TaxID=9796;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 1420;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              43; Mismatches 137; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1420 SERINE PROTEASE.
AA; 158367 MW; BE102949E03C5B0E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    108 RRRPWCYVQVGLKPLVQE--CMVHDCAD-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 477; DB 1;
Pred. No. 4.1e-30;
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1-NOV-1991 (Rel. 20, Last sequence update)
6-CT-2001 (Rel. 40, Last annotation update)
lasminogen (EC 3.4.21.7) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KRINGLE 1.
KRINGLE 2.
KRINGLE 4.
KRINGLE 6.
KRINGLE 6.
KRINGLE 7.
KRINGLE 8.
KRINGLE 9.
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ID PLMN HORSE

AC P80010;

DT 01-NOV-1991 (1)
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products.
--- ENZYME REGULATION: CONVERTED INTO PLASMIN BY PLASMINOGEN
ACTIVATORS, BOTH PLASMINOGEN AND ITS ACTIVATOR BEING BOUND TO
FIBRIN. ACTIVATED WITH CATALYTIC AMOUNTS OF STREPTOKINASE.
--- MISCELLARBOUS: PLASMIN IS INACTIVATED BY ALPHA-2-ANTIPLASMIN
IMMEDIATELY AFTER DISSOCIATION FROM THE CLOT.
--- SIMILARITY: BELONGS TO PEPTIDASE FAMILY SI. PLASMINOGEN SUBFAMILY.
--- SIMILARITY: CONTAINS AT least 1 kringle domain.
                              (PROBABLE)
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RELAY SYSTEM (BY SIMILARITY)
RELAY SYSTEM (BY SIMILARITY)
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PROSITE; PS00134; TRYPSIN DOM; 1.
PROSITE; PS00135; TRYPSIN SER; 1.
Hydrolase; Serine protease; Plasma; Glycoprotein; Fibrinolysis; Issue remodeling; Blood coagulation; Kringle; Zymogen.
NON TER 1 108 PLASMIN HEAVY CHAIN A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREPTOKINASE-BINDING SITE (PRC STREPTOKINASE-BINDING SITE (PRC STREPPOKINASE-BINDING SITE (PRC SITE OF SUBSTRATE SPECIFICITY (BY SIMILARITY).
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InterPro; IPR001314; Chymotrypsin.
InterPro; IPR0030601; Kringle.
InterPro; IPR003966; Prothxombin.
InterPro; IPR001254; Ser_protease_Try.
Pfam; PF00061; Kringle; I.
Pfam; PF00089; trypsin; I.
                MEDLINE=92052077; PubMed=1946332;
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PRINTS, PRO0018; KRINGLE.
PRINTS, PRO1505, PROTHROMBIN.
PRODOM, PD000395, Kringle; 1.
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PROSITE; PS00021; KRINGLE 1
PROSITE; PS50070; KRINGLE 2
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HSSP; P00747; SHPG.
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Gaps

39;

Score 447.5; DB 1; Length 338; Pred. No. 1.8e-28; 0; Mismatches 153; Indels 39.

19.8%; Scoi 34.1%; Pred tive 40; 1

Query Match 19.8 Best Local Similarity 34.1 Matches 120; Conservative

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64 GDVNGPWCYT-MNPQKLFDYCDVPQCESS--PFDCGKPKVEPKKCSGRIVGGCVAIAHSW 120
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CYEGNGHFYRGKASTDIMGRPCLPWNSATVLQQTYHAH---RSDALQLGLGKHNYCRNPD 106
                                             9 CMLGIGKGYQGKKATTVTGTRCQAWAA----QEPHRHSIFTPEANPWANLEKNYCRNPD 63
                                                                                                      107 -NRRRPWCYVQVGLKPLVQECMVHDCADGKLKFQCGQKTLRPR---FKIIGGEFTTIENQ
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096ef3 hamis cabal
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MEDLINE=22155945; PubMed=12149463;

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MEDLINE=22155945; PubMed=12149463;

MEDLINE=22155945; PubMed=12149463;

A Falkenberg M., Tom C., DeYoung M.B., Wen S., Linnemann R.,

Dichek D.A.;

"Increased expression of urokinase during atherosclerotic lesion of urokinase during atherosclerotic lesion growth."

The development causes arterial constriction and lumen loss, and a cocelerates lesion growth."

A EMBLARITY: DELONGS TO PEPTIDASE FAMILY SI.

"Increased expression of urokinase DoMAIN."

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InterPro; IPRO00191; KINGLE.

InterPro; IPRO00191; KRINGLE.

PRODOM; PRO0019; KRINGLE.

PRODOM; PRO00195; KRINGLE.

PRODOM; PRO00202; EGF 1; 1.

PROSITE; PSO0021; KRINGLE.

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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Lagomorpha, Leporidae, Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-WAR-2003 (TrEMBLrel. 23, Last annotation update)
Urokinase-type plasminogen activator.
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Copyright (c) 1993 - 2003 Compugen Ltd.
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Listing first 45 summaries
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5: sp_fungi:*
6: sp_numan:*
7: sp_mammal:*
7: sp_mbc:*
8: sp_organelle:*
9: sp_plant:*
10: sp_plant:*
12: sp_vrucbrate:*
13: sp_vrucbrate:*
14: sp_vruclasified:*
15: sp_archeriap:*
16: sp_bacteriap:*
17: sp_archeap:*
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Gapop 10.0 , Gapext 0.5
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2: sp_bacteria:*
3: sp_fungi:*
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Maximum DB seq length: 2000000000
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No.

Result

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MEROPS; SOL.231; -.
InterPro; IPRO01314; Chymotrypsin. ..
InterPro; IPRO00001; Kringle.
InterPro; IPRO01254; Ser_protease_Try.
Pfam; PF00051; Kringle; I.
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Best Local (
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                                                                                                                                                                                     Gaps
PROSITE; PS50240; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN H1S; 1.
PROSITE; PS00135; TRYPSIN SER; 1.
G]YCODYCLEIN; Hydrolase; Kinase; Kringle; Protease; Serine protease.
SEQUENCE 433 AA; 48375 MW; 65E64F36415549B0 CRC64;
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"Oryctolagus cuniculus urokinase-type plasminogen activator, mRNA, complete dds.";

Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.

-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.

--: SIMILARITY: CONTAINS I KRINGLE DOMAIN.

EMBL; AR092517; AAK40233.1;

EMBL; AB087224; BAC02685.1;
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                                                                                                                                  Query Match

83.5%; Score 1885; DB 6; Length 4

Best Local Similarity 82.8%; Pred. No. 2e-172;

Matches 342; Conservative 23; Mismatches 38; Indels
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Sug.ki M., Yoshida E., Anai K., Maruyama M.;
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Eu
Mammalia, Eutheria, Lagomorpha, Leporidae, Oryctolagus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Urokinase-type plasminogen activator.
UROKINASE.
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InterPro; IPR001314; EdF like.
InterPro; IPR001201; Kringle.
InterPro; IPR001254; Ser_protease_Try.
Pfam; PF00004; Kringle; 1.
PR00015; Kringle; 1.
PR10175; PR00012; CHYMOTRYPSIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                        10; Gaps
PRINTS; PR00018; KRINGLE.

ProDom; P0000395; Kringle; 1.

SMART; SM00020; Tryp_SPC; 1.

PROSITE; PS00021; EGF 1: 1.

PROSITE; PS00021; KRINGLE 1: 1.

PROSITE; PS00014; TRYPSIN_DOM; 1.

PROSITE; PS00149; TRYPSIN_DOM; 1.

PROSITE; PS001135; TRYPSIN_DOM; 1.

PROSITE; PS001135; TRYPSIN_DS; 1.

PROSITE; PS001135; TRYPSIN_SER; 1.

Glycoprotein; Hydrolase; Klinase; Kringle; Protease; Serine protease.

SEQUENCE 433 AA; 48444 MW; 6DD35A371010A6EE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PLVCSLQGRMTLTGIVSWGRGCALKDKPGVYTRVSHFLPWIRSHTKEENGLAL 403
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Mammalia, Eutheria, Lagomorpha, Leporidae, Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                 433;
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Yin J., Idell S.,

Yan J., Idell S.,

"Partial mRNA of rabbit uPA.";

Submitted (COT-1998) to the EMBL/GenBank/DDBJ databases.

-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.

-!- SIMILARITY: COTTAINS 1 KRINGLE DOMAIN.

EMBL, RRO97497, AAD39351.1; -.

HSSP, PO0749; 1EJN.
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                                                                                                                                                                                                                                                                                                                                                                                 83.3%; Score 1880; DB 6;
82.6%; Pred. No. 5.9e-172;
iive 23; Mismatches 39;
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ر ف

Gaps

81

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322 LTVILGRTYRVVPGEEEQKFEVEKYIVHKEFDDDT--YDNDIALLQLKSDSSRCAQESSV 379
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       148 RFKIIGGEFTTIENOPWFAAIYRH-RGGSVTYVCGGSLISPCWVISATHCFIDYPKKED 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   202 VYTAQNPSAQALGLGRGHNYCRNPDGDAKPWCHVLKNRRLTWEYCDVPSCSTCGLRQYSQP 261
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380 VRIVCLPPADLQLPDWTECELSGYGKHBALSPFYSERLKEAHVRLYPSSRCTSQHLLNRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     262 QFRIKGGLFADIASHPWQAAIFAKHRKSPGERFLCGGILISSCWILSAAHCFQERFPPHH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       207 YIVYLGRSRLNSNTQGEMKFEVENLILHKDYSADTLAHHNDIALLKIRSKEGRCAQPSRT
                                                                                                                                                                                                                                                                                               23 SQEIHARFRRGARSYQGCSEPRCFNGGTCQQALYFSDF-VCQCPEGFAGKCCEIDTRATC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          327 VITKMLCAAD-----PQWKT-DSCOGDSGGPLVCSLOGRWTLIGIVSWGRGCALKDKPGV
                                                                                                                                                                                                                                                     1 SNELH------QVPSNCDCLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTC
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Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                          37.8%; Score 852.5; DB 4; Length 516; 37.1%; Pred. No. 3.5e-73; ive 55; Mismatches 154; Indels 103;
PROSITE; PS50240; TRYPSIN_DOW; 1.
PROSITE; PS00134; TRYPSIN_BIS; 1.
PROSITE; PS00135; TRYPSIN_SER; 1.
PROSITE; PS00135; TRYPSIN_SER; Hydrolase; Kringle; Protease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             516 AA; 57370 MW; BAB31901FDC96800 CRC64;
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(TrEMBLrel. 19, Last sequence update)
(TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     559 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                           111 PWCYVQVGLKPLVQECMVHDCADG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10090;
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500 YTKVTNYLDWIRDNMR 515
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                                                                                                                                                                                     Best Local Similarity 37.1 Matches 184; Conservative
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TISSUE=Breast tumor;
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                                                                                               Serine protease
SEQUENCE 516
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01-DEC-2001 (
01-DEC-2001 (
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                                                                                                                                                                    Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                    67 MGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVGLKPLVQEC
                                                                                                                                                                                                                                                                                                                                                                                                                                    127 MVHDCA-----DGKLKFQCGQKTLRPRFKIIGGEFTTIENQPWFAAIYRRHRGGSVTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       180 VCGGSLISPCWVISATHCFIDYPKKEDYIVYLGRSRLNSNTQGEMKFEVENLILHKDYSA
              PRINTS; PROUZZ; CHYMOTRYPSIN.
PRINTS; PROUZZ; CHYMOTRYPSIN.
PRODO395; Kringle; 1.
SWART; SW00130; KR; 1.
SWART; SW00130; KR; 1.
PROSITE; PS00021; KRINGLE; 1.
PROSITE; PS500240; KRINGLE; 1.
PROSITE; PS500134; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_HIS; 1.
Glycoprotein; Hydrolase; Kinase; Kringle; Protease; Serine protease.
Glycoprotein; Hydrolase; Kinase; Kringle; Protease; Serine protease.
SEQÜENCE 214 AA; 24314 MW; 69975C41C3280D7E CRC64;
                                                                                                                                                                                                                                                                                                                                                            Gaps
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Homo sapiens (Human).
Eukaryota: Metakuan).
Mammalia; Putheria; Primates; Cararhini; Hominidae; Homo.
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Strausberg R.;
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
SIMILARITY: BELONGS TO PEPTIDASE FAMILY SI.
SIMILARITY: CONTAINS 2 KRINGLE DOMAINS.
REMBL; BCOOSTOS; JAAH02795.1; -..
INTEFPO: IPRO01314; Chymotrypsin.
InterPro: IPRO06210; EGF 1.
InterPro: IPRO06210; IEGF 1.
R InterPro: IPRO00210; Kringle.
R InterPro: IPRO0021; Kringle; 2.
R Pfam; PF000089; kringle; 2.
R Pfam; PF000089; kringle; 2.
R PRINTS; PR00722; CHYMOTRYPSIN.
R PRINTS; PR00139; KRINGLE.
R PRINTS; RN00189; KRINGLE.
R SWART; SM00130; KR. 2.
                                                                                                                                                                                                                                                                                                           42.2%; Score 953.5; DB 6; Length
81.3%; Pred. No. 2.3e-83;
ive 12; Mismatches 21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  240 DTLAHHNDIALLKIRSKEGRCAOPSRTIQTICLP 273
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PROSITE; PS00022; EGF 1; 1.
PROSITE; PS01186; EGF 2; 1.
PROSITE; PS00021; KRINGLE 1; 2.
PROSITE; PS50070; KRINGLE 2; 2.
                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 81.33
Matches 174; Conservative
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ICLPSMYNDPQFGTSCEITGFGKENSTDYLYPEQLKMTVVKLISHRECQQPHYYGSEVTT 329
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      92 LOLGLGKHNYCRNPDNRRRPWCYVQVGLKPLVQECMVHDCADGKLKFQCG-QKTLRPRFK 150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                210 YLGRSRLNSNTQGEMKFEVENLILHKDYSADTLAHHNDIALLKIRSKEGRCAQPSRTIQT
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                                                                                          Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           110;
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PROSITE; PS00134; TRYPSIN_HIS; 1.
PROSITE; PS00135; TRYPSIN_SER; 1.
EGF-like domain; Glycoprotein; Hydrolase; Kringle; Protease;
                                                                                                                                                                            36.5%; Score 823; DB 6; Length 564
36.3%; Pred. No. 2.6e-70;
tive 55; Mismatches 148; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5 HOVP-SNCD---CLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEID--
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Tissue-type plasminogen activator.
Oryccolagus cuniculus (Rabbit).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eut Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       564 AA; 62726 MW; 459D8BAC6D4A937C CRC64;
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SMART; SMOOTB0; KR; 2.
SMART; SMOODS0; TRYP SPC; 1.
PROSITE; PSOODS2; EGF 1; 1.
PROSITE; PSO1186; EGF 2; 1.
PROSITE; PSO1253; FIBRONECTIN 1; 1.
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Matches 178; Conserv
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SEQUENCE 564 P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SMYNDPQF----GISCELIGEGKENSTDYLYPEQLKMIVVKLISHRECQOPHYYGSEVIT 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               330 KMLCAADP----QWKTDSCQGDSGGPLVCSLQGRMTLTGIVSWGRGCALKDKPGVYTRV 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----FOCG-QKTLRPRFKIIGG 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ochsvevrscseprcfnegicogalyfsdf-vcocedgfvekredidtrafefeegeity 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         253 NSQALGLGRHNYCRNPDGDARPWCHVMKDRKLTWEYCDMSPCSTCGLRQYKRPQFRIKGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RGKASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         193 GKYTTEFCSTPACPKGKSEDCYVGKGVTYRGTHSLTTSQASCLPWNSIVLMGKSYTAWRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      155 EFTTIENQPWFAAIY-RRHRGGSVTYVCGGSLISPCWVISATHCFIDYPKKEDYIVYLGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 ELHQVP----SNCDCLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                           Probom; PRO001395; Kringle; 2.

SMART; SM0001395; RN1: 1.

SMART; SM0001395; RN1: 1.

SMART; SM00020; RV1: 1.

SMART; SM00020; Tryp SPc; 1.

RPOSITE; PSO1020; Tryp SPc; 1.

RPOSITE; PSO1020; RGF=2; 1.

RPOSITE; PSO1021; KRINGLE=1; 2.

RPOSITE; PSO0240; TRYPSIN DOM; 1.

RPOSITE; PSO0240; TRYPSIN DOM; 1.

RPOSITE; PSO0134; TRYPSIN DOM; 1.

RPOSITE; PSO0135; TRYPSIN DOM; 1.

RPOSITE; PSO0135; TRYPSIN DOM; 1.

RPOSITE; PSO0135; TRYPSIN SFR; 1.

RPOSITE; PSO0135; TRYPSIN SFR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        36.5%; Score 824.5; DB 11; Length 559; 35.5%; Pred. No. 1.9e-70; ive 63; Mismatches 150; Indels 105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 559 AA; 63122 MW; 8CCEE2BDB94514D9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    564 AA
                                        InterPro; IPR006210; IEGF.
InterPro; IPR00001; Kringle.
InterPro; IPR001254; Ser_protease_Try.
                                                                                                   Pfam; PF00008; EGF; 1.
Pfam; PF00039; fnl; 1.
Pfam; PF00081; kringle; 2.
Pfam; PF00089; trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
PRINTS; PR00018; KRINGLE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q8MKB1;
01-OCT-2002 (TrEMBLrel. 22,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                547 TNYLDWIHDNMKQ 559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SHFLPWIRSHTKE 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 35.5%
Matches 175; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                274
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q8MKB1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 6
Q8MKB1
ID Q8MKA
AC Q8MKA
DT 01-OC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8 S
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HDCADGKLK------FQCGQKTLRPRFKIIGGEFTTIENQPWFAAIYRHRGGS-VTY 179
                                       256 AQTLGLGKHNYCRNPDGDTQPWCHVLKDHKLTWEYCDLPQCVTCGLRQYKEPQFRIKGGL 315
                                                                                                           434 ANLQLPDWTECELSGYGKHEASSPFYSERLKEAHVRLYPSSRCTSKHLFNKTITNNMLCA 493
                                                                                                                                                                                                                                                                                                                335 ADPOW-----KTDSCQGDSGGPLVCSLQGRMTLTGIVSWGRGCALXDKPGVYTRVSHFL 388
             ----HDCADGKLKFQ------CGQKTLR-PRFKIIGGE 155
                                                                                                                                                                                                                                        275 MYNDPQFGTSCEITGFGKENSTDYLYPEQLKMTVVKLISHRECQQPHYYGSEVTTKMLCA 334
                                                                                                                                                                                                                                                                                                                                                    494 GDTRSGGDNANLHDACQGDSGGPLVCMKGNHMTLVGVISWGLGCGQKDVPGVYTKVTNYL 553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       90 RPCLAWNAPAVLQKPYNAHRPDAISLGLGKHNYCRNPDNQKRPWCYVQIGLRQFVQECWV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                215 RLNSNTQGEMKFEVENLILHKDYSADTLAHHNDIALLKIRSKEGRCAQPSRTIQTICLPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30 SNCGCQNGGVCVSYKYFSRIRRCSCPRKFQGEHCEIDASKTCYHGNGDSYRGKANTDTKG
                                                                                       156 FTTIENOPWFAAIY-RRHRGGSVTYVCGGSLISPCWVISATHCFIDYPKKEDYIVYLGRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9 SNCDCLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFYRGKASTDTMG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 69 RPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVGLKPLVQECMV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN=CSPRUF6J; TISSUE=Ovary;
STRAIN=CSPRUF6J; TISSUE=Ovary;
The MEDIJNE=22354683; PubMed=12466851;
The FANTOM Consortium,
the RIKEN Genome Exploration Research Group Phase I & II Team;
the RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation 60,770 full-length cDNAs.";
Nature 420:563-573(2002).
Nature 420:563-573(2002).
NATURE 420:563-573(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          231 AA; 25510 MW; 25E8980A682737F2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         08C6L2;
01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Plasminogen activator (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             35.8%; Score 808.5; DB 1.
69.5%; Pred. No. 2.1e-69;
ive 21; Mismatches 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  180 VCGGSLISPCWVISATHCFI 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    210 KCGGSLISPCWVASAAHCFI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity VIII-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                              PWIRSHTK 396
                                                                                                                                                                                                                                                                                                                                                                                                                                554 NWIRDNTR 561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                              389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQÜENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EKYSPDFCSTPACTKEKEBCYTGKGLDYRGTRSLTMSGAFCLPWNSLVLMGKIYTAWNSN 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        58
                                                           3 BLHOVP-SNCD---CLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCXEGNGHFY
431 VCLPDASLQLPDWTECELSGYGKHEEFSPVFSEQLKEAHVRLYPSSRCTPQQLKNRTVTG
                                   KMLCAADPQW-----KTDSCQGDSGGPLVCSLQGRMTLTG1VSWGRGCALKDKPGVYTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                              01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
1-plasminogen activator.
1-plasminogen activator.
Sus scrofa (Pig)
Bukatazoa; (Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SMART; SM00058; FN1; 1.

SMART; SM00050; TryP 2.

SMART; SM00050; TryP 5.

RROSITE; PS00022; EGF 1; 1.

RPOSITE; PS00021; EGF 2; 1.

RPOSITE; PS00021; KRINGLE 1: 2.

RPOSITE; PS00021; KRINGLE 2; 2.

RPOSITE; PS00134; TRYPSIN DOM; 1.

RPOSITE; PS00134; TRYPSIN DOM; 1.

RPOSITE; PS00135; TRYPSIN DOM; 1.

RPOSITE; PS00135; TRYPSIN SRR; 1.

REGF-like domain; Glycoprofein; Hydrolase; Kringle; Protease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 6; Length 562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   36.1%; Score 815.5; DB 6; Length 5 35.9%; Pred. No. 1.4e-69; ive 60; Mismatches 156; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           F9E6B4C77CB101E8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        119 LK------DLV----QECMV------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         562 AA; 63668 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00008; EGF. 1.
Pfam; PF00039; Enl: 1.
Pfam; PF00051; Kringle; 2.
Pfam; PF00089; trypsin; 1.
Probom; PD000395; Kringle; 2.
SWART; SM00181; EGF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kringle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 35.9
les 175; Conservative
                                                                                                               384 VSHFLPWIRSH 394
                                                                                                                                                   551 VVNYLGWIQQH 561
                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Serine protease.
SEQUENCE 562 A
                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9823;
                                       330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    136
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Q8SQ23
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81 KASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVGLK 140
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical 70.6 kDa protein.
Hypothetical 70.6 kDa protein.
Hypothetical 70.6 kDa protein.
Hypothetical 70.6 kDa protein.
Hypothetical 70.6 kDa protein.
Hypothetical 70.6 kDa protein.
Hypothetical 70.6 kDa protein.
Hypothetical 70.6 kDa protein.
Hypothetical 70.6 kDa protein.
Hypothetical 70.6 kDa protein.
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                                                                                                154 AA
                                                                                                                              01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last seq
01-WAR-2003 (TrEMBLrel. 23, Last ann
                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00022; EGF_1; 1.
PROSITE; PS00021; KRINGLE 1; 1.
PROSITE; PS00001; KRINGLE 2; 1.
Glycoprotein; Kinase; Kringle.
SEQUENCE 154 AA; 17305 MW;
380 TKVTNYLDWIRDNMR 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 PLVQECMVHDCADG 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LLVQECMVHDCADG 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                           Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                              NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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Q8VCS4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Loca
Matches
                                                         RESULT 10
Q96SE8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    90 DALQLGLGKHNYCRNPDNRRRPWCYVQVGLKPLVQECMVHDCADGKLKFQCG-QKTLRPR 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           202 TVILGRIYRVVPGEEEGKFECEKYIVHKEFDDDT--YDNDIALLQLKSDSSRCAQESSVV 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       88 SAQALGLGKHNYCRNPDGDAKPWCHVLKNRRLTWEYCDVPSCS-----TCGLRQYSQPQ 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FKIIGGEFTTIENQPWFAAIYRRH-RGGSVTYVCGGSLISPCWVISATHCFIDYPKKEDY 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              208 IVYLGRSRLNSNIQGEMKFEVENLILHKDYSADTLAHHNDIALLKIRSKEGRCAQPSRTI 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QTICLPSMYNDPQFGTSCEITGFGKENSTDYLYPEQLKMTVVKLISHRECQQPHYYGSEV 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TIKMLCAAD-----PQWKT-DSCQGDSGGPLVCSLQGRMTLTGIVSWGRGCALKDKPGVY 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30 WCNCPKKFGGQHCEIDKSKTCYEGNGHFYRGKASTDTMGRPCLPWNSATVLQQTYHAHRS 89
                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                         21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  34.9%; Score 788.5; DB 4; Length 395; llarity 42.9%; Pred. No. 3.4e-67; Conservative 49; Mismatches 144; Indels 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             395 AA; 44323 MW; 3FBD4A2F0B7C11C8 CRC64;
                                                           01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2003 (TrEMBLrel. 23, Last annotation update)
Neonatal thrombolytic agent alpha-form (Fragment)
Homo saplens (Human).
                         395 AA
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                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----
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hes 161; Conserv
                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                         NCBI_TaxID=9606;
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SEQUENCE
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Matches
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A Bai X., Fu J., Wang W., Xi X., Ruan C.;

A Bai X., Fu J., Wang W., Xi X., Ruan C.;

AT "Overexpression of the amino-terminal fragment of human urokinase-type plantinogen activator in breast cancer cells results in decreased at tumor invasion, growth and anglogenesis.";

AL submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.

I. SIMILARITY: CONTAINS I KRINGLE DOMAIN.

BEBL; AY020537; AAK33734.1; -

BEBL; AY020537; AAK33734.1; -

InterPro; IPR006209; EGF like.

BIT INTERPROSES KRINGLE.

Refam; PF00015; KRINGLE.

RENINTS; RR0018; KRINGLE.

RENINTS; RR0018; KRINGLE.

RENINTS; RR0018; KRINGLE.

RENINTS; RR00180; KRINGLE.

RENINTS RR00180; KRINGLE.

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RENINTS RR00180; KRINGLE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21 SNELHQVPSNCDCLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFYRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 SNEIHQVPSNCDCLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFYRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fu_J, Bai X., Ruan C.; "Cloning and expression of the amino-terminal fragment of human "Cloning and expression of the amino-terminase-type plasminogen activator."; Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Urokinase-type plasminogen activator amino-terminal fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 154;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17305 MW; A3CCF2FCFF505572 CRC64;
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13;
                                    333 CAADPQWKTDSCQGDSGGPLVCSLQGRMTLTGIVSWGRGCALKDKPGVYTRVSHFLPWIR 392
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Euteleostomi;
Sus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS00021; KRINGLE 1; I.
PROSITE; PS50070; KRINGLE 2; 1.
PROSITE; PS00240; TRYPSIN_DOW; 1.
PROSITE; PS00134; TRYPSIN_HIS; 1.
PROSITE; PS00135; TRYPSIN_SER; 1.
EGF-11ke domain; Glycoprotein; Hydrolase; Kringle; Protease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Takahashi T., Kihara T.;
"Porcine liver factor XII.";
Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
-!- SIMILARITY: CONTAINS 1 KRINGLE DOMAIN.
EMBL; AB022426; BAA37148.1; -.
HSSP; P00763; 1DPO.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chordata; Craniata; Vertebrata;
Cetartiodactyla; Suina; Suidae;
                                                                                                                                                                                                                                                                                                                                                  01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INTERIOR JERNONGES, WILLIAM THE PROPERTY INTERPROPRED TO THE PROPERTY INTERPROPRED TO THE PROPERTY INTERPROPRED TO THE PROPERTY INTERPROPRED TO THE PROPERTY INTERPROPRED TO THE PROPERTY INTERPROPRED TO THE PROPERTY INTERPROPRED TO THE PROPERTY INTERPROPRED TO THE PROPERTY INTERPROPRED TO THE PROPERTY INTERPROPRED TO THE PROPERTY INTERPROPRED TO THE PROPERTY INTERPROPRED TO THE PROPERTY INTERPROPRED TO THE PROPERTY INTERPRED TO THE PROPERTY PROPERTY INTERPRED TO THE PROSITE; PROPERTY INTERPRED TO THE PROSITE; PROPERTY INTERPRED TO THE PROSITE; PROPERTY INTERPRED TO THE PROSITE; PROPERTY INTERPRED TO THE PROSITE; PROPERTY INTERPRED TO THE PROSITE; PROPERTY INTERPRED
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EGF 2.
EGF_like.
Fibrnctnl.
FN Type_II.
IEGF.
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                                                                                                                                                                                                                                                                                                 PRELIMINARY;
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InterPro; IPR000742;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR006209;
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Matches 158; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sus scrofa (Pig).
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                         393 SHTK 396
                                                                                                                                                               641 DRIR 644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9823;
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SEQUENCE 616 A
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097507
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     57 FYRGKASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQ 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     290 EYRGVASTAASGLSCLAWNSDLLYQELHVDSVAAAVLLGLGPHAYCRNPDKDERPWCYVV 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              117 VGLKPLVQECMVHDC-----TLRPRFKII 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                350 KDNALSWEYCRLTACESLARVHSQSPEILAALPESAPAVRPTCGKRHKKRTFLRPR--II 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGEFTTIENQPWFAAIYRRHRGGSVTYVCGGSLISPCWVISATHCFIDYPKKEDYIVYLG 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RSRLNSNTQGEMKFEVENLILHKDYSADTLAHHNDIALLKIRSKEGRCAQPSRTIQTICL 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QHFFNRTTDVTQTFGIEKYVPYTLYSVFNPNNH-DLVLIRLKKKGERCAVRSQFVQPICL 520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PSMYNDPQFGTSCEITGFGKENSTDYLYPEQLKMTVVKLISHRECQQPHYYGSEVTTKML 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | Probom; P0000395; NRINGE II; | NRINGE II; | NRINGE II; | NRINGE II; | NRINGE II; | NRINGE II; | NRINGE II; | NRINGE II; | NRINGE II; | NRINGE II; | NRINGE II; | NRINGE II; | NRINGE II; | NRINGE II; | NRINGE II; | NRINGE II; | NRINGE II; | NRINGE II; | NRINGE II; | NRINGE II; | NRINGE II; | NRINGE II; | NRINGE II; | NRINGE II; | NRINGE II; | NRINGE II; | NRINGE II; | NRINGE II; | NRINGE II; | NRINGE II; | NRINGE II; | NRINGE II; | NRINGE II; | NRINGE II; | NRINGE II; | NRINGE II; | NRINGE II; | NRINGE II; | NRINGE II; | NRINGE II; | NRINGE II; | NRINGE II; | NRINGE II; | NRINGE II; | NRINGE II; | NRINGE II; | NRINGE II; | NRINGE II; | NRINGE II; | NRINGE II; | NRINGE II; | NRINGE II; | NRINGE II; | NRINGE II; | NRINGE II; | NRINGE II; | NRINGE II; | NRINGE II; | NRINGE II; | NRINGE II; | NRINGE II; | NRINGE II; | NRINGE II; | NRINGE II; | NRINGE II; | NRINGE II; | NRINGE II; | NRINGE II; | NRINGE II; | NRINGE II; | NRINGE II; | NRINGE II; | NRINGE II; | NRINGE II; | NRINGE II; | NRINGE II; | NRINGE II; | NRINGE II; | NRINGE II; | NRINGE II; | NRINGE II; | NRINGE II; | NRINGE II; | NRINGE II; | NRINGE II; | NRINGE II; | NRINGE II; | NRINGE II; | NRINGE II; | NRINGE II; | NRINGE II; | NRINGE II; | NRINGE II; | NRINGE II; | NRINGE II; | NRINGE II; | NRINGE II; | NRINGE II; | NRINGE II; | NRINGE II; | NRINGE II; | NRINGE II; | NRINGE II; | NRINGE II; | NRINGE II; | NRINGE II; | NRINGE II; | NRINGE II; | NRINGE II; | NRINGE II; | NRINGE II; | NRINGE II; | NRINGE II; | NRINGE II; | NRINGE II; | NRINGE II; | NRINGE II; | NRINGE II; | NRINGE II; | NRINGE II; | NRINGE II; | NRINGE II; | NRINGE II; | NRINGE II; | NRINGE II; | NRINGE II; | NRINGE II; | NRINGE II; | NRINGE II; | NRINGE II; | NRINGE II; | NRINGE II; | NRINGE II; | NRINGE II; | NRINGE II; | NRINGE II; | NRINGE II; | NRINGE II; | NRINGE II; | NRINGE II; | NRINGE II; | NRINGE II; | NRINGE II; | NRINGE II; | NRINGE II; | NRINGE II; | NRINGE II; | NRINGE II; | NRINGE II; | NRINGE II; | NRINGE II; | NRINGE II; | NRINGE II; | NRINGE II; | NRINGE II; | NRINGE II; 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31.7%; Score 716; DB 11; Length 653; 36.3%; Pred. No. 6e-60; tive 58; Mismatches 162; Indels 50;
                                                                                                   Strausberg R.;
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
-!- SIMILARITY: CONTAINS 1 KRINGLE DOMAIN.
EMBL; BCO19375; AAH19376.1; -.
HSSP; P00761; 1AN1.
                                                                                                                                                                                                                                                          HISSY; WOUTAL! ALM.
HISSY; WOUTAL! ALM.
INTERPRO! IPRO00742; EGF_2.
INTERPRO! IPRO00742; EGF_11ke.
INTERPRO: IPRO00609; FIDEROLLINI.
INTERPRO: IPRO00609; FIDEROLLINI.
INTERPRO: IPRO00601; KINGTO-IITREPRO: IPRO00001; KRINGTO-IITREPRO: IPRO00001; KRINGTO-IITREPRO: IPRO00001; KRINGTO-IITREPRO: IPRO00001; KRINGTO-IITREPRO: IPRO00001; KRINGTO-IITREPRO: IPRO00001; FIDEROLLINI.
PÉTAM: PRO00009; FIDEROLLINI.
PRINTS; PRO00009; TYPERI.
PRINTS; PRO000009; TYPERI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 36.3
Matches 154; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PR00013; FNTYPEII
PRINTS; PR00018; KRINGLE.
                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    153
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410 AAHCLQDRPAPEDLTVVLGQERRNHSCEPCQTLAVRSYRLHEAFS--PVSYQHDLALLRL
                                                                                                                                                                                                                                                                                    SLERCSAPDVHGSSILPGMLCAGFLEGGTDACQGDSGGPLVCEDQAAERRLTLQGIISWG
                                                                                                                                      SHRECOOPHYYGSEVITRMLCAADPOWKIDSCOGDSGGPLVCSLOG----RMILIGIVSWG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS00021; KRINGLE 1; T.
PROSITE; PS50070; KRINGLE 2; 1.
PROSITE; PS50240; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN HIS; 1.
PROSITE; PS00135; TRYPSIN HIS; 1.
EGF-like domain; Glycoprofein; Hydrolase; Kringle; Protease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Schloesser M., Schwager S., Engel W.;
Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
-!- SIMILARITY: CONTAINS 1 KRINGLE DOMAIN.
EMBL: X99571; CA67881.1; -.
HSSP; P00760; 1AQ7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              597 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MGD; MGI:1891012; F12.
InterPro; IPR0011314; CHymotrypsin.
InterPro; IPR001039; EGF like.
InterPro; IPR000083; Fibrnctni.
InterPro; IPR000082; Fibrnctni.
InterPro; IPR0000562; FN Type_II.
InterPro; IPR000001; Kringle.
InterPro; IPR00001254; Ser_protease_Try.
Pfam; PF00008; EGF; 2.
Pfam; PF00039; fn1; 1.
Pfam; PF00039; fn1; 1.
Pfam; PF00089; trypsin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                   613
                                                                                                                                                                                                                                                                                                                                                                                            588 SGCGDRNKPGVYTDVAYYLAWIREHT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SMART; SM00020; Tryp_SPc; 1.
PROSITE; PS00022; EGF 1; 2.
PROSITE; PS01186; EGF 2; 1.
PROSITE; PS01253; FIBRONECTIN 1; 1.
PROSITE; PS00023; FIBRONECTIN 2; 1.
                                                                                                                                                                                                                                                                                                                                                       370 RGCALKDKPGVYTRVSHFLPWIRSHT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
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PRINTS; PRO0013; FNTYPBII.
PRINTS; PR00018; KRINGLE.
ProDom; PD000995; FN Type II; 1.
ProDom; PD000395; KrIngle; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SMART; SM00181; EGF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SMART; SM00058; FN1;
SMART; SM00059; FN2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         247 DIALLKIR-SKEGRCAQPSRTIQTICLP---SMYNDPQFGTSCEITGFGKENSTDYLYPE 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             296 QTPTQAAPPTPVSPRLHVPLMPAQPAPPKPQPTTRTPPQSQTPGALPAKREQPPSLTRNG 355
                                                                                                                                                                                                                                                                                                                                                          -----CQQKTLRPRF----KIIGGEFTTIBNQPWFAAIYRRHRGGSVTYVÇGGSLI 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                402 APCWVLTAAHCLQNRPAPEELTVVLGQDRHNQSCBQCQTLAVRSYRLHESYSPKTYQH-- 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QLKMTVVKLISHRECQQPHYYGSEVITKMLCAADPQWKTDSCQGDSGGPLVC---SLQGR 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          137 KPOCGO----KTLRPRFKIIGGEFTTIENOPWFAAIYRRHRGGSVTYVCGGSLISPCWVIS 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PLSCGORLRKSLSSMTRVVGGLVALRGAHPYIAALYWGHS-----FCAGSLIAPCWVLT 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   194 ATHCFIDYPKKEDYIVYLGRSRLNSNTQGEMKFEVENLILHKDYSADTLAHHNDIALLKI 253
      OVCSTNPCLNGGSCLQTE---GHRLCRCPTGYAGRLCDVDLKERCYSDRGLSYRGMAQTT 232
                                                                                                                                                                                                                                                                                       289 YCRLARCQAPIGEAPPILTPTQSPSEHQDSPLLSREPQPTTQTPSQNLTSAWCAPPEQRG 348
                                                                                                                                                                                                                                                                                                                                                                                                                       401
                                                                                                    TMGRPCLPWNSATVLQQTY-HAHRSDALQLGLGKHNYCRNPDNRRRFWCYVQVGLKPLVQ 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     349 PLPSAGLVGCGQR-LRKRLSSLNRIVGGLVALPGAHPYIAALYWGQN-----FCAGSLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SPCWVISATHCFIDYPKKEDYIVYLGRSRLNSNTQGEMKFEVENLILHKDYSADTLAHHN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               519 FLOEAQVPLISPERCSAADVHGAAFTPGMLCAGFLEGGTDACQGDSGGPLVCEDETAERO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PWAS----EATYRNVTAEQARNWGLGGHAFCRNPDNDIRPWCFVLNRDRLSWEYCDLAQC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Craniata, Vertebrata, Euteleostomi,
Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.

Wada H., Nishioka J., Nakatani K., Kasai Y., Abe Y., Nobori T.;

"Molecular chracterization of coaggulation factor XII-Mie.";

Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.

EMBL; AB095845; BAC23095.1; -

SEQUENCE 615 AA, 67735 MW; 030508870A0C7EDB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30.0%; Score 678; DB 4; Length 615; 34.1%; Pred. No. 2.5e-56; ive 57; Mismatches 159; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              360 MTLTGIVSWGRGCALKDKPGVYTRVSHFLPWIRSHT 395
                                                                                                                                                                                                                          ----ADGKLKFQ----
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Homo sapiens (Human).
Bukaryota, Metazoa; Chordata; Mammalla; Butheria; Primates; NCBI_TaxID=9606;
                                                                                                                                                                                                                                 125 ECMVHDC------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (TrEMBLrel. 23, (TrEMBLrel. 23, (TrEMBLrel. 23,
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Matches 152; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
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01-MAR-2003 (
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C081225
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                100020, Tryp SPc; 1
PS00022, EGF 1; 3.
PS01186; EGF 2; 2.
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                                     PROSITE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----LKPLV----QE------CMVH---DCADGKLKFQ------CGQ---KTLRPRFKI 151
                                                                                                                                                                                                                                                                                                                 QTPTFAPLVVPESQEESPSQAPSLSHAPNDSTDHQTSLSKTNTMGCGQRFRKGLSSFMRV 355
                                                                                                                                                                                                                                                                                                                                                                                            356 VGGLVALPGSHPYIAALYWGNN-----FCAGSLIAPCWVLTAAHCLQNRPAPEELTVVL 409
                                                                                                                                                                                                                                                                                                                                                                                                                                    GRSRLNSNTQGEMKFEVENLILHKDYSADTLAHHNDIALLKIR-SKEGRCAQPSRTIQTI 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3.1 MLCAADPQWKTDSCQGDSGGPLVC---SLQGRMTLTGIVSWGRGCALKDKFGVYTRVSHF 387
                                                                                                                   72
                                                                                                                                                                                                                                                                                                                                                       152 IGGEFTTIENOPWFAAIYRRHRGGSVTYVCGGSLISPCWVISATHCFIDYPKKEDYIVYL
                                                                                                                                                                                             PWNSATVLQQTY-HAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVG-------
                                                                                                                                                                                                                                     240 RW----TVEATYRNMTEKQALSWGLGHHAFCRNPDNDTRPWCFVWSGDRLSWDYCGLEQC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLPSGAAPPSETVLCEVAGWGHQLEGAEEYSTFLQEAQVPFIALDRCSNSNVHGDAILPG
                                                                                                                 CLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFYRGKASTDTMGRPCL
                                                                             Gaps
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                             90;
                                     Length 597;
                                     29.6%; Score 66%; DB 11; Length 59
35.6%; Pred. No. 2.2e-55;
ive 61; Mismatches 154; Indels
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  65638 MW; F3AC07C37D0C0FBA
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PR001254; Ser_protease_Try.
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InterPro; IPR000742; EGF 2.
InterPro; IPR006209; EGF Ca.
InterPro; IPR006209; EGF like.
InterPro; IPR006210; EGF InterPro; IPR006101; Kaingle.
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PRINTS; PRO0018; KRINGLE.
PRODOM; PD000395; Kringle; 1.
SWART; SM00181; EGF; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-OCT-2002 (TrEMBLrel. 22, 01-OCT-2002 (TrEMBLrel. 22, 01-MAR-2003 (TrEMBLrel. 23, Hypothetical protein. Mus musculus (Mouse).
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Pfam, PF00051, kringle, 1.
Pfam, PF00089, trypsin, 1.
                                                          Local Similarity 35.6
hes 152; Conservative
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  597 AA;
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TISSUE=Kidney;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     227 EVENLILHKDYSADTLAHHNDIALLKIRSKEGRCAQPSRTIQTICLPSMYNDP-QFGTSC 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        348 RVEKILKYSQYNERDEIPHNDIALLKLKPVGGHCALESRYVKTVCLPS---DPFPSGTEC 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 127 MVHDCADGKLKF------QCGQKTLRPRF--KIIGGEFTTIENQPWFAAIY---- 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            170 ---RRHRGGSVTYVCGGSLISPCWVISATHCFIDYPKKEDYIVYLGRSRLNSNTQGEMKF 226
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            72
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         294 LITSMPQG----HFCGGALIHPCWVLTAAHC-TDINTKHLKVV-LGDQDLKKTESHEQTF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               116 CQNGGVCSRHRRRSRF-TCACPDQYKGKFCEIGPD-DCYVGDGYSYRGKVSKTVNQNPCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            234 PVPDTPNPVESLLEPVMELPGFESCGKTEVAEHAVKRIYGGFKSTAGKHPWQVSLQTSLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       73 PWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVGLKPL-----VQEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13 CLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFYRGKASTDTMGRPCL
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MEDLINE=96425001; PubMed=8827452;
Choi-Miura N.H., Tobe T., Sumiya J., Nakano Y., Sano Y., Mazda T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606,
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FROMEIR; PSONOOL; KRINGLE 1; 1.
PROSITE; PSONOOL; KRINGLE 1; 1.
PROSITE; PSONOOL; KRINGLE 2; 1.
PROSITE; PSONOOL; TRYPEIN_LOM; 1.
PROSITE; PSONOOL4; TRYPEIN HIS; 1.
PROSITE; PSONOOL35; TRYPEIN HIS; 1.
PROSITE; PSONOOL35; TRYPEIN JES; 1.
KRINGLE; PSONOOL35; TRYPEIN JES; 1.
KRINGLE; PSONOOL35; TRYPEIN JES; 1.
KRINGLE; PSONOOL35; TRYPEIN JES; 1.
KRINGLE; PSONOOL35; TRYPEIN JES; 1.
KRINGLE; PSONOOL35; TRYPEIN JES; 1.
KRINGLE; PSONOOL35; TRYPEIN JES; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 43;
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01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
HGF activator like protein (Hyaluronan binding protein 2).
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                          DB 11; Length
                                                                                                                                                                                                                                                                                                                                                                  Query Match
29.4%; Score 664.5; DB 11; Length
Best Local Similarity 36.9%; Pred. No. 3.9e-55;
Matches 154; Conservative 57; Mismatches 163; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (MAR-1995) to the EMBL/GenBank/DDBJ databases
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73 PWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVGLKPLVQECWVHDCA 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 AWDSPTVLLKMYHAHRSDAIQLGLGKHNYCRNPDNQRRPWCYVQIGLKQFVQFCMVQDCS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13 CLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFYRGKASTDTMGRPCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 CLNGGKCVTYKYFSNIQRCSCPKKFQGEHCEIDTSKTCYQGNGHSYRGKANRDLSGRPCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Povidea; Bovidea; Boxidea;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Lagomorpha, Leporidae, Oryctolagus.
                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
TISSUB-Skeletal muscle;
MEDLINE=21071388; PubMed=11204721;
Balcerzak D., Querenguesser L., Dixon W.T., Baracos V.E.;
Coordinate expression of matrix-degrading proteinases and their activators and inhibitors in bovine skeletal muscle.";
J. Anim. Sci. 79:94-107(2001).
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STRAIN=New Zealand White;
MEDLINE=9906775; PubMed=9837780;
Reno C., Boykiw R., Martinez M.L., Hart D.A.;
"Temporal alterations in mRNA levels for proteinases and inhibit and their potential regulators in the healing medial collateral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 157;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17858 MW; A768D6C72C1FBFB7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAY-2003 (TrEMBLrel. 23, Last annotation update)
Urokinase (Fragment).
Cryctolagus cuniculus (Rabbit).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 VGKSPSSPREKEEFQCGQKALRPRFKIVGGQVTNAEN 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    133 DGKL-----KFQCGQKTLRPRFKIIGGEFTTIEN 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ligament.";
Biochem. Biophys. Res. Commun. 252:757-763(1998).
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY SI.
EMBL; AF069711; AAC95003.1; -.
HSSP, P00749; 1EJN.
MEROPS; S01.231; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match

28.3%; Score 638; DB 6;
Best Local Similarity 70.7%; Pred. No. 3.1e-53;
Matches 111; Conservative 14; Mismatches 24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                J. Anim. Sci. 79:94-10712001).

-i- SIMILARITY: CONTAINS 1 KRINGLE DOMAIN.
EMBL; AF144761; AAD30301.1; -
HSSP; P00749; 1URK.
ILLEPPO: JER006209; EGF_like.
ILLEPPO: JER006001; Kringle.
PRINTS; PR00018; KRINGLE.
PROMO18; KRINGLE.
PROSITE; PS000215; KRINGLE.
PROSITE; PS00021; KRINGLE.
PROSITE; PS00021; KRINGLE.
PROSITE; PS00021; KRINGLE.
PROSITE; PS00021; KRINGLE.
NON TER
IST 157
SEQÜENCE 157 AA; 17858 MW; A768D6C72C1FB
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Urokinase plasminogen activator (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                    NCBI_TaxID=9913;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    277 SAQDVAYPEESPTEPSTKLPGFDSCGKTEIAERKIKRIYGGFKSTAGKHPWQASLQ---- 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                174 GGSVT-----YVCGGSLISPCWVISATHCFIDYPKKEDYIVYLGRSRLNSNTQGEMK 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                333 -SSLPLTISMPQGHFCGGALIHPCWVLTAAHC-TDI-KTRHLKVVLGDDDLKKEEFHEQS 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    226 FEVENLILHKDYSADTLAHHNDIALLKIRSKEGRCAQPSRTIQTICLPSMYNDPQF--GT 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        390 FRVEKIFKYSHYNERDEIPHNDIALLKLKPVDGHCALESKYVKTVCLP----DGSFPSGS 445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                284 SCEITGFGKENSTDYLYPEQLKMTVVKLISHRECQQPHYYGSEVTTKMLCAADPQWK-TD 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            159 CONGATCSRHKRRSKF-TCACPDOFKGKFCEIG-SDDCYVGDGYSYRGKMNRTVNQHACL 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            73 PWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVGLKPLVQE-CMVHDC 131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13 CLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFYRGKASTDTMGRPCL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 4; Length 560;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS50240; TRYPSIN_DOM, 1.
PROSITE; PS00134; TRYPSIN HS; 1.
PROSITE; PS00135; TRYPSIN BER; 1.
EGF-like domain; Glycoprotein; Hydrolase; Kringle; Protease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ouery Match
28.9%; Score 651.5; DB 4; Length :
Best Local Similarity 36.4%; Pred. No. 7.7e-54;
Matches 152; Conservative 58; Mismatches 161; Indels
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Last sequence update)
Last annotation update)
                                                                    157 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                560 AA; 62671 MW;
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01-MAY-2000 (TYEMBLY 13,
01-MAY-2000 (TYEMBLY 13,
01-MAR-2003 (TYEMBLY 1, 23,
        SEQUENCE FROM N.A.
TISSUE=Colon, and Kidney;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
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SEQUENCE 560 A
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Q9TVA8
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DR DR DR KW KW KW SQ SQ

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  112 WCYVQVGLKPLVQECMYHDCADGKLKFQCGQKTLRPR---FKIIGGEFTTIENQPWFAAI 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   169 YRRHRGGSVTYVCGGSLISPCWVISATHCFIDYPKKEDYIVYLGRSRLNSNTQGEMKFEV 228
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         344
                                                                                                                                                                                                                                                                                                                                                                                                                                                           428 NPDGDKGPWCYTTDPSVRWEYCNLKRCSETGGSVVELPTVSQEPSGPSDSETDCMYGNGK 487
                                                                                                                                                                                                                                                                                                                                                                                                       56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          57 FYRGKASTDIMGRPCLPWNSAIVLQQIYHAHRSDALQ----LGLGKHNYCRNPD-NRRRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   488 DYRGKTAVTAAGTPCOGWAA-----OEPHRHSIFTPOTNPRAGLEK-NYCRNPDGDVNGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 542 WCYT-INPRKLYDYCDIPLCASAS-SFECGKPOVEPKKCPGRVVGGCVANPHSWPWQISL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     229 ENLILHKDYSADTLAHHNDIALLKIRSKEGRCAQPSRTIQTICLPSMYNDPQF----GTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CEITGFGKENSTDYLYPEQLKMTVVKLISHRECQQPHYYGSEVTTKMLCAADPQWKTDSC
                                                                                                                                                                                                                                                                                                                                                                                                10 NCDCLNGGTCVSNKYFSNIHWCNCPK--KFGGQHCEI------DKSKTCYEGNGH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rattus norvegicus (Rat).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                        54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              345 QGDSGGPLVCSLQGRMTLTGIVSWGRGCALKDKPGVYTRVSHFLPWI 391
PROSITE; PSS0070; KRINGLE 2; 5.
PROSITE; PSS0240; TRYPSIN DOM; 1.
PROSITE; PSS0134; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN LIS; 1.
Glycoprotein; Hydrolase; Kringle; Protease; Serine protease.
SEQUENCE 812 AA; 90781 MW; 24173260B6A2FFD2 CRC64;
                                                                                                                                                                                                                                                                  Length 812;
                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bangert K., Johnsen A.H., Thorsen S.;
"Rat plasminogen: cDNA and gene structure.";
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2003 (TrEMBLrel. 23, Last annotation update)
Plasminogen protein precursor (EC 3.4.21.7).
PLASMINOGEN.
                                                                                                                                                                                                                                                                  22.4%; Score 505; DB 11; I
33.2%; Pred. No. 1.4e-39;
tive 48; Mismatches 170;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              812 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        receptor site for plasminogen";
J. Blol. Chem. 266:10829-10829 (1991).
-1- SIMILARITY: CONTAINS 5 KRINGLE DOWAINS.
EMBL; AJ242649; CAB46014.1;
-15. PROPATY: 1PMR.
InterPro; IPR001314; Chymctrypsin.
InterPro; IPR001314; Chymctrypsin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=91250378; PubMed=1645711;
                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 33.2%
Matches 135; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 rissum=Liver
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              O9R0W3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 MKFEVEQLILHEGYRADTLAHHNDIALLKILSNNGQCAQPSRSIQTICLPPWNADPNFGT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 WFAAIYRRHRGGSVTYVCGGSLISPCWVVSATHCFINHQKKEDYIVYLGRSRLNSMTPGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               164 WFAAIYRRHRGGSVTYVCGGSLISPCWVISATHCFIDYPKKEDYIVYLGRSRLNSNTQGE
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PLG.
Mus musculus (Mouse).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=129/Sv;
Brathwaite M., Waeltz P., Qian Y., Dudekula D., Schlessinger D.,
Nagaraja R.;
"Genomic Sequence Analysis in the Mouse t-complex Region.";
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
-:- SIMILARITY: CONTAINS 5 KRINGLE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0
                                                                                                                                                                                                                                                                                                                                                                                                              Length 128;
                                                                                                                                                                                                                                                                                                                                                                                                          ' Match 25.9%; Score 585; DB 6; Length 12
Local Similarity 84.4%; Pred. No. 2.9e-48;
les 108; Conservative 6; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Strausberg R.;
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                   128 128
128 AA; 14328 MW; 1BC7ED30E071A06D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
             InterPro; IPR001314; Chymotrypsin.
InterPro; IRR001234; Ser_protease_Try.
Pfam; PR00199; trypsin; 1.
PRINTS; PR00722; CHYMOTRYESIN.
SMART; SM00020; Tryp_SPc; 1.
PROSITE; PS00134; TRYPSIN DOM; 1.
Hydrolase; Kinase; Protease; Serine protease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MGD: MGI:97620; PIG.
MGD: MGI:97620; PIG.
InterPro; IRRO101314; Chymotrypsin.
InterPro; IRR000001; Kringle.
InterPro; IRR003044; PAN.
InterPro; IRR003966; Frothrombin.
InterPro; IRR001254; Ser_protease_Try.
InterPro; IRR001254; Ser_protease_Try.
InterPro; IRR001400; Somatotropin.
Pfam; PF00054; Kringle; S.
Pfam; PF00054; PAN; 1.
Pfam; PF00089; trypsin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
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PRINTS; PRO0189; KRINGLE.
PRINTS; PRO1505; PROTHROMBIN.
PRODOM; PD000395; KRINGLE, 5.
PROSITE; PS00021; KRINGLE_1; 5.
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01-DEC-2001 (TrEMBLrel. 19,
01-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SCEITGFG 291
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NON TER
SEQUENCE
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Matches
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OQ91WJS
DD OQ1-DE
DD O1-DE
DD
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WCYVQVGLKPLVQECMVHDCADGKLKFQCGQKTLRPR---FKIIGGEFTTIENQPWFAAI 168
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          169 YRRHRGGSVTYVCGGSLISPCWVISATHCFIDYPKKEDYIVYLGRSRLNSNTQGEMKFEV 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SRLFLEPT-----RKDIALLKLSSP----AVITDKVIPACLPS----PNYVVADRTE 698
                                                                                                                                      DR EMBL, W14220, AAA34451.1;

DR HSSP; P00747; 2PK4.

BR HSSP; P00747; 2PK4.

BR HSSP; P00747; 2PK4.

DR HSSP; P00747; 2PK4.

BR InterPro; IPR001314; Chymotrypsin.

BR InterPro; IPR003014; PAN.

BR InterPro; IPR003016; Pan app.

BR InterPro; IPR003186; Prochrombin.

BR InterPro; IPR001254; Ser_prothease_Try.

BR Fam; PF00051; kringle; 5.

BR Fam; PF00051; kringle; 5.

BR PRINTS; PR00018; KRINGLE.

BR PRINTS; PR00018; KRINGLE.

BR PRINTS; PR00195; KRINGLE.

BR PRINTS; PR00195; KRINGLE.

BR PRINTS; PR00195; KRINGLE.

BR PRINTS; PR00196; KRINGLE.

BR PRINTS; PR00113; PAN AP; 1.

BR PROSITE; PS00101; KRINGLE.

BR PROSITE; PS00101; KRINGLE.

BR PROSITE; PS00114; TRYPSIN HIS; 1.

BR PROSITE; PS00113; TRYPSIN JER; 1.

BR PROSITE; PS00113; TRYPSIN JER; 1.

BR PROSITE; PS00113; TRYPSIN JER; 1.

BR PROSITE; PS00113; TRYPSIN JER; 1.

BR PROSITE; PS00113; TRYPSIN JER; 1.

BR PROSITE; PS00113; TRYPSIN JER; 1.

BR PROSITE; PS00113; TRYPSIN JER; 1.

BR PROSITE; PS00113; TRYPSIN JER; 1.

BR PROSITE; PS00113; TRYPSIN JER; 1.

BR PROSITE; PS00113; TRYPSIN JER; 1.

BR PROSITE; PS00113; TRYPSIN JER; 1.

BR PROSITE; PS00113; TRYPSIN JER; 1.

BR PROSITE; PS00113; TRYPSIN JER; 1.

BR PROSITE; PS00113; TRYPSIN JER; 1.

BR PROSITE; PS00113; TRYPSIN JER; 1.

BR PROSITE; PS00113; TRYPSIN JER; 1.

BR PROSITE; PS00113; TRYPSIN JER; 1.

BR PROSITE; PS00113; TRYPSIN JER; 1.

BR PROSITE; PS00113; TRYPSIN JER; 1.

BR PROSITE; PS00113; TRYPSIN JER; 1.

BR PROSITE; PS00113; TRYPSIN JER; 1.
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Browne M.J., Chapman C.G., Dodd I., Carey J.E., Lawrence G.M.P., Mitchell D., Robinson J.H.; "Expression of recombinant human plasminogen and aglycoplasminogen in HeLa cells ":
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10 NCDCLNGGTCVSNKYFSNIHWCNCPKKFGGQ------HCEIDKSKTCYEGNGH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NPDADKGPWCFTTDPSVRWEYCNLKKCSGTEASVVAPPPVVLLPDVETPSEEDCMFGNGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        57 FYRGKASTDTMGRPCLPWNSATVLQQTYHAHR----SDALQLGLGKHNYCRNPD-NRRRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               188 GYRGKRATIVIGIPCQDWAA-----QEPHRHSIFIPEINPRAGLEK-NYCRNPDGDVGGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               229 ENLILHKDYSADTLAHHNDIALLKIRSKEGRCAQPSRTIQTICLPSMYNDPQF----GTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CEITGFGKENSTDYLYPEQLKMTVVKLISHRECQQPHYYGSEVTTKMLCAADPQWKTDSC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QGDSGGPLVCFEKDKYILQGVTSWGLGCARPNKPGVYVRVSRFVTWI 803
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 810;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    910 PLASMINOGEN.
90555 MW, B05C7D4B0D020B3C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22.1%; Score 498; DB 4; Lv 33.4%; Pred. No. 6.7e-39; ive 45; Mismatches 170;
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                                                                                                                                 S KRINGLE DOMAINS
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01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                             Fibrinolysis 0:0-0(1991)
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810 AA;
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Matches 136; Conserv
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Q95M89
ID Q95M8
AC Q95M8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 72 LPWNSATVLQQTYHAHRSDALQ----LGLGKHNYCRNPD-NRRRPWCYVQVGLKPLVQEC 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          503 QEWAA-----QEPHSHRIFTPQTNPRAGLEK-NYCRNPDGDVNGPWCYT-MNPRKLYDYC 555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SLISPCWVISATHCFIDYPKKEDYIVYLGRSR---LNSNTQGEMKFEVENLILHKDYSAD 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 297 DYLYPEQLKMTVVKLISHRECQQPHYYGSEVTTKMLCAADPQWKTDSCQGDSGGPLVCSL 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P--GAGRIKEAQLPVÍENKVČNRABYLNNRVKSTELCAGHLAGGIDSCÓGDSGGPLVČFE 770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SVRWEYCNLKRCSETGGGVAESAIVPQVPSAPGTSETDCMYGNGKEYRGKTAVTAAGTPC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27 NIHW--CN---CPKKFGG--QHCEIDK-----SKT-CYEGNGHFYRGKASTDTMGRPC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    127 MVHDCADGKLKFQCGQKTLRPR---FKIIGGEFTTIENQPWFAAIYRRHRGGSVTYVCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       241 TLAHHNDIALLKIRSKEGRCAQPSRTIQTICLPSMYNDPQF----GTSCEITGFGKENST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               667 -----DIALLKL----SRPATITONVIPACLPS----PNYVVADRTLCYITGWGETKGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                         Glycoprotein; Hydrolase; Kringle; Protease; Serine protease; Signal SIGNAL 1 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 812;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
22.2%; Score 500; DB 11; Length 81
Best Local Similarity 33.8%; Pred. No. 4.3e-39;
Matches 136; Conservative 56; Mismatches 148; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QGRMTLTGIVSWGRGCALKDKPGVYTRVSHFLPWIRSHTKEE 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   90535 MW; 8C703C51410EBC9E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
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                               InterProj IPR003609; Pan_app.
InterProj IPR001366; Prochrombin.
InterProj IPR001254; Ser_Drotease_Try.
InterProj IPR001254; Ser_Drotease_Try.
InterProj IPR001400; Somatotropin.
Pfam; PF00024; Pan; 1.
Pfam; PF00029; Prypsin; 1.
PRINTS; PR00122; CHYMOTRYPSIN,
PRINTS; PR010129; KRINGLE.
PRINTS; PR010185; KRINGLE.
PRODOM; PR001095; KRINGLE.
SMART; SM00130; KR; 4.
SMART; SM00130; KR; 4.
SMART; SM00120; Tryp_SPC; 1.
PROSITE; PS00021; KRINGLE_1; 5.
PROSITE; PS00021; KRINGLE_1; 5.
PROSITE; PS00039; SONATOTROPIN_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PLASMINOGEN
                                                                                                                                                                                                                                                                                                                                                                 PSS0240; TRYPSIN_DOM, 1.
PS00134; TRYPSIN_HIS; 1.
PS00135; TRYPSIN_SER; 1.
:ein: Hv4m?
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01-NOV-1996 (TrEMBLrel. 01,
01-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
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01-NOV-1996 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Plasminogen precursor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          812 AA;
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SEQUENCE FROM N.A.
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PROSITE;
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Q15146;
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487 111

26

654 284

Gaps

23;

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121 CEPCQTLAVRSYRLHEAFS--PVSYQHDLALLRLQEDADGSCALLSPYVQPVCLPSGAAR 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            160 ENQPWFAAIYRRHRGGSVTYVCGGSLISPCWVISATHCFIDYPKKEDYIVYLGRSRLNSN 219
                                                                                                                                                                                                                                                                           220 TOGEMKFEVENLILHKDYSADTLAHHNDIALLKIR-SKEGRCAOPSRTIQTICLPSMYND 278
                                                                                                103 RNPDNRRRPWCYVQVGLKPLVQECMVHDCADGKLKFQCGQ---KTLRPRFKIIGGEFTTI
                                                                                                                                                                                                                  67 GAHPYIAALYWGHS-----FCAGSLIAPCWVLTAAHCLQDRPAPEDLTVVLGQERRNHS
                                                                                                                                         15 RTPPOSOTP-----GALPAKREOPPSLTRNGPL--SCGORLRKSLSSMTRVVGGLVALR
                                                                                                                                                                                                                                                                                                                                                                279 POFGISCEITGFGKENSIDYLYPEQLKMTVVKLISHRECQOPHYYGSEVTIKMLCAADPQ
                                                                                                                                                                                                                                                                                                                                                                                                         179 PSETTLCQVAGWGHQFEGAEEYASFLQEAQVPFLSLERCSAPDVHGSSILPGMLCAGFLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                     339 WKIDSCOGDSGGPLVCSLOG---RMILIGIVSWGRGCALKDKPGVYTRVSHFLPWIRSHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cox L.A., Jett C., Hixson J.E.; "Molecular Basis of the Apolipoprotein (a) Null Phenotype: A Splice Site Mutation is Associated with Deletion of a Single Exon in a Null
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Merazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae,
Cercopithecinae, Papio.
                DB 4; Length 300;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A InterProj TRYO(1314) Chymotrypsin.

A InterProj IPRO(01314) Chymotrypsin.

InterProj IPRO(0001) Kringle.

R Pfam, PF(00051) Kringle, 2.

R PRINTS; PRO(016) KRINGLE.

R PRINTS; PRO(016) KRINGLE.

R PRINTS; PRO(016) KRINGLE.

R PRANT; SM(0020) TRYP_SPC; 1.

R PROSITE; PS(0021) KRINGLE_1; 2.

R PROSITE; PS(0021) KRINGLE_2; 2.

R PROSITE; PS(01015) TRYPSIN_DOM; 1.

R PROSITE; PS(0115) TRYPSIN_DOM; 1.

R PROSITE; PS(0115) TRYPSIN_SER; 1.

R PROSITE; PS(0115) TRYPSIN_SER; 1.
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                21.9%; Score 493.5; DB 4; Length 3
37.3%; Pred. No. 5.2e-39;
tive 46; Mismatches 119; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          50041 MW; 974E30744C187B2F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-JUN-1993 (TrEMBLrel. 23, Last annotation update)
Apolipoprotein a (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 493; DB 6;
Pred. No. 9.8e-39;
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                Query Match 21.9%;
Best Local Similarity 37.3%;
Matches 112; Conservative 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         454 AA;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
                                                                                                                                                                                           X MEDLINE=21314992; PubMed=11421942;
X MEDLINE=21314992; PubMed=11421942;
A MEDLINE=21314992; PubMed=11421942;
Shubitowski D. M. Venta P.J., Douglass C.L., Zhou R.-X., Ewart S.L.;
A min Genet. 32:78-78 (2001).

- - SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
- - SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
- - SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
REMBL, AYO08803; AAK14840.1; JOINED.
REMBL, AYO08803; AAK14840.1; JOINED.
REMBL, AYO08803; AAK14840.1; JOINED.
REMBL, AYO08803; CHYMOTRYPSIN.
REMBL, PRO01254; SEPT.
REMBL, PRO01254; SEPT.
REMBL, PRO01254; SEPT.
REMBL, PRO01254; CHYMOTRYPSIN.
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REMBL, PRO012555, CHYMOTRYPSIN.
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REMBL, PRO012555, CHYMOTRYPSIN.
REMBL, PRO012555, CHYMOTRYPSIN.
REMBL, PRO012555, CHYMOTRYPSIN.
REMBL, PRO012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hypothetical protein.
Hypothetical protein.
Homo sapiens (Human).
Eukarosapiens (Human).
Mammalia, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia, Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                       Eguus caballus (Horse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Perissodactyla, Equidae, Equus.
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Strauberg M.

Strauberg M.

Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.

-1 - SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.

REMBL: BC012390; AAH12390.1; -

REMBL: BC012390; AAH12390.1; -

REMBL: BC012390; AAH12390.1; -

REMBL: BC012390; AAH12390.1; -

REMBL: BC001230; AHNOOLS4; Ser_protease_Try.

REMBL: MORO0124; Ser_protease_Try.

REMBL: MORO0125; CHYMOTRYPSIN.

REMBL: MORO0120; TRYPSIN. 1.

REMBL: MORO0130; TRYPSIN DOM; 1.

REMSITE; PSS00134; TRYPSIN HIS; 1.

REMSITE; PSS00135; TRYPSIN BER; 1.

REMSITE; PSS00135; TRYPSIN BER; 1.

REMSITE; PSS00135; TRYPSIN BER; 1.

REMSITE; PSS00135; TRYPSIN M; FFC2BDF9332F636A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21.9%; Score 495; DB 6; Length 103; 87.4%; Pred. No. 9.7e-40; ive 7; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            224 MKFEVENLILHKDYSADTLAHHNDIALLKIRSKEGRCAQPSRT 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MKFEVEKLILHEDYSADTLAHHNDIALLKISSSTGQCAQPSRS 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11525 MW; 0B739514F6331180 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
Last sequence update)
Last annotation update)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update) 01-MAR-2003 (TrEMBLrel. 23, Last annotation update) Plasminogen activator urokinase (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hydrolase; Kinase; Protease; Serine protease.
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01-DEC-2001 (TEMBLrel. 19,
01-DEC-2001 (TEMBLrel. 19,
01-MAR-2003 (TEMBLrel. 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   90; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            103 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
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                                                                                                                                                NCBI_TaxID=9796;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            103
    01-DEC-2001
01-MAR-2003
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NON TER
SEQUENCE
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266 SSKQERDVTKII---KGPAGT----DIALLKL----DRPALINDKVSPVCLPEKDYIVP 313
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Papio hamadryas (Hamadryas baboon).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Butele
Mammalia, Butheria, Primates, Catarrhini, Cercopithecidae,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
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36.2%; Pred. No. 2.8e-38;
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MEROPS; S01.233; -.
Interpro; IPR001314; Chymotrypsin.
Interpro; IPR000001; Kringle.
Interpro; IPR001966; Prothrombin.
Interpro; IPR001264; Ser_protease_Tr
F&an; PF00051; Kringle; I.
Pfam; PF00089; trypsin; I.
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Best Local Similarity 36.29
Matches 129; Conservative
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01-JUN-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     161 NQPWFAAIYRRHRGGSVTYVCGGSLISPCWVISATHCFIDYPKKEDYIVYLGRSRLNSNT 220
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                   14;
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                                                                                                                                                                      156
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                                                                                           CYEGNGHFYRGKASTDIMGRPCLPWNSATVLQ--QTYHAHRSDALQLGLGKHNYCRNPDN 107
                                                                                                                                                                                                                                             --GKLKFQCGQ 142
                                                                                                                                                                                                                                                                                                                     DTGPWCFT---MDPSVRWEYCNLTRCSDTEGTVVTPLTVIPIPSLEARSGQASSSFDCGK 213
                                                                                                                                                                                                                                                                                                                                                                                        KTLRPR---FKIIGGEFTTIENQPWFAAIYRRRGGSVTYVCGGSLISPCWVISATHCFI 199
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Hannmanthaiah R., Day K., Jagadeeswaran P.,

"Comprehensive analysis of blood coagulation pathways in teleostei:

"Comprehensive analysis of blood coagulation of zebrafish
factor VIII.";

Blood Cells Mol. Dis. 0:0-0(2002).

EMBL, AFSIS276; AAN71006.1;

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                                                                                                                                                      CYHGDGQSYRGSFSTTVTGRICQSWSSMTPHQHKRIPENHPNDGLIM-----NYCRNPDA
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01-MAR.2003 (TrEMBLrel. 23, Last sequence update)
01-MAR.2003 (TrEMBLrel. 23, Last sequence update)
101-MAR.2003 (TrEMBLrel. 23, Last annotation update)
101-MAR.2003 (TrEMBLrel. 23, Last annotation update)
101-MAR.2003 (TrEMBLrel.)
101-MAR.2003 (Example 1)
102-MAR.2003 (Example 1)
102-MAR.2003 (Example 2)
101-MAR.2003 (Example 2)
10
                       Gaps
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                           Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QPWFAAIYRRHRGGSVTYVCGGSLISPCWVISATHCFIDYPKKEDYIVYLGRSRLNSNTQ 221
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                                                                                                                                                                                                 428
                                                                                                                                     397
281 FGTSCEITGFGKENST---DYLYPEQLKMTVVKLISHRECQQPHYYGSEVTTKMLCAADP 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                106 D-NRRRPWCYVQVGLKPLVQECMVHDCADGKLKFQCGQKTLRPR----FKIIGGEFTTIEN
                                                                                                                                                                                   369 EGGNDSCQGDSGGPLVCYAQNTFVLQGVTSWGLGCANAMKPGVYTRVSKFVDWIERSIKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CMFGNGKRYRGKKATTVTGTPCQEWAA----KEPHSHLIFTPETYPRAGLEK-NYCRNP
                                                                                                                                         338 QWKTDSCOGDSGGPLVCSLOGRMTLTGIVSWGRGCALKDKPGVYTRVSHFLPWIRSHTKE
                                                           314 SNİBCYVİĞMĞETQDİGGEGY----LKEİGFPVİENKUCNRPSFLNGRVKDHEMCAĞNI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COX L.A., Jett C., Hixson J.E.; "Molecular Basis of the Apolipoprotein (a) Null Phenotype: A Splice Site Mutation is Associated with Deletion of a Single Exon in a Null
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRINTS; PRO0722; CHYMOTRYPSIN.
R PRINTS; PRO018; KRINGLE.
R RINTS; PRO0195; KRINGLE.
R RAMAR; SMO0130; KR; 1.
SMART; SMO0130; KR; 1.
R SMART; SMO0130; KR; 1.
R RAMAR; SMO0020; KRINGLE 1; 1.
R RAMAR; SMO0021; KRINGLE 1; 1.
R ROSITE; PS50070; KRINGLE 2; 1.
R RPOSITE; PS50140; TRYPSIN LIS; 1.
R ROSITE; PS00134; TRYPSIN LIS; 1.
R ROSITE; PS00135; TRYPSIN LIS; 1.
R ROSITE; PS00135; TRYPSIN LIS; 1.
R GIYCODOCCER; HYGLOLAGE; Kringle; Protease; Serine protease.
T NON TER 1 1 1
NON TER 1 1 1
SEQUENCE 334 AA; 36791 MW; C7DC06E03B965286 CRC64;
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SEQUENCE FROM N.A.

STRAIN=white spot;

RX MEDLINE=99423646; PubMed=10491255;

RX Ohashi M., Kawamura K., Fujii N., Yubisui T., Fujiwara S.;

Ohashi M., Kawamura K., Fujii N., Yubisui T., Fujiwara S.;

RI "A retinoic acid-inducible modular protease in budding ascidians.";

RI "A retinoic acid-inducible modular protease in budding ascidians.";

RI "A SIMILARITY: BELONGS TO PEPTIDASE FAMILY SI.

EX MEL; AB030007; BAA82522.1;

EX MEL; AB030007; BAA82522.1;

EX MEL; AB030007; BAA82522.1;

EX MESP; PRO063114; Chymotrypsin.

RINEEPRO; IPR001134; Chymotrypsin.

RINEEPRO; IPR001134; Chymotrypsin.

RINEEPRO; IPR001134; Ser_protease Try.

BR FAM; PR001254; SRCR; 2.

BR FAM; SM00403; SRCR; 2.

BR RINTS; PR00261; LDLRECEPTOR.

BR RINTS; PR00261; LDLRECEPTOR.

BR RART; SM00403; SRCR; 2.

BR RART; SM00403; SRCR; 2.

BR RART; SM00403; SRCR; 2.

BR RART; SM00404; SRCR; 2.

BR RROSITE; PS00406; LDLRA-1; 3.

BR RROSITE; PS00406; LDLRA-1; 3.

BR RROSITE; PS004034; TRYPSIN LDM; 1.

BR RROSITE; PS00134; TRYPSIN LSK; 1.

RR PROSITE; PS00135; TRYPSIN LSK; 1.

RR PROSITE; PS00135; TRYPSIN SER; 1.

KWANLER, SM0135; TRYPSIN SER; 1.

KWANLER, SM0136; TRYPSIN SER; 1.

KWANLER, SM0136; TRYPSIN SER; 1.

KWANLER, SM0136; TRYPSIN SER; 1.

KWANLER, SM0136; TRYPSIN SER; 1.

KWANLER, SM0136; TRYPSIN SER; 1.

KWANLER, SM0136; TRYPSIN SER; 1.

KWANLER, SM0136; TRYPSIN SER; 1.

KWANLER, SM0136; TRYPSIN SER; 1.

KWANLER, SM0136; TRYPSIN SER; 1.

KWANLER, SM0136; TRYPSIN SER; 1.

KWANLER, SM0136; TRYPSIN SER; 1.

KWANLER, SWANLER, SWANLER, SWANLER, SWANLER, SWANLER, SWANLER, SWANLER, SWANLER, SWANLER, SWANLER, SWANLER, SWANLER, SWANLER, SWANLER, SWANLER, SWANLER, SWANLER, SWANLER, SWANLER, SWANLER, SWANLER, SWANLER, SWANLER, SWANLER, SWANLER, SWANLER, SWANLER, SWANLER, SWANLER, SWANLER, SWANLER, SWANLER, SWANLER, SWANLER, SWANLER, SWANLER, SWANLER, SWANLER, SWANLER, SWANLER, SWANLER, SWANLER, SWANLER, SWANLER, SWANLER, SWANLER, SWANLER, SWANLER, SWANLER, SWANLER, SWANLER, SWANLER, SWANLER, SWANLER, SWANLER, SWANLER, SWANLER, SWANL
                                     608 JAPOWVLTAAHCLERSQWPGAYKVILG-------LHREVNPESYSQE
                                                                                                                                                                                                                                                                                     648 IGVSRLFKGPLAADIALLKL----NRPAAINDKVIPACLPSQDFMVPDRTLCHVTGWGDT
                                                                                                                                                                                                                                                                                                                                                                                         129 HDCADGKLKFQCGQKTLRPR---FKIIGGEFTTIENQPWFAAIYRRHRGGSVTYVCGGSL
                                                                                                                                                                                                                                ------NDIALLKIRSKEGRCAQPSRTIQTICLPSMYNDPQFGTSCEITGFGKE
                                                                                                                                                                                                                                                                                                                                                    294 NSTDYLYPE-QLKMTVVKLISHRECQQPHYYGSEVTTKMLCAADPQWKTDSCQGDSGGPL
                                                                                                                   ISPCWVISATHCFIDYPKKEDYIVYLGRSRLNSNTQGEMKFEVENLILHKDYSADTLAHH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ol-MOV-1999 (TrEMBLrel. 12, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Tunicate retinoic acid-inducible modular protease precursor.
TRAMP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20.2%; Score 457; DB 5; Length 86:
39.2%; Pred. No. 6.3e-35;
cive 43; Mismatches 100; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          353 VCSLQGRMTLTGIVSWGRGCALKDKPGVYTRVSHFLPWIRSHTK 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         761 iCFEDDKYVLQGVTSWGLGCARPNKPGVYVRVSRVISWIEDVMK 804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Polyandrocarpa misakiensis.
Bukaryota, Metazoa, Chordata, Urochordata, Ascidiacea,
Stolidobranchia, Styelidae, Polyandrocarpa.
NGBI_TaxID=7723;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL.
F71462865F36A6CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     868 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1999 (TrEMBLrel. 12, Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 39.2
Matches 104; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
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Q9Y1V3
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RAM R.W., Schwartz K., Patthy L.;

"Convergent evolution of apolipoprotein(a) in primates and hedgehog.";

RCC. Mall. Acad. Sci. US.A. 94:11992-11997(1997).

PRILARITY: CONTAINS 5 KRINGLE DOWAINS.

EMBL; AF012297; AAB65760.1; -...

RESP; POONT47; SHPG.

RINGEPCO; IPR001314; Chymotrypsin.

RINGPOS; S01.23; -..

RINGPOS; S01.23; -..

RINGPOS; S01.23; -..

RINGPOS; S01.23; -..

RINGPOS; S01.23; -..

RINGPCOS; S01.23; -..

RINGPCOS; S01.23; -..

RINGPCOS; S01.23; -..

RINGPCOS; S01.23; -..

RINGPCOS; S01.23; -..

REAM; PR00129; FR00136; FRINGLE

BR PRINTS; PR00136; FRINGLE

BR PRINTS; PR00136; KRINGLE

BR PRINTS; PR00136; KRINGLE

BR PRART; S000136; KRINGLE

BR SWART; S000136; KRINGLE

BR PROSITE; PS500140; TRYPSIN DOM; I.

RROSITE; PS500140; TRYPSIN DOM; I.

RROSITE; PS500140; TRYPSIN DOM; I.

RROSITE; PS500140; TRYPSIN DOM; I.

ROSITE; PS500140; TRYPSIN DOM; I.

ROSITE; PS500140; TRYPSIN DOM; I.

ROSITE; PS500140; TRYPSIN DOM; I.

ROSITE; PS500140; TRYPSIN HIS; I.

RW ROSITE; PS500140; TRYPSIN BR; I.

RW ROSITE; PS500140; TRYPSIN BR; I.

RW ROSITE; PS500140; TRYPSIN BR; I.

RW ROSITE; PS500140; TRYPSIN BR; I.

RW ROSITE; PS500140; TRYPSIN BR; I.

RW ROSITE; PS500140; TRYPSIN BR; I.

RW ROSITE; PS500140; TRYPSIN BR; I.

RW ROSITE; PS500140; TRYPSIN BR; I.

RW ROSITE; PS500140; TRYPSIN BR; I.

RW ROSITE; PS500140; TRYPSIN BR; I.

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RW ROSITE; PS500140; TRYPSIN BR; I.

RW ROSITE; PS500140; TRYPSIN BR; I.

RW ROSITE; PS500140; TRYPSIN BR; I.

RW ROSITE; PS500140; TRYPSIN BR; I.

RW ROSITE; PS500140; TRYPSIN BR; I.

RW ROSITE; PS500140; TRYPSIN BR; I.

RW ROSITE; PS500140; TRYPSIN BR; I.

RW ROSITE; PS500140; TRYPSIN BR; I.

RW ROSITE; PS500140; TRYPSIN BR; I.

RW ROSITE; PS500140; TRYPSIN BR; II

RW ROSITE; PS500140; TRYPSIN BR; II

RW ROSITE; PS500140; TRYPSIN BR; II

RW ROSITE; PS500140; TRYPSIN BR; II

RW ROSITE; PS500140; TRYPSIN BR; II

RW ROSITE; PS500140; TRYPSIN BR; II

RW ROSITE; PS500140; TRYPSIN BR; II

RW ROSITE; PS500140; TRYPSIN 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AWTA----QEPHRHIIFTPDIYFRAGLEENYCRNFDGDPNGFWCYT-TNFKKLFDYCDI 552
                                                                                          213
                                     GEMKFE -- VENLILHKDYSADTLAHHNDIALLKIRSKEGRCAQPSRTIQTICLPSMYNDP 279
                                                                                                                                                        280 QF----GTSCEITGFGKENSTDYLYPEQLKMTVVKLISHRECQQPHYYGSEVTTKMLÇAA 335
                                                                                                                                                                                                          214 NYVVADRTECFITGWGETQGT--YGAGLLKEARLPVIENKVCNRYEFLNGRVKSTELCAG 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFYRGKASTDTMGRPCL
                                                                          HLAGGTDSCQGDSGGPLVCFEKDKYILQGVTSWGLGCARPNKPGVYRVSRFVTWI 327
                                                                                                                                                                                                                                                                      336 DPQWKTDSCOGDSGGPLVCSLQGRMTLTGIVSWGRGCALKDKPGVYTRVSHFLPWI 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Metatheria; Diprotodontia; Macropodidae; Macropus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        67;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 908
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Macropus eugenii (Tammar wallaby)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JAN-1998 (TrEMBLrel. 05, 01-JAN-1998 (TrEMBLrel. 05, 01-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
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les 129; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9315;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Plasminogen.
                                                                                                                                                                                                                                                                                                                                    272
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                                                                                                                                                           663 AHCFVREYPIR-DYIIRLGDHIIGVDDETEQLFKIAEIIKH-DYNVIT--KENDIALLRI 718
                                                                                                                                                                                                                                                                                                                                                          SHRECQQPHYYGSEVTTKMLCAADPQWKTDSCQGDSGGPLVCSLQG--RMTLTGIVSWGR 370
                                                                                                                                                                                                                                                                                                                                                                                                         ANKKCLRDSEY-TQLGPTMFCAGYLTGGKDSCQGDSGGFLSCRDQSDDRYYVWGIVSWGN 837
                                                                                                                                                                                                                                    254 RSKEGRCAQPSRTIQTICLPSMYNDPQFGTSCEITGFGKENSTDY-LYPEQLKMTVVKLI 312
QCGQKTL----RPRFKIIGGEFTTIENQPWFAAIYRRHRGGSVTYVCGGSLISPCWVISA 194
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                                         :||:||:|
ECGRXPVIEAPLPTARIVGGSGTEPHEWPWQAGIWL----PWTYWCGGSLIHPCWVLTA
                                                                                                                                                                                                                                                                                                 719 ENDARECATITPEVOTVCLPKSSSOFDAKTICEVTGWGKDSATAVRAYVPVLQEAEIPLI
                                                                                                                     THCFI - DYPKKEDYIVYLGRSRLNSNTQGEMKFEVENLILHKDYSADTLAHHNDIALLKI
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01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Similar to protesse, serine, 8 (Prostasin) (Fragment).
Homo sapiens (Hunan).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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19.7%; Score 445.5; DB 4; Length 3
Best Local Similarity 38.3%; Pred. No. 2.4e-34;
Matches 105; Conservative 36; Mismatches 100; Indels
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Strausberg R.;
Strausberg R.;
Submitted (AUG-2002) to the EMBL/GenBank/DDBJ of the SMILMRITY: BELONGS TO PEPTIDASE FAMILY SI EMBL; BC036846; AAH36846.1;
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INTERPRO 1 PRO01354; Ser_protease_Try.
Pran, PRO0089; trypsin, 1.
PRINTS; PRO0122; trypsin, 1.
PROSTE; PRO0122; CHYMOTRYPSIN.
SMART; SM00020; Tryp SPC; 1.
PROSITE; PS50240; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN_HIS; 1.
PROSITE; PS00135; TRYPSIN_HIS; 1.
PROSITE; PRO0134; TRYPSIN_ERR; 1.
Hydrolase; Protease; Serine protease.
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                                                                                                                                                                                                                         Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
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                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                        Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           243 WVLVGVVSWGKGCALPNRPGVYTSVATYSPWIQA 276
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290 WVLVGVVSWGKGCALPNRPGVYTSVATYSPWIQA 323
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                                                                                                                                         01-OCT-2002 (TrEMBLrel.
                                                                                                                                                        01-OCT-2002 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
                                                                                                                                                                                                                Homo sapiens (Human)
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Sequence

Sequence 12, Appl Sequence 12, Appl Sequence 8, Appli

sequence 3, Appli Sequence 3, Appli Sequence 10, Appl

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Sequence 3,

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Sequence 1 Sequence 1

Sequence

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| Sequence 6, Application US/09880503
| Sequence 6, Application US/09880503
| Patent No. US2002011964A1
| Patent No. US2002011964A1
| APPLICANT CINES, Douglas B
| APPLICANT: HIGAZI, Abd Al-Roof
| TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING MUSCLE CELL AND
| TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING MUSCLE CELL AND
| FILE REFRENCE: 9596-331
| CURRENT FILING DATE: 2001-06-13
| FRIOR APPLICATION NUMBER: US 60/212,847
| PRIOR FILING DATE: 2000-06-20
| SOFTWARE: Patentin Ver. 2.1
| SOFTWARE: Patentin Ver. 2.1
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100.0%; Score 2257; DB 10;
Best Local Similarity 100.0%; Pred. No. 1.4e-190;
Matches 403; Conservative 0; Mismatches 0;
                                                         US-09-914-20-145
US-09-914-20-145
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     TYPE: PRT
ORGANISM: Homo sapiens
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Sequence 149, App
Sequence 4, Appli
Sequence 2, Appli
Sequence 1, Appli
Sequence 7, Appli
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Sequence 21, Appl
Sequence 2, Appli
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Sequence 3, Appli
                                                                                                                     2003, 14:43:04 ; Search time 41.3738 Seconds (without alignments) 1811.566 Million cell updates/sec
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                                                                                                                                                                                       US-09-880-503-6
2257
1 SNELHQVPSNCDCLNGGTCV......VSHFLPWIRSHTKEENGLAL 403
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(c) 1993 - 2003 Compugen Ltd.
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US-09-880-503-3
US-10-301-822-161
US-10-131-985-21
US-10-076-421-2
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US-10-193-656-4
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US-10-264-4688-1
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APPLICANT: Millennium rammaceucicais, .....
APPLICANT: Millennium rammaceucicais, .....
APPLICANT: Guillemete, Tracy L.
APPLICANT: Guillemete, Tracy L.
APPLICANT: Kamatkar, Shubhangi
APPLICANT: Ronahan, John E.
APPLICANT: Schegel, Robert
APPLICANT: Thibodeau, Stephen N.
APPLICANT: Thibodeau, Stephen N.
APPLICANT: Thibodeau, Stephen N.
APPLICANT: Thibodeau, Stephen N.
APPLICANT: Thibodeau, Stephen N.
APPLICANT: THERRY OF COLON CANCER
TITLE OF INVENTION: THERRY OF COLON CANCER
TITLE OF INVENTION: THERRY OF COLON CANCER
FILE REFERENCE: MPM01-029P2RNM
CURRENT APPLICATION NUMBER: US 60/339, 971
PRIOR APPLICATION NUMBER: US 60/331, 978
PRIOR FILING DATE: 2002-03-05
PRIOR FILING DATE: 2002-03-05
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Pred. No. 2.6e-189;
0; Mismatches 0;
                                                                                                        APPLICANT: Millennium Pharmaceuticals, Inc. APPLICANT: Berger, Allison
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 4
US-10-131-985-21
Sequence 21, Application US/10131985
Publication No. US20030199440A1
GENERAL INFORMATION:
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Best Local Similarity 98.1%;
Matches 403; Conservative
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APPLICANT: Davies, Michael J
APPLICANT: Fish, Paul V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-301-822-161
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APPLICANT: CITNES, Abd Al-Roof
APPLICANT: HIGAZI, Abd Al-Roof
TITLE OF INVENTION: TORPOSITIONS AND METHODS FOR MODULATING MUSCLE CELL AND
TITLE OF INVENTION: TISSUE CONTRACTABILITY
FILE REPERENCE: 9596-331
CURRENT APPLICATION NUMBER: US/09/880,503
CURRENT APPLICATION NUMBER: US 60/212,847
PRIOR FILING DATE: 2000-06-20
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PALENTIN Ver. 2.1
SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PLVQECMVHDCADGK-----LKFQCGQKTLRPRFKIIGGEFTTIENQPWFAAIYRRH 172
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                                               CGGSLISPCWVISATHCFIDYPKKEDYIVYLGRSRLNSNTQGEMKFEVENLILHKDYSAD
CGGSLISPCWVISATHCFIDYPKKEDYIVYLGRSRLNSNTQGEMKFEVENLILHKDYSAD
                                                                                                                            TLAHHNDIALLKIRSKEGRCAQPSRTIQTICLPSMYNDPQFGTSCEITGFGKENSTDYLY
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Pred. No. 2.5e-189;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 3, Application US/09880503; Patent No. US20020131964A1; GENERAL INFORMATION:
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98.1%;
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Best Local Similarity 98.1
Matches 403; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
CORGANISM: Homo sapiens
US-09-880-503-3
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APPLICANT: Chen, Yan
APPLICANT: Chen, Yan
APPLICANT: Chen, Yan
APPLICANT: Amarkar, Subbhangi
APPLICANT: Amarkar, Subbhangi
APPLICANT: Amarkar, Subbangi
APPLICANT: Gannavarapu, Manjula
APPLICANT: Gannavarapu, Manjula
APPLICANT: Hoersh, Sebastian
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
TITLE OF INVENTION: OF CERVICAL CANCER
FILE REFERENCE: MINGER: US/10/171,311
CURRENT APPLICATION NUMBER: US 60/298,159
PRIOR PLING DATE: 2001-06-13
PRIOR APPLICATION NUMBER: US 60/298,155
PRIOR PLING DATE: 2001-06-13
PRIOR PLING DATE: 2001-06-13
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PRIOR FILING DATE: 2001-06-13
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ilarity 98.1%; Pred. No. 2.6e-189;
Conservative 0; Mismatches 0;
                                                        Score 2243; DB 14;
Pred. No. 2.6e-189;
0; Mismatches 0;
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GENERAL INFORMATION: APPLICANT: SCALEGE!, Robert APPLICANT: Chen, Yan
                                                              99.4%;
                                                        Query Match
Best Local Similarity 98.1
Matches 403; Conservative
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US-10-171-311-184
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Best Local Similarity
Matches 403; Conserva
      US-10-076-421-2
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US-10-076-421-2

Sequence 2, Application US/10076421

PUDLication No. US20220193304A1

GENERAL INFORMATION:
APPLICANT: WADA, WANBU

TITLE OF INVENTION: ANTI-HIV AGENTS
FILE REFERENCE: HAYAK-9

CURRENT FILING DATE: 2002-05-17

PRIOR APPLICATION NUMBER: US/10/076,421

CURRENT FILING DATE: 2001-02-20

PRIOR FILING DATE: 2001-02-20

PRIOR FILING DATE: 2001-06-19

NUMBER OF SEQ ID NOS: 5

SEQ ID NO 2

LENGTHARE: PATENTIN US: 2

LENGTH: 431
APPLICANT: Huggins, Jonathan P
APPLICANT: McIntosh, Fraser S
APPLICANT: Occleton, Nicholas L
TILE OF INVENTION: Composition
FILE REFERENCE: PCS 10391A
CURRENT APPLICATION NUMBER: US/10/131,985
CURRENT FILING DATE: 2002-04-25
PRIOR PILING DATE: 2000-11-30
PRIOR PLING DATE: 1999-12-29
NUMBER OF SEQ ID NOS: 60
SOFTWARE: PatentIn Ver: 2.1
SOFTWARE: PatentIn Ver: 2.1
LENGTH: 431
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ORGANISM: Homo sapiens
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US-10-131-985-21
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61 KASTDIMGRPCLPWNSAIVLQQIYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVGLK 120
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                                      261 LHKDYSADTLAHHNDIALLKIRSKEGRCAQPSRTIQTICLPSMYNDPQFGTSCEITGFGK
                                                                                    ENSTDYLYPEQLKMTVVXLISHRECQQPHYYGSEVTTKMLCAADPQWKTDSCQGDSGGPL
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               LHKDYSADTLAHHNDIALLKIRSKEGRCAQPSRTIQTICLPSMYNDPQFGTSCEITGFGK
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                                                                                                                                                                                                                                                                           Sequence 4, Application US/10193656; publication No. US20030096733A1; GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: WY. TOT
APPLICANT: LI, JINAN
TITLE OF INVENTION: NOVEL DRUG TARGETS FOR ARTHRITIS
FILE REFERENCE: 3810/1J577-US3; CURRENT APPLICATION NUMBER: US/10/193,656
CURRENT FILING DATE: 2002-07-10
PRIOR APPLICATION NUMBER: US 60/304,461
PRIOR APPLICATION NUMBER: US 60/304,490
PRIOR PRILING DATE: 2001-07-10
PRIOR FILING DATE: 2001-07-10
PRIOR FILING DATE: 2001-07-10
PRIOR FILING DATE: 2001-07-10
PRIOR FILING DATE: 2001-07-10
PRIOR FILING DATE: 2001-07-10
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PRIOR FILING DATE: 2001-07-10
PRIOR FILING DATE: 2001-07-11
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Pred. No. 4.8e-189;
1; Mismatches 0;
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ORGANISM: Homo sapiens
PARBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: GenBank / P007499
DATABASE ENTRY DATE: 1986-07-21
RELEVANT RESIDUES: (1)..(431)
US-10-193-656-4
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Best Local Similarity 97.8%;
Matches 402; Conservative
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                                                                            PLVQECMVHDCADGK-----LKFQCGQKTLRPRFKIIGGEFTTIENQPWFAAIYRRH 172
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SNETHQVPSNCDCLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFYRG
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Sequence 149, Application US/10247671
Fublication No. US20030194721A1
GENERAL INFORMATION:
APPLICANT: Shiffan, Dov
APPLICANT: Shiffan, Dov
APPLICANT: Raser, Matthew R.
FILE REFERENCE: PA-0550 US
FILE REFERENCE: PA-0550 US
CURRENT APPLICATION NUMBER: US/10/247,671
CURRENT FILING DATE: 2002-09-18
PRIOR APPLICATION NUMBER: 60/323,784
PRIOR FILING DATE: 2001-09-19
NUMBER OF SEQ ID NOS: 186
SOFTWARR: PERL PROGram
SEQ ID NO 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20030194721A1 1453334CD1
US-10-247-671-149
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US-10-247-671-149
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APPLICANT: Johnson Jr., Robert W.
APPLICANT: Holzman, Thomas F.
ITLE OF INVENTION: HIGHLY CRYSTALLINE UROKINASE
FILE REPERBNCE: 6310.US.P1
CURRENT APPLICATION NUMBER: US/09/264,468B
CURRENT FILING DATE: 1999-03-05
PRIOR APPLICATION NUMBER: US 09/036,361
PRIOR FILING DATE: 1999-03-06
NUMBER OF SEQ ID NOS: 23
SOFTWARE FASTEGE for Windows Version 4.0
                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Homo sapiens
PEATURE:
NAME/KEY: SIGNAL
LOCATION: (1)...(20)
OTHER INFORMATION: Leader sequence
NAME/KEY: VARIANT
LOCATION: (279)...(279)
OTHER INFORMATION: Xaa = any amino acid
NAME/KEY: VARIANT
LOCATION: (302)...(302)
                                                                                                                                                                                                                                                                                                                                                                                                                                                , LUCATION: (302) ...(302) ; OTHER INFORMATION: Xaa = any amino acid US-09-264-468B-1
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Best Local Similarity 97.6
Matches 401; Conservative
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US-09-880-503-7
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                                                                                                                     SUBJICATION US 103003021938641

Publication No. US2003021938641

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: IDELL, STEVEN

TITLE OF INVENTION: TO ITS SOLUBLE RECEPTOR PROTECTS AGAINST PLEURAL

TITLE OF INVENTION: ADDISONS IN TETRACYCLINE-INDUCED PLEURITIS IN RABBITS

FILE REFERENCE: UTSN.022US

CURRENT APPLICATION NUMBER: US/10/407,821

CURRENT FILING DATE: 2003-04-04

PRIOR PILING DATE: 2002-09-27

PRIOR PILING DATE: 2002-09-27

PRIOR PILING DATE: 2002-09-05

NUMBER OF SEQ ID NOS: 3

SOFTWARE: Patentin Ver. 2.1

SSOFTWARE: Patentin Ver. 2.1

LENGTH 4.1
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        381 VCSLQGRMTLTGIVSWGRGCALKDKPGVYTRVSHFLPWIRSHTKEENGLAL 431
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Patent No. US/0020106775A1
Patent No. US/0020106775A1
PAPLICANT: Wang, Jieyi
APPLICANT: Winabarr, Vicki L.
APPLICANT: Smith, Tack
APPLICANT: Smith, Richard A.
APPLICANT: Smith, Richard A.
APPLICANT: Severin, Jean M.
APPLICANT: Severin, Jean M.
APPLICANT: Bdalji, Rohinton
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US-10-407-821-2
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US-09-264-468B-1
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US-10-407-821-2
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Sequence 7, Application US/09880503
Sequence 7, Application US/09880503
Patent No. US20020131964A1
GENERAL INFORMATION
APPLICANT: CINES, Douglas B
APPLICANT: HIGAZI, Abd Al-Roof
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING MUSCLE CELL AND
TITLE OF INVENTION: TISSUE CONTRACTABILITY
FILE REFERENCE: 9596-331
CURRENT APPLICATION NUMBER: US/09/880,503
CURRENT FILING DATE: 2001-06-13
PRIOR APPLICATION NUMBER: US 60/212,847
PRIOR FILING DATE: 2000-06-20
                                                                                                                                                                                                                                                                                                            81 KASTDIMGRPCLPWNSAIVLQQIYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVGLK 140
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                                                                                                                                      1 SNELHQVPSNCDCLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFYRG
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                                                                      Gaps
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       Length 431;
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                                                                   Indels
98.6%; Score 2225; DB 10; 97.6%; Pred. No. 1e-187; tive 0; Mismatches 2;
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Publication No. US20030219386A1

GENERAL INFORMATION:
APPLICANT: IDELL, STEVEN
TITLE OF INVENTION: TO ITS SOLUBLE RECEPTOR PROTECTS AGAINST PLEURAL
TITLE OF INVENTION: TO ITS SOLUBLE RECEPTOR PROTECTS AGAINST PLEURAL
TITLE OF INVENTION: ADHESIONS IN TETRACYCLINE-INDUCED PLEURITIS IN RABBITS
                                                                                 172
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Sequence 5. Application US/09880503

Patent No. US20020131964A1

SERENAL INFORMATION:

APPLICANT: CINES, Douglas B

APPLICANT: CINES, Douglas B

APPLICANT: CINES, Douglas B

APPLICANT: CINES, DOUGLAS B

APPLICANT: TISSUE CONTRACTABILITY

FILE REFERENCE: 9596-331

CURRENT APPLICATION WUMBER: US/99/880,503

CURRENT FILING DATE: 2001-06-13

PRIOR PLING DATE: 2000-06-20

WINNED OF SEC 75 00-06-20

WINNED OF SEC 75 00-06-20
                     147 PLVQECMVHDCADGKKPSSPPEELKFQCGQKTLRPRFKIIGGEFTTIENQPWFAAIYRRH
                                                                                                                                                                                                    207 RGGSVTYVCGGSLISPCWVISATHCFIDYPKKEDYIVYLGRSRLNSNTQGEMKFEVENLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8 ELKFÓCGÓKTLRPRFKIIGGEFTTIENÓPWFAAIYRRHRGGSVTYVCGGSLISPCWVISA
KASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVGLK
                                                                                    -----LKFQCGQKTLRPRFKIIGGEFTTIENQPWFAAIYRH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        135 KLKFQCGQKTLRPRFKIIGGEFTTIENQPWFAAIYRHRGGSVTYVCGGSLISPCWVISA
                                                                                                                                                                        173 RGGSVTYVCGGSLISPCWVISATHCFIDYPKKEDYIVYLGRSRLNSNTQGEMKFEVENLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Gaps
                                                                                                                                                                                                                                                                                         267 LHKDYSADTLAHNDIALLKIRSKEGRCAQHPGLYRPSACPRCITIPSL 315
                                                                                                                                                                                                                                                             233 LHKDYSADTLAHHNDIALLKIRSKEGRCAQ-----PSRTIQTICLPSM 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 276;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 64.9%; Score 1465; DB 10; Best Local Similarity 99.6%; Pred. No. 5.3e-121; Matches 268; Conservative 1; Mismatches 0;
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                                                                                         PLVQECMVHDCADGK-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin Ver. 2.
SEQ ID NO 5
LENGTH: 276
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                             RESULT 13
US-09-880-503-5
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TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptide
TITLE REFERENCE: PA005P1
CURRENT APPLICATION NUMBER: US/10/106,698
CURRENT FILING DATE: 2002-03-27
PRIOR PILING DATE: 2000-09-28
PRIOR PILING DATE: 1999-09-29
PRIOR PILING DATE: 1999-10-29
PRIOR PILING DATE: 1999-11-03
NUMBER OF SEQ ID NOS: 8564
SOFTWARE: Patentin Ver. 3.0
SEQ ID NO 6266
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               221 PEQLKMITVVKLISHRECQQPHYYGSEVTIKMLCAADPQWKIDSCQGDSGGPLVCSLQGRM 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181 CGGSLISPCWVISATHCFIDYPKKEDYIVYLGRSRLNSNTQGEMKFEVENLILHKDYSAD 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            241 TLAHHNDIALLKIRSKEGRCAQPSRTIQTICLPSMYNDPQFGTSCEITGFGKENSTDYLY 300
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                                                                                                                                                                                                                                                                                                                                                        61 KASTDIMGRPCLPWNSAIVLQQIYHAHRSDALQLGLGKHNYCRNPDNRRPWCYVQVGLK 120
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                                                                                                                                                                                                                                                                 1 SNELHQVPSNCDCLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFYRG
                                                                                                                                                                                                                                                                                                                                                                                                                                               121 PLVQECMVHDCADGKLKFQCGQKTLRPRFKIIGGEFTTIENQPWFAAIYRRHRGGSVTYV
                                                                                                                                                                                                                                                                                                                                                                                                    ------BSSb------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                       1 SNELHQVPSNCDCLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSK----
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Pred. No. 5.9e-122;
3; Mismatches 5;
                                                                                                                                                                             Score 1703; DB 10;
Pred. No. 6.9e-142;
2; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 6266, Application US/10106698 Publication No. US20030109690A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 92.4%;
Matches 267; Conservative
                                                                                                                                                                                  Query Match
Best Local Similarity 79.2%;
Matches 319; Conservative
                            SOFTWARE: Patentin Ver. 2. SEQ ID NO 7 LENGTH: 323 LENGTH: PRT ORGANISM: Homo sapiens
           NUMBER OF SEQ ID NOS: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Homo sapiens
US-10-106-698-6266
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US-10-106-698-6266
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APPLICANT: Fernandes, Elha
APPLICANT: Fernandes, Elha
APPLICANT: Fernandes, Elha
APPLICANT: Fastelli, Luca
APPLICANT: Garlach, Valorie L
APPLICANT: Garlach, Valorie L
APPLICANT: Garlach, Valorie L
APPLICANT: Granden, Valorie L
APPLICANT: Granden, Valorie L
APPLICANT: MacDougall, John R
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING THE SAME
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING THE SAME
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING THE SAME
TILE OF INVENTION: NUCLEIC ACIDS ENCODING THE SAME
TILE REPERBENCE: 15966-598 CIP
CURRENT APPLICATION NUMBER: US.S.N. 60/165,986
PRIOR APPLICATION NUMBER: US.S.N. 60/194,839
PRIOR PELING DATE: 2000-04-05. N. 60/195,637
PRIOR APPLICATION NUMBER: US.S.N. 60/195,637
PRIOR APPLICATION NUMBER: US.S.N. 60/195,637
PRIOR APPLICATION NUMBER: US.S.N. 60/191,347
PRIOR APPLICATION NUMBER: US.S.N. 60/191,347
PRIOR APPLICATION NUMBER: US.S.N. 60/194,195
PRIOR APPLICATION NUMBER: US.S.N. 60/194,195
PRIOR APPLICATION NUMBER: US.S.N. 60/194,195
PRIOR APPLICATION NUMBER: US.S.N. 60/194,195
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PRIOR APPLICATION NUMBER: US.S.N. 60/194,195
PRIOR APPLICATION NUMBER: US.S.N. 60/194,195
PRIOR APPLICATION NUMBER: US.S.N. 60/194,195
PRIOR PLILNG DATE: 2000-07-03
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PRIOR PLING DATE: 2000-0
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                                                                                                                                                                                                                                                                                                                          331 MLCAADPQWKTDSCQGDSGGPLVCSLQGRMTLTGIVSWGRGCALKDKPGVYTRVSHFLPW 390
                                                                                         211 LGRSRLNSNTQGEMKFEVENLILHKDYSADTLAHHNDIALLKIRSKEGRCAQPSRTIQTI 270
1 IIGGEFTTIENQPWPAAIYRRHRGGSVTYVCGGSLISPCWVISATHCFIDYPKKEDYIVY
                                                                                                                        61 LGRSRLNSNTQGEMKFEVENLILHKDYSADTLAHHNDIALLKIRSKEGRCAQPSRTIQTI
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Pred. No. 4e-108;
1; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 47, Application US/09898837A Publication No. US20030077697A1 GENERAL INFORMATION:
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APPLICANT: Spytek, Kimberly A.
APPLICANT: Majumder, Kumud
APPLICANT: Vernet, Corine
APPLICANT: Herrmann, John L.
APPLICANT: Burgess, Catherine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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US-09-898-837A-47
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Best Local Simi
Matches 240;
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Best Local Similarity 100.0%; Pred. No. 6.3e-121;
Matches 268; Conservative 0; Mismatches 0; Indels 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Nienaber, Vicki L.
APPLICANT: Henkin, Jack
APPLICANT: Henkin, Jack
APPLICANT: Smith, Richard A.
APPLICANT: Severin, Jean M.
APPLICANT: Severin, Jean M.
APPLICANT: Goldin, Robinton
APPLICANT: Goldin, Robinton
APPLICANT: Johnson Jr., Robert W.
APPLICANT: HOLlamar, Thomas F.
ITILE OF INVENTION: HIGHLY CRYSTALLINE UROKINASE
FILE REPERENCE: 6310.US.P1
CURRENT APPLICATION NUMBER: US/09/264,468B
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Pred. No. 2e-109;
0; Mismatches 2;
      FILE REFERENCE: UTSN:022US
CURRENT APPLICATION NUMBER: US/10/407,821
CURRENT FILING DATE: 2003-04-04
PRIOR PPLICATION NUMBER: 60/414,202
PRIOR FILING DATE: 2002-09-27
PRIOR APPLICATION NUMBER: 60/370,466
NUMBER OF SEQ ID NOS: 3
SOFTWARE: PARENTIN Ver: 2.1
SEQ ID NO 3
LENGTH: 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  241 DKPGVYTRVSHFLPWIRSHTKEENGLAL 268
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PRIOR FILING DATE: 1998-03-06
NUMBER OF SEQ ID NOS: 23
SOFTWARE: PastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2, Application US/09264468B Patent No. US20020106775A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     59.1%;
99.2%;
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) TYPE: PRT

) ORGANISM: Homo sapiens

US-09-264-468B-2
                                                                                                                                                                                                                                                                                                                                TYPE: PRT
CRGANISM: Homo sapiens
US-10-407-821-3
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Best Local Similarity
Matches 244; Conserval
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151 IIGGEFTTIENQPWFAAIYRRHRGGSVTYVCGGSLISPCWVISATHCFIDYPXXEDYIVY 210

151 IIGGEFTTIENQPWFAAIYRRRGGSVTYVCGGSLISPCWVISATHCFIDYPKKEDYIVY 210

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                                                                                                       AD----POWKT-DSCOGDSGGPLVCSLOGRMTLTGIVSWGRGCALKDKPGVYTRVSHFL 388
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                  334
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APPLICANT: Jiradej Manostoi
APPLICANT: Jiradej Manostoi
APPLICANT: Chactania Trapajuatana
APPLICANT: Chactania Trapajuatana
APPLICANT: Chactania Trapajuatana
APPLICANT: Chactania Trapajuatana
APPLICANT: Friedrich Goetz
APPLICANT: Friedrich Goetz
APPLICANT: Friedrich Goetz
APPLICANT: Friedrich Goetz
APPLICANT: Friedrich Goetz
APPLICANT: Folf-Guenther Werner
TITLE OF INVENTION: Methods for Large Scale Production of Recombinant
TITLE OF INVENTION: DNA-Derived tPA or K2S Molecules
FILE REFERENCE: 0652.2190001
CURRENT FILING DATE: 2001-11-14
FRIOR FILING DATE: 2001-11-14
FRIOR FILING DATE: 2000-11-14
FRIOR FILING DATE: 2000-11-14
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 19
LENGTH: S27
TYPE: PRT
TYPE: PRT

CRAMISM: Homo sapiens
                                                                                                                                    42 QCHSVPVKSCSEPRCFNGGTCQQALYFSDF-VCQCPEGFAGKCCEIDTRATCYEDGGISY
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                                               399 ADLQLPDWTECELSGYGKHEALSPFYSERLKEAHVRLYPSSRCTSQHLLNRTVTDNMLCA
                     275 MYNDPQFGTSCEITGFGKENSTDYLYPEQLKMTVVKLISHRECQQPHYYGSEVTTKMLCA
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Sequence 19, Application US/09987455
Publication No. US20030049729A1
GENERAL INFORMATION:
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DWIRDNMR 526
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Manosroi, Jiradej
APPLICANT: Manosroi, Jiradej
APPLICANT: Tayapiwatana. Chatchai
APPLICANT: Goetz, Friedrich
TITLE OF INVENTION: Methods for Large Scale Protein Production in Prokaryotes
TITLE OF INVENTION: Methods for Large Scale Protein Production in Prokaryotes
TITLE OF INVENTION: MUMBER: US/09/987,457
CURRENT FILING DATE: 2001-11-14
FRIOR APPLICATION NUMBER: G0/268,573
PRIOR APPLICATION NUMBER: GB 00 27 782.2
PRIOR APPLICATION NUMBER: GB 00 27 782.2
PRIOR FILING DATE: 2000-11-14
SOPTWARE: PATENTIN VEY: 2.1
SEQ ID NOS: 18
SOPTWARE: PATENTIN VEY: 2.1
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1 IIGGEFTTIENQPWFAAIYRRHRGGSVTYVCGGSLMSPCWVISATHCFIDYPKKEDYIVY
                                                                      LGRSRLNSNTQGEMKFEVENLILHKDYSADTLAHHNDIALLKIRSKEGRCAQPSRTIQTI
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Publication No. US20030013150A1
GENERAL INFORMATION:
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CRGANISM: Homo sapiens (tPA)
US-09-987-457-18
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Best Local Similarity 37.5'
Matches 183; Conservative
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RESULT 21
US-10-443-701-4
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                 459 GDTRSGGPQANLHDACQGDSGGPLVCLNDGRMTLVGIISWGLGCGQKDVPGVYTKVTNYL 518
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         434 ADLQLPDWTECELSGYGKHEALSPFYSERLKEAHVRLYPSSRCTSQHLLNRTVTDNMLCA 493
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  494 GDTRSGGPQANLHDACQGDSGGPLVCLNDGRMTLVGIISWGLGCGQKDVPGVYTKVTNYL 553
AD----PQWKT-DSCQGDSGGPLVCSLQGRMTLTGIVSWGRGCALKDKPGVYTRVSHFL 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 ELHQVP-SNCD---CLNGGTCVSNKYPSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFY 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 77 ochsvevkscseprcfndgrcooalyfsdf-vcoceegragkceidtratcyedggisy
                                                                                                                                                                                                                   APPLICANT: Pfizer Inc. (All designated States except GB and EP (GB)),
APPLICANT: Pfizer Limited (GB and EP (GB) only)
TITLE OF INVENTION: Pharmaceutical Combinations
FILE REPERBNCE: PSC10951APME
CURRENT APPLICATION NUMBER: US/09/969,271
CURRENT FILING DATE: 2001-10-01
PRIOR APPLICATION NUMBER: GB 0025473.0
PRIOR FILING DATE: 2000-10-17
NUMBER: OF SEQ ID NOS: 7
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97;
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38.0%; Score 858.5; DB 9; Length
Best Local Similarity 37.5%; Pred. No. 3.4e-67;
Matches 183; Conservative 56; Mismatches 152; Indels
                                                                                                                                                                        ; Sequence 7, Application US/09969271
; Patent No. US20020098179A1
; GENERAL INFORMATION:
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, ORGANISM: Homo sapiens
US-09-969-271-7
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DWIRDNMR 561
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RESULT 20 US-09-974-298-145

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 ELHQVP-SNCD---CLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFY
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NAME/KEY: misc_feature
CTHER INFORMATION: Incyte ID No. US20020156263A1 1001470CD1
US-09-974-298-145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      atch 38.0%; Score 858.5; DB 10; Length cal Similarity 37.5%; Pred. No. 3.4e-67; 183; Conservative 56; Mismatches 152; Indels
Sequence 145, Application US/09974298
Patent No. US20020156263A1
GENERAL INFORMATION:
APPLICANT: Chen, Huei-Mei
TITLE OF INVENTION: GENES EXPRESSED IN BREAST CANCER
FILE REPERENCE: PA-0037 P
CURRENT APPLICATION NUMBER: US/09/974,298
CURRENT FILING DATE: 2001-10-04
PRIOR FILING DATE: 2000-10-10
NUMBER OF SEQ ID NOS: 194
SOFTWARE: PERL PROGRAM
SEQ ID NO 145
LENGTH. 642
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Publication No. US20030199016A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             389 PWIRSHTK 396
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TYPE: PRT
CORGANISM: Homo sapiens
US-09-880-503-4
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US-09-880-503-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        156 FITIENQPWFAAIYRRH-RGGSVTYVCGGSLISPCWVISATHCFIDYPKKEDYIVYLGRS 214
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GKYSSEFCSTPACSEGNSDCYFGNGSAYRGTHSLTESGASCLPWNSMILIGKVYTAQNPS
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                                                                                                                                                                                                                                                                                              Length 562;
                                                                                                                                                                                                                                                                                                                                               152; Indels
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Sequence 8, Application WS/10193656

Publication No. US20030096733A1

GENERAL INFORMATION:

APPLICANT: NY, TEX

APPLICANT: LI, Jinan

ITLE OF INVENTION: NOVEL DRUG TARGETS FOR ARTHRITIS

FILE REFERENCE: 3810/1557-US3

CURRENT APPLICATION NUMBER: US/10/193.656

CURRENT FILING DATE: 2002-07-10

PRIOR PILING DATE: 2001-07-10

PRIOR PILING DATE: 2001-07-10

PRIOR FILING DATE: 2001-07-10

PRIOR FILING DATE: 2001-07-10

PRIOR PILING DATE: 2001-07-13

NUMBER OF SEQ ID NOS: 18

SOFTWARE: PRECHTIN VETSION 3.1

FENANCE: PROFILE PROFILE PROFILE PROFILE PROFILE PROFILE PROFILE PROFILE PROFILE PROFILE PROFILE PROFILE PROFILE PROFILE PROFILE PROFILE PROFILE PROFILE PROFILE PROFILE PROFILE PROFILE PROFILE PROFILE PROFILE PROFILE PROFILE PROFILE PROFILE PROFILE PROFILE PROFILE PROFILE PROFILE PROFILE PROFILE PROFILE PROFILE PROFILE PROFILE PROFILE PROFILE PROFILE PROFILE PROFILE PROFILE PROFILE PROFILE PROFILE PROFILE PROFILE PROFILE PROFILE PROFILE PROFILE PROFILE PROFILE PROFILE PROFILE PROFILE PROFILE PROFILE PROFILE PROFILE PROFILE PROFILE PROFILE PROFILE PROFILE PROFILE PROFILE PROFILE PROFILE PROFILE PROFILE PROFILE PROFILE PROFILE PROFILE PROFILE PROFILE PROFILE PROFILE PROFILE PROFILE PROFILE PROFILE PROFILE PROFILE PROFILE PROFILE PROFILE PROFILE PROFILE PROFILE PROFILE PROFILE PROFILE PROFILE PROFILE PROFILE PROFILE PROFILE PROFILE PROFILE PROFILE PROFILE PROFILE PROFILE PROFILE PROFILE PROFILE PROFILE PROFILE PROFILE PROFILE PROFILE PROFILE PROFILE PROFILE PROFILE PROFILE PROFILE PROFILE PROFILE PROFILE PROFILE PROFILE PROFILE PROFILE PROFILE PROFILE PROFILE PROFILE PROFILE PROFILE PROFILE PROFILE PROFILE PROFILE PROFILE PROFILE PROFILE PROFILE PROFILE PROFILE PROFILE PROFILE PROFILE PROFILE PROFILE PROFILE PROFILE PROFILE PROFILE PROFILE PROFILE PROFILE PROFILE PROFILE PROFILE PROFILE PROFILE PROFILE PROFILE PROFILE PROFILE PROFILE PROFILE PROFILE PROFILE PROFILE PROFILE PROFILE PROFILE PROFILE PROFILE PROFILE PROFILE PROFILE PROFILE PROFILE PROFILE PROFILE PROFILE PROFILE PROFI
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11arity 37.5%; Pred. No. 3.4e
Conservative 56; Mismatches
                                    60/163,607
PRIOR FILING DATE: 2000-11-01
PRIOR APPLICATION NUMBER: US 60,
PRIOR FILING DATE: 1999-11-04
NUMBER OF SEQ ID NOS: 4
SEQ ID NO 4
LENGTH: 562
                                                                                                                                                                             ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-443-701-4
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183; Conserv
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US-10-193-656-8
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Best Local S:
Matches 183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  156 FTTIENQPWFAALYRRH-RGGSUTYVCGGSLISPCWVISATHCFIDYPKKEDYIVYLGRS 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     335 AD-----PQWKT-DSCQGDSGGPLVCSLQGRMTLTGIVSWGRGCALKDKPGVYTRVSHFL
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                                                                                                                                                                                                                                               DB 15; Length 562;
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                                                                                                                                                                                                                                         Query Match
38.0%; Score 858.5; DB 15; Length
Best Local Similarity .37.5%; Pred. No. 3.4e-67;
Matches 183; Conservative 56; Mismatches 152; Indels
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Fatent No. US20020131964A1
GENERAL INFORMATION
JAPULCANT: CINES, Douglas B
APPLICANT: HIGAZI, Abd Al-Roof
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: COMPOSITIONS
CURRENT APPLICATION NUMBER: US/09/880,503
CURRENT FILING DATE: 2001-06-13
FRIOR FILING DATE: 2001-06-13
FRIOR FILING DATE: 2000-06-20
NUMBER OF SEQ ID NOS: 18
SEQ ID NO 4
TYPE: PRT
ORGANISM: Homo sapiens
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: GenBank / P00750
DATABASE ENTRY DATE: 1986-07-21
RELEVANT RESIDUES: (1)..(562)
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Best Local Similarity
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Fournier, Alain
Guitton, Jean-Dominique
Jung, Gerard
Yeh, Patrice
Yeh, Patrice
TITLE OF INVENTION: NOVEL BIOLOGICALLY ACTIVE POLYPEPTIDES,
CONTAINING SAID PHARMACEUTICAL COMPOSITION
CONTAINING SAID POLYPEPTIDES
                                                                                                                              64 KASTDIMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVGLK 123
                    9
                                                           SNELHQVPSNCDCLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKICYEGNGHFYRG 63
                                                                                                          KASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVGLK
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100.0%; Pred. No. 3.6e-62;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CUMPUTER: TACETY USES
COMPUTER: TACETY USES
COMPUTER: Macintosh
OPERATING SYSTEM: System 7.1
SOFTWARE: Word 5.1 (Patentin)
CURRENT APPLICATION DATA:
PRIOR APPLICATION NUMBER: US/08/797,689
FILING DATE: 31-JAN-1997
APPLICATION NUMBER: US/08/797,689
FILING DATE: 31-JAN-1994
APPLICATION NUMBER: US/08/256,927
FILING DATE: 28-JUL-1994
APPLICATION NUMBER: PR 92/01064
FILING DATE: 28-JUN-1993
APPLICATION NUMBER: PR 92/01064
FILING DATE: 31-JAN-1993
APPLICATION NUMBER: PR 92/01064
FILING DATE: 31-JAN-1993
APPLICATION NUMBER: PR 92/01064
FILING DATE: 31-JAN-1993
APPLICATION NUMBER: PR 92/01064
FILING DATE: 31-JAN-1993
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NAME: Smith Ph.D., Julie K.
REGISTRATION NUMBER: P-38,619
REFERENCE/DOCKET NUMBER: ST92006-US
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESSE:
ADDRESSEE: Rhone-Poulenc Rorer Inc.
STREET: 500 Arcola Road, 3C43
CITY: Collegeville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (610) 454-3839
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 19426
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                              Sequence 12, Application US/10237667
Publication No. US20030022308A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 454-3808
                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Fleer, Reinhard
                                                                                                                                                                                             121 PLVQECMVHDCADGK 135
                                                                                                                                                                                                                                      124 PLVQECMYHDCADGK 138
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SEQUENCE CHARACTERISTICS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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Best Local Similarity
Matches 135; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: PA
COUNTRY: U
                                                                                                                                                                                                                                                                                                       RESULT 25
US-10-237-667-12
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Patent NO. US20020151011A1

GENERAL INFORMATION: VS20020151011A1

GUITLE OF INVENTION: NOVEL BIOLOGICALLY ACTIVE POLYPEPTIDES,

CONTAINING SAID POLYPEPTIDES

CONTAINING SAID POLYPEPTIDES
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                                                                                                                              KASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVGLK 120
                                                                                                                                                        KASTDIMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNRRPWCYVQVGLK 120
                                                                                1 SNELHQVPSNCDCLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFYRG 60
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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Indels
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100.0%; Pred. No. 3.6e-62;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/797,689
FILING DATE: 31-JAN-1997
APPLICATION NUMBER: US 08/256,927
FILING DATE: 28-UGL-1994
APPLICATION NUMBER: FR 92/01064
FILING DATE: 31-JAN-1992
APPLICATION NUMBER: PCT/FR93/00085
FILING DATE: 28-JAN-1993
ATTONNEY/AGENT INFORMATION:
NAME: SMITH Ph. D., JULIE K.
REGISTRATION NUMBER: P.38,619
REFERENCE/DOCKET NUMBER: ST92006-US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: Macintosh Computers Macintosh CopeRATING SYSTEM: System 7.1 SOFTWARE: Word 5.1 (Patentin) CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/964,186 FILLING DATE: 29-00t-2001 CLASSIFICATION: AUKNOWN>PRIOR APPLICATION DATA:
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein
SEQUENCE DESCRIPTION; SEQ ID NO: 12:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rhorne-Poulenc
STREET: 500 Arcola Road,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 19426
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 138 amino acids
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SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Collegeville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
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Best Local Similarity 100.
Matches 135; Conservative
  Conservative
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  135;
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Matches
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PREPARATION THEREOF AND PHARMACEUTICAL COMPOSITION CONTAINING SAID POLYPEPTIDES
                                                                                           61 KASTDIMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVGLK 120
                                                                                                                                                           64 KASTDÍMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVGLK 123
                  SNELHQVPSNCDCLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFYRG 63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fournier, Alain
Guitton, Jean-Dominique
Jung, Gerard
Yeh, Patrice
TITLE OF INVENTION: NOVEL BIOLOGICALLY ACTIVE POLYPEPTIDES,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 35.1%; Score 793; DB 15; Best Local Similarity 100.0%; Pred. No. 3.6e-62; Matches 135; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/797,689
FILING DATE: 31-74N-1997
APPLICATION NUMBER: US 08/256,927
FILING DATE: 28-701-1994
APPLICATION NUMBER: FR 92/01064
FILING DATE: 31-74N-1992
APPLICATION NUMBER: PR 92/01064
FILING DATE: 28-74N-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: Macintcsh
COMPUTER: Macintcsh
CORFWARE: Word 5.1 (Patentin)
CURRENT APPLICATION DATA: US/10/237,866
FILING DATE: 10-56p-2002
CLASSIFICATION: <university control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of th
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REGISTRATION NUMBER: P-38,619
REFERENCE/DOCKET NUMBER: ST92006-US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSE: Rhone-Poulenc Rorer Inc.
STREET: 500 Arcola Road, 3C43
CITY: Collegeville
STATE: PA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-10-237-866-12
                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 27
US-10-237-866-12
Sequence 12, Application US/10237866
Publication No. US20030036171A1
GENERAL INFORMATION:
APPLICANT: Fleer, Reinhard
Fournier, Reinhard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (610) 454-3839
TELEFAX: (610) 454-3808
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                                                                                                                                                                                                                                              121 PLVQECMVHDCADGK 135
                                                                                                                                                                                                                                                                                                124 PLVQECMVHDCADGK 138
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COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Fleet, Alain Fournier, Alain Guitton, Jean-Dominique Guitton, Jean-Dominique Jung, Gerard Yeh, Patrice Yeh, Patrioe NOVEL BIOLOGICALLY ACTIVE POLYPEPTIDES, TITLE OF INVENTION: PREPARATION THEREOF AND PHARMACEUTICAL COMPOSITION CONTAINING SAID POLYPEPTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                      64 KASTDIMGRPCLPWNSATVLQQIYHAHRSDALQLGLGKGHNYCRNPDNRRRPWCYVQVGLK 123
                                                                                                                                        KASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVGLK 120
9
   SNELHQVPSNCDCLNGGTCVSNKYPSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFYRG
                                                                        SNELHOVPSNCDCLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFYRG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURKENT APPLICATION DATA:
CURKENT APPLICATION DATA:
TLING DATE: 10-Sep-2002
CLASSIEFCATION: CURKNOWN:
PRIOR APPLICATION NATA:
APPLICATION NUMBER: US/08/797,689
TILING DATE: 31-JAN-1997
APPLICATION NUMBER: US 08/256,927
TILING DATE: 28-JUL-1994
APPLICATION NUMBER: PS 24/01064
FILING DATE: 28-JUL-1994
APPLICATION NUMBER: PCT/FR93/00085
FILING DATE: 38-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Smith Ph.D., Julie K.
REGISTRATION NUMBER: P-38,619
REFERENCE/DOCKET NUMBER: ST92006-US
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (610) 454-3808
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHEACTERSITICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: RACOLE-Poulenc Rorer Inc.
STREET: 500 Arcola Road, 3C43
CITY: Collegeville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 19426
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Macintosh
OPERATING SYSTEM: System 7.1
SOFTWARE: WORD 5.1 (Patentin)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (PatentIn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 12, Application US/10237708
Publication No. US2030036170A1
GENERAL INFORMATION:
APPLICANT: Fleer, Reinhard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 138 amino acids
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Best Local Similarity
Matches 135; Conservat
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US-10-237-708-12
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Length 138;

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AFFLICANT.

FOURTILE, Alain
Guitton, Jean-Dominique
Jung, Gerard
Yeh, Partice
TITLE OF INVENTION: NOVEL BIOLOGICALLY ACTIVE POLYPEPTIDES,
CONTAINING SAID POLYPEPTIDES
CONTAINING SAID POLYPEPTIDES
                      120
                                                               64 KASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVGLK 123
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35.1%; Score 793; DB 15;
Best Local Similarity .100.0%; Pred. No. 3.6e-62;
Matches 135; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CUMPUTER: Macintosh OPERATING SYSTEM: System 7.1 SOFTWARE: Word 5.1 (Patentin) CURRENT APPLICATION DATA:

- APPLICATION NUMBER: US/10/237,624 FILING DATE: 10-8ep-2002 CLASSIFICATION: «Unknown»

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/757,689 FILING DATE: 31-JAN-1997 APPLICATION NUMBER: US/08/256,927 FILING DATE: 28-JUL-1994 APPLICATION NUMBER: FR 92/01064 FILING DATE: 31-JAN-1992 APPLICATION NUMBER: PCT/FR93/00085 FILING DATE: 28-JAN-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Smith Ph.D., Julie K.
REGISTRATION NUMBER: P-38,619
REFERENCE/DOCKET NUMBER: ST92006-US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rhone-Poulenc Rorer Inc.
STREET: 500 Arcola Road, 3C43
CITY: Collegeville
STATE: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ), MOLECULE TYPE; protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 12:
WS-10-237-624-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 19426
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                US-10-237-624-12
Sequence 12, Application US/10237624
Publication No. US20030082747A1
GENERAL INFORMATION:
APPLICANT: Fleer, Reinhard
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                                                                                                                                                          124 PLVQECMYHDCADGK 138
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SEQUENCE CHARACTERISTICS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AND PHARMACEUTICAL COMPOSITION
                                                                         64 KASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVGLK 123
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SNELHQVPSNCDCLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFYRG 63
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Guitton, Jean-Dominique
Jung, Geared
Yeh, Patrice
TITLE OF INVENTION: NOVEL BIOLOGICALLY ACTIVE POLYPEPTIDES,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 138;
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100.0%; Pred. No. 3.6e-62;
tive 0; Mismatches 0;
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COMPUTER: Macintosh
OPERATING SYSTEM: System 7.1
SOFTWARE: Word 5.1 (Patentin)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/237,871
FILING DATE: 10-Sep-2002
CLASSIPICATION ATA:
PRIOR APPLICATION ATA:
APPLICATION NUMBER: US/08/797,689
FILING DATE: 28-JUL-1997
APPLICATION NUMBER: US 08/256,927
FILING DATE: 28-JUL-1994
APPLICATION NUMBER: RR 92/01064
FILING DATE: 28-JUL-1994
APPLICATION NUMBER: CR 92/01064
FILING DATE: 28-JUL-1993
APPLICATION NUMBER: CR 92/01064
FILING DATE: 28-JUL-1993
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NAME: SMITH Ph.D., Julie K.
REGISTRATION NUMBER: P-39,619
REFERENCE/DOCKET NUMBER: ST92006-US
TELECOMMUNICATION INFORMATION:
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ADDRESSEE: Rhone-Poulenc Rorer Inc.
STREET: 500 Arcola Road, 3C43
CITY: COllegeville
STATE: PA
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SEQUENCE DESCRIPTION: SEQ ID NO: 12:
                                                                                                                                                                                                                                    RESULT 28
US-10-237-871-12
; Sequence 12, Application US/10237871
; Publication No. US20030036172A1
; GENERAL INFORMATION:
APPLICANT: Fleer, Reinhard
Fournier, Alain
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 138 amino acids
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SEQUENCE CHARACTERISTICS
                                                                                                                                    121 PLVQECMVHDCADGK 135
                                                                                                                                                                            124 PLVQECMVHDCADGK 138
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Best Local Similarity
Matches 135; Conserva
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RESULT 30

US-09-880-503-8

Sequence 8, Application US/09880503

Patent No. US2020131964A1

Sequence 8, Application US/09880503

Patent No. US2020131964A1

GENERAL INFORMATION:

APPLICANT: CINES, Douglas B

APPLICANT: TISSUE CONFOSITIONS AND METHODS FOR MODULATING MUSCLE CELL AND

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING MUSCLE CELL AND

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING MUSCLE CELL AND

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING MUSCLE CELL AND

FILE REPERENCE: 2501-06-13

CURRENT APPLICATION NUMBER: US/09/880,503

CURRENT FILING DATE: 2001-06-13

PRIOR FILING DATE: 2001-06-20

NUMBER OF SEQ ID NOS: 18

SOFTWARR: PatentIN Ver. 2.1

SED ID NO 8

LENGTH: 143

TYPE: PRT

TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 KASTDIMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVGLK 120
61 KASTDIMGRPCLPWNSAIVLQQIYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVGLK 120
                            64 KASTDIMGRPCLPWNSATVLQQIYHAHRSDALQLGLGKGNYCRNPDNRRRPWCYVQVGLK 123
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35.1%; Score 793; DB 10; Length 143;
Best Local Similarity 100.0%; Pred. No. 3.8e-62;
Matches 135; Conservative 0; Mismatches 0; Indels 0
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Sequence 43, Appl
Sequence 50, Appl
Sequence 50, Appl
Patent No. 5185259
Patent No. 5200340
Patent No. 5244676
Sequence 15, Appl
Sequence 15, Appl
Sequence 17, Appl
Sequence 17, Appl
Sequence 17, Appl
Sequence 17, Appl
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Patent No.
Patent No.
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Sequence 73, Application US/09101272G
Patent No. 6509445;
GENERAL INFORMATION:
TITLE OF INVENTION: CANCEROUS METASTASIS INHIBITOR
TITLE REPERENCE: G50979
CURRENT APPLICATION NUMBER: US/09/101,272G
CURRENT APPLICATION NUMBER: US/09/101,272G
CURRENT APPLICATION NUMBER: US/09/101,272G
PRIOR PRIOR PILING DATE: 1996-01-08
NUMBER OF SEQ ID NOS: 107
SEQ ID NO 73
LENGTH: 200
TYPE: PRI
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100.0%; Score 837; DB 4;
Best Local Similarity 100.0%; Pred. No. 4.2e-76;
Matches 143; Conservative 0; Mismatches 0;
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US-09-101-272G-98
Sequence 98, Application US/09101272G
Fatent No. 6509445
GENERAL INFORMATION:
APPLICANT: Nissin Food Products Co., Ltd.
ITILE OF INVENTION: CANCEROUS METASTASIS INHIBITOR
FILE REPERENCE: 650979
CURRENT APPLICATION WHERE: US/09/101,272G
CURRENT FILING DATE: 1998-07-08
                                                                                                                                                                                                                       PCT-US94-05669A-15
PCT-US94-05669A-17
US-08-438-745-13
US-09-219-019-13
PCT-US94-05669A-13
                  5200340-6
US-08-811-949-43
US-08-560-098A-50
US-08-883-795A-38
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US-08-438-745-15
US-08-438-745-17
US-09-219-019-15
US-09-219-019-17
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5200340-2
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OTHER INFORMATION: ATF domain of uPA
              ORGANISM: Homo sapiens
 US-09-101-272G-73
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                                                                                                               3, 2003, 14:35:43; Search time 7.39655 Seconds (without alignments) 818.010 Million cell updates/sec
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                                                                                                                                                                                                                        1 SNELHQVPSNCDCLNGGTCV......QECMVHDCADGKKPSSPPEE 143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 4
Patent No.
Sequence 2
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/cgn2_6/ptodata1/liaa/PCTUS_COMB.pep:*
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                  GenCore version 5.1.6
(c) 1993 - 2003 Compugen Ltd
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US-08-087-163-1

US-08-153-799-18

US-08-157A-3

US-07-942-157A-3

US-09-101-272G-1

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US-09-101-272G-1

US-08-101-272G-1

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Maximum Match 100%
Listing first 45 summaries
                                                                                   using sw model
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                              seq length: 0
seq length: 200000000
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Match Length
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                                                                                                                      December
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score
                                                                                   protein
                                                                                                                                                                                                                                                                                                                                                                              Minimum DB
Maximum DB
                                                                                                                                                                                                                          Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Database
                                                                                                                                                                                                                                                                                                            Searched:
                                                                                                                    Run on:
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ô 9 80

Gaps

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61 KASTDIMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVGLK 120
                                                                                                                                                                                                      61 KASTDIMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVGLK 120
                                                                                                                                                   1 SNELHQVPSNCDCLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFYRG 60
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                                                                                                        1 SNELHQVPSNCDCLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFYRG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 18, Application US/08286748B
Patent No. 5759542
GENERAL INFORMATION:
APPLICANT: Victor Gurewich
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DELIVERY
TITLE OF INVENTION: OF DRUGS BY PLATELETS FOR THE TREATMENT OF
TITLE OF INVENTION: CARDIOVASCULAR AND OTHER DISEASES
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
                                                             ..
0
            Length 411;
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          ; Score 837; DB 1;
; Pred. No. 9.4e-76;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
100.0%; Score 837; DB 1;
Best Local Similarity 100.0%; Pred. No. 9.4e-76;
Matches 143; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: 0.s....
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: 1BM PS/2 Model 502 or 55SX
COPERATING SYSTEM: MS-DOS (Version 5.0)
SOSTIWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/286,748B
TT-ING DATE: August 5, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: J. Peter Fasse
REGISTRATION NUMBER: 32,983
REFERENCE/DOCKET NUMBER: 04547/013001
TELECOMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEPHONE: (617) 542-8906
                                                                                                                                                                                                                                                                                                  121 PLVQECMVHDCADGKKPSSPPEE 143
                                                                                                                                                                                                                                                                                                                                             121 PLVOECMVHDCADGKKPSSPPEE 143
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STREET: 225 Franklin Street
CITY: Boston
          100.0%;
ilarity 100.0%;
Conservative 0;
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CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
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INFORMATION FOR SEQ 1D NO:
SEQUENCE CHARACTERISTICS:
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U.S.A.
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STRANDEDNESS: single
TOPOLOGY: linear
       Query Match
Best Local Similarity
Matches 143; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-286-748B-18
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                                                                                                                                                                                                                                                                                                                                                                                                                            2 SNELHQVPSNCDCLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFYRG 61
                                                                                                                                                                                                                                                                                                                                                                                        1 SNELHQVPSNCDCLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFYRG
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0
                                                                                                                                                                                                                                                                                             Length 208;
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                                                                                                                                                                                                                                                                                          Query Match 100.0%; Score 837; DB 4; : Best Local Similarity 100.0%; Pred. No. 4.4e-76; Matches 143; Conservative 0; Mismatches 0;
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ZIP: 02110-2804

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/087,163
FILING DATE: 07/02/93
CLASSIFICATION: 514
PRICR APPLICATION: 514
PRICR APPLICATION UNBER:
FILING DATE:
FILING DATE:
APPLICATION NUMBER:
FILING DATE:
ANDER TORNEY AGENT INFORMATION:
                                                                                                                                                                                            ; FEATURE:
; OTHER INFORMATION: ATFHI-ML chimeric protein
US-09-101-272G-98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1, Application US/08087163
Patent No. 5472692
GENERAL INFORMATION:
APPLICANT: Liu, Jian-Ning
APPLICANT: Gurewich, Victor
TITLE OF INVENTION: PRO-UROKINASE MUTANTS
WUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        04353/003001
PRIOR APPLICATION NUMBER: JP 1059/1996
PRIOR FILING DATE: 1996-01-08
NUMBER OF SEQ ID NOS: 107
SOFTWARE: Patentin version 3.1
SEQ ID NO 98
LENGTH: 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 PLVQECMVHDCADGKKPSSPPEE 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              122 PLVQECMVHDCADGKKPSSPPEE 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Fasse, J. Peter
REGISTRATION NUMBER: 32,983
REPREDICE/DOCKET NUMBER: 0435
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Fish & Richardson STREET: 225 Franklin Street CITY: Boston STATE: Massachusetts COUNTRY: U.S.A.
                                                                                                                                              TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEX: 200154
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TOPOLOGY: N/A
US-08-087-163-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 3
US-08-087-163-1
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61 KASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVOVGLK 120
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Best Local Similarity 100.0%; Pred. No. 9.9e-76;
Matches 143; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/942,157A
FILING DATE: 1992098
CLASSIFICATION 1435
PRIOR APPLICATION NUMBER: US 07/631673
APPLICATION NUMBER: US 07/631673
APPLICATION NUMBER: US 07/631673
APPLICATION NUMBER: 31,284
REGISTRATION NUMBER: 31,284
RESPERNCE/DOCKET UNBER: TS1108CONT.
TELEPHONE: (444)815-6508
                                                                                                          Sequence 3, Application US/07942157A
Patent No. 5648253
GENERAL INFORMATION:
TITLE OF INVENTION: Inhibitor-Resistant Urokinase
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: ALIBETISK & COdy
STREET: 1100 Peachtree Street Suite 2800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /label= peptide /
/note= "WAP signal"
121 PLVQECMVHDCADGKKPSSPPEE 143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                COUNTRY: USA
ZIP: 30309-4530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 430 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 430 amino aride
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: Peptide
                                                                                                                                                                                                                                                                                                                              CITY: Atlanta
STATE: Georgia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 SNELHQVPSNCDCLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFYRG 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
ZIP: 07974
COMPUTER: TEADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/153,799
FILING DATE:
                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Ballance, David J
APPLICANT: Ballance, David J
APPLICANT: Goodey, Andrew R
TITLE OF INVENTION: Polypeptides
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: R Hain Swope, BOC Health Care Inc
STREET: 100 Mountain Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
PRICR APPLICATION DATA:
APPLICATION DATA:
APPLICATION MDER: 10 07/847975
FILING DATE: 06-MAR.1992
PRICR APPLICATION NDER: 68 990916.2
FILING DATE: 29-APR.1992
PRICR APPLICATION NDMER: 29-APR.1990
PRICR APPLICATION NDMER: PCT/GB90/00650
FILING DATE: 26-APR.1990
PRICR APPLICATION NDER: 26-APR.1990
PRICR APPLICATION NDER: 26-APR.1990
PRICR APPLICATION NDER: 36-APR.1990
PRICR APPLICATION NDER: 29-CCT-1991
ATTORNEY/AGENT INFORMATION:
REFERENCE/DOCKET NUMBER: 92H894
REFERENCE/DOCKET NUMBER: 92H832
TELECPAX: (908) 771 6159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 PLVQECMVHDCADGKKPSSPPEE 143
                                                                     121 PLVOECMVHDCADGKKPSSPPEE 143
                                                                                                                                     RESULT 5
US-08-153-799-18
'Sequence 18, Application US/08153799
'Patent No. 5766883
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : 411 amino acids
amino acid
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-153-799-18
                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Murray Hill
STATE: New Jersey
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US-09-181-816-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        81 KASTDIMGRPCLPWNSATVLQQIYHAHRSDALQLGLGKGHNYCRNPDNRRRPWCYVQVGLK 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 KASTDIMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVGLK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 SNELHQVPSNCDCLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFYRG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21 SNELHQVPSNCDCLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFYRG 80
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: Urokinase-type plasminogen activator (uPA):-09-101-272G-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 100.0%; Score 837; DB 4; Length 431; Best Local Similarity 100.0%; Pred. No. 1e-75; Matches 143; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: KOBAYASHI, YO-ICHI,OMORI, MUNEKI;YAMADA, CHIKAKO
TITLE OF INVENTION: RAPIDLY ACTING PROUROKINASE
NUMBER OF SEQUENCES: 23
             Sequence 1. Application US/09101272G
Patent No. 6509445
GENERAL INFORMATION:
APPLICANT: Nissin Food Products Co., Ltd.
TITLE OF INVENTION: CANCEROUS METASTASIS INHIBITOR
FILE REFERENCE: 050979
CURRENT APPLICATION NUMBER: US/09/101,272G
CURRENT FILING DATE: 1998-07-08
PRIOR PRILICATION NUMBER: UP 1059/1996
PRIOR FILING DATE: 1996-01-08
NUMBER OF SEQ ID NOS: 107
SOFTWARE: Patentin version 3:1
SEQ ID NO!
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 PLVQECMVHDCADGKKPSSPPEE 143
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APPLICATION NUMBER: US/07/340,007
FILING DATE: 18-AUG-1988
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION: (21)..()
OTHER INFORMATION:
NAME/KEY: misc_feature
LOCATION: (20)..()
                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Patent No. 5188829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 431
-09-101-272G-1
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61 KASTDIMGRPCLPWNSAIVLQQIYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVGLK 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                 APPLICANT: WAZAR, Andrew P.
APPLICANT: WAZAR, Andrew P.
APPLICANT: JONES, Terence R.
TITLE OF INVENTION: CYCLIC PEPTIDE LIGANDS THAT TARGET UROKINASE
TITLE OF INVENTION: DASSMINOSEN ACTIVATOR RECEPTOR
FILE REFERENCE: 32904200300 SIDN 1-7
CURRENT APPLICATION NUMBER: US/09/181,816
CURRENT PILING DATE: 1998-10-29
NUMBER OF SEQ ID NOS: 2.0
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Pred. No. 9.4e-75;
0; Mismatches 1; Indels
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ZIP: 2005
ZIP: 2005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/560,098A
FLING DATE: 17-NOV-1995
PRIOR APPLICATION DATA:
FLING DATE: 17-NOV-1994
ATTORNY AGENT INFORMATION:
NAME: EVANS, Joseph D.
REGISTRATION UNMER: 148/42448
TELECOMONICATION UNDERRE: 148/42448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: WIENDY, Stephan
APPLICANT: WIENDY, Stephan
APPLICANT: HEINZEL-WIELAND, Regina
APPLICANT: HEINZEL-WIELAND, Regina
APPLICANT: STEFFENS, Gard Josef
ATTLE OF INVENTION: Coagulation-inhibiting Properties
ITILE OF INVENTION: Coagulation-inhibiting Properties
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: ADDRESS:
ADDRESSEE: ADDRESSE:
ADDRESSEE: ADDRESSE:
ADDRESSEE: ADDRESSE:
ADDRESSEE: ADDRESSE:
ADDRESSEE: ADDRESSE:
ADDRESSEE: ADDRESSE:
COUNTRY: USA
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; Sequence 48, Application US/08560098A
; Parent No. 5976841
; GENERAL INFORMATION:
; Sequence 1, Application US/09181816; Patent No. 6277818; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 99.3%;
Matches 142; Conservative (
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ORGANISM: Homo sapiens
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61 KASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVGLK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 KASTDIMGRPCLPWNSAYVLQQIYHAHRSQALQLGLGKHNYCRNPQNRRRPWCYYQVGLK 120
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Patent No. 5876969
GENERAL INFORMATION:
APPLICANT: Fleer, Reinhard
APPLICANT: Guitton, Jaan-Dominique
APPLICANT: Guitton, Jaan-Dominique
APPLICANT: Veh, Patrice
ITILE OF INVENTION: NOVUL BIOLOGICALLY ACTIVE POLYPEPTIDES,
TITLE OF INVENTION: CONTAINING SAID POLYPEPTIDES
ITILE OF INVENTION: CONTAINING SAID POLYPEPTIDES
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rhone-Poulenc Rorer Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 SNELHQVPSNCDCLNGGTCVSNKYFSNIHWCNCPKKFGGOHCEIDKSKTCYEGNGHFYRG
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97.2%; Pred. No. 7.9e-74;
tive 0; Mismatches 4;
                                                                                                                                            SOFTWARE: ASCII TEXT
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/142,590B
FILING DATE: 25-00T-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/042,318
FILING DATE: 02-ARR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Myers, Paul L.
REGISTRATION NUMBER: 35,965
REFERENCE/DOCKET NUMBER: MGP-009CP
TELECOMMUNICATION INFORMATION:
TELEPHORE: (617) 227-7400
TELEFRAX: (617) 227-5940
INFORMATION FOR SEQ ID NO: 25:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E: Rhone-Poulenc Rorer Inc.
500 Arcola Road, 3C43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 PLVQECMVHDCADGKKPSSPPEE 143
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                                                                                   3: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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Word 5.1 (PatentIn)
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amino acid
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Best Local Similarity 97.2
Matches 139; Conservative
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FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS LENGTH: 157 amino aci
    Massachusetts
                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 19426
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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OPERATING SYSTEM: SY
SOFTWARE: Word 5.1 (
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                                                                                                                              OPERATING SYSTEM:
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US-08-142-590B-25
Sequence 25, Application US/08142590B
Sequence 25, Application US/08142590B
Parent No. 6120765
GENERAL INFORMATION:
APPLICANT: HIBINO, Tashihiko; TAKAHASHI, Tadahito; HORII, Izumi, and GOET;
TITLE OF INVENTION: UROKINASE PLASMINOGEN ACTIVATOR FRAGMENTS
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
STREET: 28 State Street
CITY: BOSLON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ξ,
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                                                                                                                                                                                                                                                                                                                                        1 SNELHQVPSNCDCLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFYRG 60
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Pred. No. 3.5e-74;
0; Mismatches 0; Indels 1;
                                                                                                                                                                                                                  Length 411;
                                                                                                                                                                                         Score 826; DB 2; Length 41.
Pred; No. 1.2e-74;
17 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5219569-2
;Patent No. 5219569
; APPLICANT: BLABER, MICHAEL;HEYNEKER, HERBERT L.;VEHAR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: PROTEASE RESISTANT URCKINASE NUMBER OF SEQUENCES: 6
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/766,858
FILING DATE: 16-AUG-1985
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 725,468
FILING DATE: 22-APR-1985
                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 PLVQECMVHDCADGKKPSSPPEE 143
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                                                                                                                                                                                                            98.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 99.3%;
Matches 142; Conservative
TELEFAX: (202) 628-8844
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                               LENGTH: 411 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                            Query Match
Best Local Similarity 99.3
Matches 142; Conservative
                                                                                                                                                 ; MOLECULE TYPE: protein US-08-560-098A-48
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61 KASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVGLK 120
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Patent No. 5976841
GENERAL INFORMATION:
APPLICANT: WENENDT, Stephan
APPLICANT: HEINZEL-WIELAND, Regina
APPLICANT: STEFFENS, Gerd Josef
TITLE OF INVENTION: Proteins having Fibrinolytic and
TITLE OF INVENTION: Coagulation-inhibiting Properties
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: 1200 G Street, N.W., Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
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                                                                                                                                                                                                                                                                                                                                                                    Sequence 96, Application US/09101272G
Parent No. 650944S
GENERAL INFORMATION:
APPLICANT: NISSIN FOOD PRODUCTS CO., Ltd.
TITLE OF INVENTION: CANCEROUS METASTASIS INHIBITOR
FILE REPERENCE: 050997
CURRENT APPLICATION NUMBER: US/09/101,272G
CURRENT FILING DATE: 1996-07-08
PRIOR APPLICATION NUMBER: UP 1059/1996
PRIOR APPLICATION NUMBER: 1996-07-08
NUMBER OF SEQ ID NOS: 107
SSOFTWARE: ParentIn version 3.1
SEQ ID NO 96
LENGTH: 201
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COMPUTER REARABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT.
ORGANISM: Artificial Sequence
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Best Local Similarity 100.03
Matches 134; Conservative
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US-09-101-272G-96
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 SNELHQVPSNCDCLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFYRG 63
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APPLICANT: Nissin Food Products Co., Ltd.
ITILE OF INVENTION: CANCEROUS METASTASIS INHIBITOR
FILE REFERENCE: 050979
CURRENT APPLICATION NUMBER: US/09/101,272G
CURRENT FILING DATE: 1998-07-08
PRIOR APPLICATION NUMBER: UP 1059/1996
PRIOR FILING DATE: 1996-01-08
NUMBER OF SEQ ID NoS: 107
SOPTWARE: Patentin version 3.1
SEQ ID NO 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                94.1%; Score 788; DB 4; I
100.0%; Pred. No. 3.1e-71;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. 6.7e-72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           94.7%; Score 793; DB
100.0%; Pred. No. 6.7
ive 0; Mismatches
                CARGAIN THELLAND DATA CARGAIN CARGAIN AND CARGAIN AND CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN CARGAIN 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 57
TELECOMMUNICATION INFORMATION:
TELEPHONE: (610) 454-3839
TELEFAX: (610) 454-3808
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 PLVQECMVHDCADGK 135
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CURRENT APPLICATION DATA: APPLICATION NUMBER: US
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Best Local Similarity 100.
Matches 134; Conservative
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Matches 135; Conservative
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US-09-101-272G-80
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62 KASTDIMGRPCLPWNSAIVLQQIYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVGLK 121
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Gaps . 0

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APPLICANT: STEFFENS, GERD J.
APPLICANT: WINENDT, STEPHANS
APPLICANT: WINENDT, STEPHANS
APPLICANT: SCHNEIDER, JOHANNES
APPLICANT: HEINZEL-WIELAND, REGINA
APPLICANT: BAUNDERS, DEREK J.
TITLE OF INVENTION: IMPROVED FIRENDLYTIC CHARACTERISTICS AND THROMBIN
TITLE OF INVENTION: IMPROVED FIRENDLYTIC CHARACTERISTICS AND THROMBIN
TITLE OF INVENTION: IMPROVED FIRENDLYTIC CHARACTERISTICS AND THROMBIN
TITLE OF INVENTION: IMPROVED FIRENDLYTIC CHARACTERISTICS AND THROMBIN
TITLE OF INVENTION: IMPROVED FIRENDLYTIC CHARACTERISTICS AND THROMBIN
TITLE OF INVENTION: IMPROVED FIRENDLYTIC CHARACTERISTICS AND THROMBIN
TITLE OF INVENTION: MARKEOWN, Edwards & Lenahan
STREET: 1200 G Street, N. W. Suite 700
COUNTRY: Washington, D.C.
COUNTRY: U.S.
                                                                                                                                                                                                                                                                                                                                                                                                          47 SKTCYEGNGHFYRGKASIDIMGRPCLPWNSAIVLQQTYHAHRSDALQLGLGKHNYCRNPD 106
                                                                                                                                                                                                                                                                                                                                                                                                                                         1 SKTCYEGNGHFYRGKASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPD 60
                                                                                                                                                                                                                                                                                                  Length 365;
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COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/720,012
FILING DATE: 27-SEP-1996
CLASSIFICATION 1435
PRIOR APPLICATION 1435
PRIOR APPLICATION NUMBER: US 08/093,741
FILING DATE: 20-JUL-1993
APPLICATION NUMBER: DE P43 23 754.1
FILING DATE: 15-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: EVANS, JOSEPh D.
REGISTRATION NUMBER: 26,269
REFERENCE/POCKET NUMBER: 148/41345
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    107 NRRRPWCYVQVGLKPLVQECMVHDCADGKKPSSPPEE 143
                                                                                                                                                                                                                                                                                                     Score 558; DB 1; L
Pred. No. 5.7e-48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 NRRRPWCYVQVGLKPLVQECMVHDCADGKKPSSPPEE 97
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66.7%; Score 558; DB

Best Local Similarity 100.0%; Pred. No. 5.77

Matches 97; Conservative 0; Mismatches
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REFERENCE/DOCKET NUMBER: 148/41345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 83, Application US/08720012; Patent No. 5747291
                 TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)628-8800
FELEPAX: (202)628-8844
INFORMATION FOR SEQ ID NO: 83: SEQUENCE CHARACTERISTICS:
LENGTH: 365 amino acids
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amino acid
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                       TOPOLOGY:
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APPLICANT: STEFFENS, GERD J.
APPLICANT: STEFFENS, GERD J.
APPLICANT: SCHNEIDER, JOHANNES
APPLICANT: BEINZEL-WIELAND, REGINA
APPLICANT: SAUNDERS, DEREK J.
ITILE OF INVENTION: INPROVED FIBRINOLYTIC CHARACTERISTICS AND THROMBIN
ITILE OF INVENTION: INHIBITING EFFECT
NUMBER OF SEQUENCES: 83
CORRESPONDENCE ADDRESS:
ADDRESSEE: Evenson, McKeown, Edwards & Lenahan
STREET: 1200 G Street, N. W. Suite 700
CITY: Washington, D.C.
COUNTRY: U.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                73 PWNSATVLOOTYHAHRSDALOLGLGKHNYCRNPDNRRRPWCYVQVGLKPLVQECMVHDCA 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              94 PWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVGLKPLVQECMVHDCA 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13 CLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFYRGKASTDTMGRPCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6; Gaps
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/093,741
FILING DATE: CO-JUL-1993
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match
66.8%; Score 559; DB 2;
Best Local Similarity 77.1%; Pred. No. 5.5e-48;
Matches 101; Conservative 8; Mismatches 16
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P43 23 754.1
FILING DATE: 15-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: EVANS, JOSEPH D.
REGISTRATION NUMBER: 26,269
                            FILING DATE: 17-NOV-1995
REOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: P 44 40 892.7
FILING DATE: 17-NOV-1994
ATTORNEY/AGENT INNOV-1994
ATTORNEY/AGENT INNOVENTION:
NAME: EVANS, JOSEPH DI.
REGISTRATION NUMBER: 26,269
REFERENCE/DOCKET NUMBER: 148/42448
TELECHOME: (202) 628-8800
TELECHOME: (202) 628-8800
TELECHOME: (202) 628-8844
INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
LENGTH: 432 amino acids
     US/08/560,098A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: PLOPPY DERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 83, Application US/08093741
Patent No. 5681721
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 432 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          133 DGKKPSSPPEE 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           154 DGKKPSSPPEE 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear MOLECULE TYPE: protein
     APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-560-098A-47
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47 SKTCYEGNGHFYRCKASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPD 106
                                                                  47 SKTCYEGNGHFYRGKASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPD 106
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                                                                                                        1 SKICYEGNGHFYRGKASIDIMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPD 60
                        Gaps
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CCMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CCMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (BPO)
SOFTWARE: Patentin Release #1.0, Version #1.30 (BPO)
CURRENT APPLICATION NAMER: US/08/560,098A
APPLICATION NUMBER: P 44 40 892.7
FILING DATE: 17-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAMM: BVANS, USSEPPD D.
REGISTRATION NUMBER: 148/42448
FEFERENCE/DOCKET NUMBER: 148/42448
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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100.0%; Pred. No. 5.7e-48;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: WIRNDT, Stephan
APPLICANT: HINCEL-WIELAND, Regina
APPLICANT: STEFFENS, Gerd Josef
TITLE OF INVENTION: Proceins having Fibrinolytic and
TITLE OF INVENTION: Coagulation-inhibiting Properties
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          107 NRRRPWCYVQVGLKPLVQECMVHDCADGKKPSSPPEE 143
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                                                                                                                                                                        107 NRRRPWCYVQVGLKPLVQECMVHDCADGKKPSSPPEE 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SSEE: Evenson, McKeown, Edwards & Lenahan
F: 1200 G Street, N.W., Suite 700
Washington
                                                                                                                                                                                                              61 NRRRPWCYVQVGLKPLVQECMVHDCADGKKPSSPPEE 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6.2e-48;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 20
US-08-967-024C-24
; Sequence 24, Application US/08967024C
                                                                                                                                                                                                                                                                                                         RESULT 19
US-08-560-098A-44
'Sequence 44', Application US/08560098A
'Parent No. 5976841
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
LENGTH: 393 amino acids
TYPE: amino acids
     Best Local Similarity 100.
Matches 97, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino STRANDEDNESS
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47 SKTCYEGNGHFYRGKASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPD 106
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Sequence 25, Application US/08967024C

Patent No. 613011

GENERAL INFORMATION:
APPLICANT: STEFFENS, Gerd Josef
APPLICANT: ADAOCHA, ENLY
ITILE OF INVENTION: Chimeric Proteins having Fibrinolytic
ITILE OF INVENTION: Chimeric Proteins having Fibrinolytic
MUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Evenson, McKeown, Edwards & Lenahan
STREET: 1200 G Street, N.W., Suite 700
STREET: 000
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APPLICANT: WNENDT, Stephan
APPLICANT: STEFFENS, Gerd Josef
APPLICANT: STEFFENS, Gerd Josef
APPLICANT: JANOCHA, Elke
APPLICANT: HEINZEL-WILMD, Regina
TITLE OF INVENTION: Chimeric Proteins having Fibrinolytic
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Evenson, MCKcown, Edwards & Lenahan
STREET: 1200 G Street, N.W., Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match

Best Local Similarity 100.0%; Pred. No. 6.2e-48;
Matches 97; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/967,024C
CLASSTORY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     107 NRRRPWCYVQVGLKPLVQECMVHDCADGKKPSSPPEE 143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: P 44 42 665.8
FILING DATE: 30-NOV-1994
ATTORNEY/AGENI INFORMATION:
NAME: EVANS, JOSEPH D.
REGISTRATION NUMBER: 148/42444
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-8800
TELEPHONE: (202) 628-8800
TELEPHONE: (202) 628-8800
TELEPHONE: (202) 628-8844
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 393 amino acids
TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 20005
COMPUTER READABLE FORM:
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61 RNPDNRRRPWCYVQVGLKPLVQECMVHDC 89

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       47 SKTCYEGNGHFYRGKASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPD 106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        66.7%; Score 558; DB 3; Length 393;
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; OTHER INFORMATION: residues 43-131 of the ATF domain of uPA
US-09-101-272G-62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 89;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
          COMPUTER: 18M PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/967,024C
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 22
US-09-101-272G-62
Sequence 62, Application US/09101272G
Fatent No. 6509445
GENERAL INFORMATION:
APPLICANT: Nissin Food Products Co., Ltd.
TITLE OF INTENTION: CANCEROUS METASIS INHIBITOR
FILE REFERENCE: Q50979
CURRENT APPLICATION NUMBER: US/09/101,272G
CURRENT FILLING DATE: 1998-07-08
FRIOR APPLICATION NUMBER: JP 1059/1996
FRIOR PILING DATE: 1996-01-08
NUMBER OF SEQ 1D NOS: 107
SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         107 NRRRPWCYVQVGLKPLVQECMVHDCADGKKPSSPPEE 143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6.2e-48;
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                                                                                                                                                                                                                                                                                                                                         148/42444
                                                                                                                                                              CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UNMBER: P 44 42 665.8
FILING DATE: 30-NOV-1994
ATTORNEY/ACHT INFORMATION:
NAME: EVANS, JOSEPh D.
REGISTRATION NUMBER: 26,269
                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 26,269
REFERENCE/DOCKET NUMBER: 148/4;
TELECOMMUNICATION INFORMATION:
TELEFAN: (202) 628-8844
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 393 amino acide
Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 393 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ) TOPOLOGY: linear; MOLECULE TYPE: protein US-08-967-024C-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Homo sapiens
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Best Local Similarity
Matches 89; Conserva
MEDIUM TYPE:
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LENGTH: 89
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Sequence 16, Application US/07609510B; Patent No. 5326700; GENERAL INFORMATION:
GENERAL TROUGHTION:
FAPLICANTE BEIGG et al.
TITLE OF INVENTION: Method for Altering Post-Translational Processing of Tissue; NUMBER OF SEQUENCES: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           59 RGKASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGGKHNYCRNPDNRRPWCYVQVG 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            78 OCHTVPVKSCSELRČFNGGTČWQAASPSDF-VČQČPKGYTGKQČEVĎTHAŤČÝKDQGVTY 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 BLHQVP----SNCDCLNGGTCVSNKYFSNIHWCNCPKKFGGQHCBIDKSKTCYEGNGHFY 58
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/560,098A

FILING DATE: 17-NOV-1995

PRIOR APPLICATION NUMBER: US/08/560,098A

FILING DATE: 17-NOV-1995

FILING DATE: 17-NOV-1994

APPLICATION NUMBER: P 44 40 892.7

FILING DATE: 17-NOV-1994

ATTCANEY/AGENT INFORMATION:

NAME: EVANS, Joseph D.

REGISTRATION NUMBER: 26,269

REFERENCE/DOCKET NUMBER: 148/42448

TELECHONE: (202) 628-8800

TELECHONE: (202) 628-8800

TELECHONE: (202) 628-8800

TELECHONE: (202) 628-8804

INFORMATION FOR SEQ ID NO: 51: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
40.1%; Score 335.5; DB 2; Length 4
Best Local Similarity 46.3%; Pred. No. 1.2e-25;
Matches 62; Conservative 17; Mismatches 50; Indels
                                                                                                                         APPLICANT: WNENDT, Stephan
APPLICANT: HEINZEL-WIELAND, Regina
APPLICANT: STEFFENS, Gerd Joseft
TITLE OF INVENTION: Proteins having Fibrinolytic and
TITLE OF INVENTION: Coagulation-inhibiting Properties
NUMBER OF SEQUENCES: 60
CORRESPONDENTS ADDRESS:
ADDRESSEE: Evenson, McKeown, Edwards & Lenahan
                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Evenson, McKeown, Edwards & Lenahan STREET: 1200 G Street, N.W., Suite 700 CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                          Sequence 51, Application US/08560098A Patent No. 5976841
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                                                                                                       GENERAL INFORMATION:
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RESULT 23
US-08-560-098A-51
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42 OCHSVPVKSCSEPRCFNGGTCQQALYFSDF-VCQCPEGFAGKCCEIDTRATCYEDQGISY 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 ELHQVP-SNCD---CLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFY 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 39.2%; Score 328.5; DB 1; Length 527; Best Local Similarity 46.3%; Pred. No. 6.9e-25; Matches 63; Conservative 14; Mismatches 54; Indels 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: SAITO, YOSHIMASA
APPLICANT: SAITO, YOSHIMASA
APPLICANT: SAITO, YOSHIMASA
APPLICANT: HAYASHI, MASAKO
APPLICANT: HAYASHI, MASAKO
APPLICANT: NOTANI, JOUTI
APPLICANT: NOTANI, JOUTI
TITLE OF INVENTION: TISSUE PLASMINOGEN ACTIVATOR
NOMBER OF SEQUENCES: 67
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADI,
                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.0 Mb storage COMPUTER: Macincoan admincan coperating SYSTEM: Macincoan COPERATING SYSTEM: Macincoan COPERATING SYSTEM: Macincoan COPERATING SYSTEM: Macincoan COPERATION DATA:
CURRENT APPLICATION DATA:
APPLICATION: 435
INPORMATION FOR SEQ ID NO: 16: SEQUENCE CHARACTERISTICS:
LENGTH: 527 amino acids
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I: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
ARLINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/811,949
FILING DATE: 05-MAR-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ell Lilly and Company STREET: Lilly Corporate Center CITY: Indianapolis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 39, Application US/08811949
Patent No. 5840533
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 527 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-609-5108-16
                                                                                                                   U.S.A.
                                                                                                                                        46285
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                                                                                               STATE: IN.
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42 ochsvevkscseprcendercogalyesde-vooceegerackceidtratoyedgisy 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Geneticech, Inc.
TITLE OF INVENTION: Tissue Plasminogen Activator Having Fibrin TITLE OF INVENTION: Tissue Plasminogen Activator Having Fibrin TITLE OF INVENTION: 2 CORRESPONDENCE ADDRESS: 2 CORRESPONDENCE ADDRESSE: Genericech, Inc. STREET: 460 Point San Bruno Blvd CITY: South San Francisco CITY: South San Francisco COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                              DB 2; Length 527;
                                                                                                                                                                                                                                                                                                                                                                                        Query Match 39.2%; Score 328.5; DB 2; Length 5: Best Local Similarity 46.3%; Pred. No. 6.9e-25; Matches 63; Conservative 14; Mismatches 54; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk COMPUTER: IBM PC compactible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/01025A
FILING DATE: 19910214
CLASSIFICATION 1435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/486,657
FILING DATE: 1 March 1990
ATTORNEY/AGENT INFORMATION:
NAME: Hasak, Janet B.
REGISTRATION NUMBER: 28 616
REGISTRATION NUMBER: 28 616
REGISTRATION NUMBER: 28 616
REGISTRATION NUMBER: 454P2
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TT-US91-01025A-2
Sequence 2, Application PC/TUS9101025A
GENERAL INFORMATION:
                                                                                                                                          TELEFAX: 703-413-2220

INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 527 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-811-949-39
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REPERROKE/DOCKET UMBER: 18-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         119 LKPLVQECMVHDCADG 134
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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AMINO ACID
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us-09-880-503-8.rai

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42 QCHSVPVKSCSEPRCFNGGTCQQALYFSDF-VCQCPEGFAGKCCEIDTRATCYEDQGISY 100
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                                                                                                                               42 QCHSVPVKSCSEPRČFNGGTCQQALYFSDF-VCQCPEGFAGKCCEIDTRATCYEDQGISY 100
                                                                                                                                                                                               59 RGKASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVG 118
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                                                                                                3 ELHQVP-SNCD---CLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFY 58
                                                     Gaps
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1 Similarity 46.3%; Pred. No. 6.9e-25;
63; Conservative 14; Mismatches 54; Indels 5;
39.2%; Score 328.5; DB 5; Length 527; 46.3%; Pred. No. 6.9e-25; tive 14; Mismatches 54; Indels 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ent No. 5185259
APPLICANT: GOEDDEL, DAVID V.;KOHR, WILLIAM J.;PENNICA, DIANE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5520913-1
;Patent No. 5520913
Patent No. 5520913
The Applicant: Anderson, Stephen, Bennett, William F.; Botstein, Dayld; Higgins, Deborat L.; Paoni, Nicholas F.; Zoller, Mark J. Title Of Invention: Tissue plasminogen activator Having; ZYMOGENIC PROPERTIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R, GORDON A.
TITLE OF INVENTION: TRUNCATED HUMAN TISSUE PLASMINOGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 15
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/489,855
FILING DATE: 02-MAR-1990
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/88,451
FILING DATE: 06-JUL-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: 12,694
FILING DATE: 09-FEB1987
APPLICATION NUMBER: 483,052
FILING DATE: 07-APR-1983
APPLICATION NUMBER: 398,003
FILING DATE: 14-UUL-1982
APPLICATION NUMBER: 374,860
FILING DATE: 05-MAY-1982
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APPLICATION NUMBER: 770,510
FILING DATE: 03-0CT-1991
APPLICATION NUMBER: 384,608
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161 GKYSSEFCSTPACSEG 176
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          Query Match
Best Local Similarity 46.3%
Matches 63; Conservative
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Patent No.
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5185259-8
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59 RGKASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVG 118
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                                                                                                                                                                                                                                                                                                                                   59 RGKASTDIMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVG 118
                                                                                                                                                                                                                                                                                                                                                         77 gchsypykscseprcfndgicogalyfsdf-vcgcpegfagkcceidtratcyedgisy 135
                                                                                                                                                                                                                                           3 ELHQVP-SNCD---CLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFY 58
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                                                                                                                                              Similarity 46.3%; Score 328.5; DB 6; Length 527; Similarity 46.3%; Pred. No. 6.9e-25; Conservative 14; Mismatches 54; Indels 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              39.2%; Score 328.5; DB 6; Length 546; 46.3%; Pred. No. 7.2e-25; ative 14; Mismatches 54; Indels 5-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2200340-6; Patent No. 5200340
; Patent No. 5200340
; APPLICANT: FOSTER, DONALD C.; MULVIHILL, EILEEN R.; O'HARA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PATRICK J. PINGEL, KURT, YOSHITAKE, SHINJI
, TITLE OF INVENTION: THROMBIN-ACTIVATED TISSUE PLASMINGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: P.C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: NIWA, MINEO
APPLICANT: SATTO, YOSHIMASA
APPLICANT: SASAKI, HITOSHI
APPLICANT: HASAKI, HITOSHI
APPLICANT: NOTANI, JOUJI
APPLICANT: NOTANI, JOUJI
APPLICANT: NOTANI, JOUJI
APPLICANT: NOTANI, JOUJI
APPLICANT: NOTANI, JOUJI
APPLICANT: NOTANI, JOUJI
APPLICANT: NOTANI, JOUJI
APPLICANT: NOTANISHI, MASAKAZU
APPLICANT: NOTANISHI, MASAKAZU
APPLICANT: NOTANISHI, MASAKAZU
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/53,412
FILING DATE: 22-MAY-1987
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                 APPLICATION NUMBER: 240,856
FILING DATE: 02-SEP-1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        161 GKYSSEFCSTPACSEG 176
                                                                                                                                                                                                                                                                                                                                                                                                                            119 LKPLVQECMVHDCADG 134
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FILING DATE: 24-JUL-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 46.3%
les 63; Conservative
                                                                                                                                                                                                 63; Conservative
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                                                                                        LENGTH: 527
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US-08-811-949-43
                                                                                                                                                        Query Match
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                                                                  SEQ ID NO:1:
                                                                                                                                                                                   Local
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(without alignments)
2097.294 Million cell updates/sec
                                                                                                    December 3, 2003, 14:34:23 ; Search time 17.5948 Seconds
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                     830525 segs, 258052604 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                   - protein search, using sw model
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sp_virus:*
sp_verrebrate:*
sp_unclassified:*
sp_rvirus:*
sp_bacteriap:*
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Gapop 10.0 , Gapext 0.5
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sp bacteria:*
sp bungi:*
sp fungi:*
sp human:*
sp mammal:*
sp mammal:*
sp organelle:*
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Perfect score:
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                                                                                                          Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Q96se8 homo sapien	Q8mil0 oryctolagus	Q8mhy7 oryctolagus	Q9tva8 bos taurus	Q8c612 mus musculu	Q9xt70 oryctolagus	O9bu99 homo sapien	Q91vp2 mus musculu	Q8sq23 sus scrofa	Q8mkbl oryctolagus	Q8k0d2 mus musculu	Q14520 homo sapien	097507 sus scrofa	Q8vcs4 mus musculu	O35727 mus musculu	Q9bzwl homo sapien
	at	Q96SE8	OBMILO	Q8MHY7	Q9TVA8	QBC6L2	Q9X170	Q9BU99	Q91VP2	Q8SQ23	QBMKB1	QBK0D2	014520	097507	Q8VCS4	035727	Q9BZW1
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	Query Match Length DB	154	433	433	157	231	214	516	559	562	564	517	260	919	653	597	395
ų	Query Match	93.0	74.9	74.9	68.8	68.0	40.3	38.5	37.7	37.2	36.0	31.7	31.5	30.8	29.9	29.9	27.8
	Score	778	627	627	576	569	337.5	322.5	315.5	311.5	301.5	265	263.5	258	250.5	250	233
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Q81ZZ5 Q8NG20 Q90675 Q8AXX3	Q8AXY6 Q91691 Q8WMR1	Q9R0W3 Q90Y90 Q9brb6 Q8bnp9	Q8BG10 046506 Q9UIR5	Q15146 Q91WJ5 Q8K0Q8	Q8C3W2 Q8BSP6 Q9UIR7 P70006	Q13208 Q9H1V4 Q8AV69 Q8N2J4	Q96GL8 Q9BTP9 Q8NCW1
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615 90 202 421	947 716 359	812 452 393 937	937 454 113	810 812 801	944 944 1113	567 648 930 381	399 420 420 424
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ALIGNMENTS

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996SE8

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1D 01-DEC-2001 (TrEMBLE-11 19, Last sequence update)

1D 01-DEC-2001 (TrEMBLE-11 19, Last sequence update)

1D 10-DEC-2001 (TrEMBLE-11 19, Last sequence update)

1D 10-MAR-2003 (TrEMBLE-11 19, Last sequence update)

1D 10-MAR-2003 (TrEMBLE-11 19, Last sequence update)

1D 10-MAR-2003 (TrEMBLE-11 19, Last sequence update)

1D 10-MAR-2003 (TrEMBLE-11 19, Last sequence update)

1D 10-MAR-2003 (TrEMBLE-11 19, Last sequence update)

20 Mannalia; Eucheria; Primates; Catarrhini; Hominidae; Homo.

21 Mannalia; Eucheria; Primates; Catarrhini; Hominidae; Homo.

22 Mannalia; Eucheria; Primates; Catarrhini; Hominidae; Homo.

23 Mannalia; Eucheria; Primates; Catarrhini; Hominidae; Homo.

24 Mannalia; Eucheria; Primates; Catarrhini; Hominidae; Homo.

25 Mannalia; Eucheria; Primates; Catarrhini; Hominidae; Homo.

26 Mannalia; Eucheria; Primates; Catarrhini; Hominidae; Homo.

27 Mannalia; Eucheria; Primates; Catarrhini; Hominidae; Homo.

28 Mannalia; Eucheria; Primates; Mannalia; Tragment of human urokinase-type plasminogen activator in Decast cancer cells results in decreased

28 Mannalia; Mannalia; Eucheria; Eucheria; Eucheria; Eucheria; Eucheria; Eucheria; Eucheria; Eucheria; Eucheria; Eucheria; Eucheria; Eucheria; Eucheria; Eucheria; Eucheria; Eucheria; Eucheria; Eucheria; Eucheria; Eucheria; Eucheria; Eucheria; Eucheria; Eucheria; Eucheria; Eucheria; Eucheria; Eucheria; Eucheria; Eucheria; Eucheria; Eucheria; Eucheria; Eucheria; Eucheria; Eucheria; Eucheria; Eucheria; Eucheria; Eucheria; Eucheria; Eucheria; Eucheria; Eucheria; Eucheria; Eucheria; Eucheria; Eucheria; Eucheria; Eucheria; Eucheria; Eucheria; Eucheria; Eucheria; Eucheria; Eucheria; Eucheria; Eucheria; Eucheria; Eucheria; Eucheria; Eucheria; Eucheria; Eucheria; Eucheria; Eucheria; Eucheria; Eucheria; Eucheria; Eucheria; Eucheria; Eucheria; Eucheria; Eucheria; Eucheria; Eucheria; Eucheria; Eucheria; Eucheria; Eucheria; Eucheria; Eucheria; Eucheria; Eucheria; Eucheria; Eucheria; Eucheria; Eucheria; Eucheria; Eu
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DP DP ò

Вb ò

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RGKASTDIMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVG 118
                                                                                                                                                                                                                                                                                                                                                                     Oryctolagus cuniculus (Rabbit).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
NCBI_TaxID=9986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.

Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.

- SIMILARITY: CONTAINS I KRINGLE DOMAIN.

E HEBL; AVC29517; AAK40239-11; -

R InterPro; IPR001314; Chymctrypsin.

R InterPro; IPR001314; Chymctrypsin.

R InterPro; IPR001254; Ser_like.

R InterPro; IPR001259; Ser_like.

R InterPro; IPR001259; Ser_like.

R Pfam; PF00051; Kringle.

R Pfam; PF000151; Kringle.

R PRINTS; PR00125; CHYMCTRYPSIN.

R PRINTS; PR00139; KRINGLE.

R PROSTIE; PS000130; KRINGLE.

R PROSTIE; PS00013; KRINGLE.

R PROSTIE; PS00014; TRYPSIN.—DW; I.

R PROSTIE; PS0014; TRYPSIN.—DW; I.

R PROSTIE; PS0014; TRYPSIN.—DW; I.

R PROSTIE; PS0014; TRYPSIN.—DW; I.

R PROSTIE; PS0014; TRYPSIN.—DW; I.

R PROSTIE; PS0014; TRYPSIN.—DW; I.

R PROSTIE; PS0014; TRYPSIN.—SER; I.

Glycoprotain; Hydrolase; Kinase; Kringle; Protease; Serine I SEQUENCE 433 AA; 48444 MW; 6DD35A371010A6EE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 433;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
Sugiki M., Yoshida E., Anai K., Maruyama M.;
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                         01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ouery Match 74.9%; Score 627; DB 6; Best Local Similarity 76.2%; Pred. No. 1.5e-59; Matches 109; Conservative 11; Mismatches 21;
                                                                                                                                                                                                                                     433 AA
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                                                                                                                             141 LKOLIQECKVHDCSSGKKPALPP 163
                                                                                       119 LKPLVQECMVHDCADGKKPSSPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                  61 KASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVGLK 120
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RA MEDLINE-2215945; PubMed=12149463;
RA Falkenberg M., Tom C., DeYoung M.B., Wen S., Linnemann R.,
RA Jotchek D.A.;
Thereased expression of uroxinase during atherosclerotic lesion development causes arterial constriction and lumen loss, and development causes arterial constriction and lumen loss, and development causes arterial constriction and lumen loss, and development causes arterial constriction and lumen loss, and development causes arterial constriction and lumen loss, and large arcelerates lesion growth.;

RT "Increment Acad. Sci. Ut.S.", 99:10665-10670(2002).

CC -:- SIMILARITY: CONTAINS I KRINGLE DOMAIN.

DR FMILARITY: CONTAINS I KRINGLE DOMAIN.

DR FMILARITY: CONTAINS I KRINGLE DOMAIN.

DR InterPro; IPRO00219; Edf=1/1.

DR PRO00219; Kringle; I.

DR PRINTS: PRO00215; Kringle; I.

DR PROMO109; KRINGLE.

DR PROSITE; PS00022; Edf=1/1.

DR PROSITE; PS00021; KRINGLE 1/1.

DR PROSITE; PS00021; KRINGLE 1/1.

DR PROSITE; PS00134; TRYPSIN LIS; I.

DR PROSITE; PS00134; TRYPSIN LIS; I.

DR PROSITE; PS00134; TRYPSIN LISR: I.

DR PROSITE; PS00134; TRYPSIN LISR: I.

DR PROSITE; PS00134; TRYPSIN LISR: I.

DR PROSITE; PS00134; TRYPSIN LISR: I.

DR PROSITE; PS00134; TRYPSIN LISR: I.

DR PROSITE; PS00134; TRYPSIN LISR: I.

DR PROSITE; PS00134; TRYPSIN LISR: I.

DR PROSITE; PS00134; TRYPSIN LISR: I.

DR PROSITE; PS00134; TRYPSIN LISR: I.

DR PROSITE; PS00134; TRYPSIN LISR: I.

DR PROSITE; PS00134; TRYPSIN LISR: I.

DR PROSITE; PS00134; TRYPSIN LISR: I.

DR PROSITE; PS00134; TRYPSIN LISR: I.

DR PROSITE; PS00134; TRYPSIN LISR: I.

DR PROSITE; PS00134; TRYPSIN LISR: I.

DR PROSITE; PS00134; TRYPSIN LISR: I.

DR PROSITE; PS00134; TRYPSIN LISR: I.

DR PROSITE; PS00134; TRYPSIN LISR: I.

DR PROSITE; PS00134; TRYPSIN LISR: I.

DR PROSITE; PS00134; TRYPSIN LISR: I.

DR PROSITE; PS00134; TRYPSIN LISR: I.

DR PROSITE; PS00134; TRYPSIN LISR: I.

DR PROSITE; PS00134; TRYPSIN LISR: I.

DR PROSITE; PS00134; TRYPSIN LISR: I.
                                                                                                                                                                               21 SNELHQVPSNCDCLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFYRG 80
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                                                                                                                                                      1 SNELHQVPSNCDCLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFYRG
                                                                                                                Gaps
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Lagomorpha, Leporidae, Oryctolagus.
NCBI_TaxID=9986;
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                                                                     Length 154;
                                                                                                                1; Indels
                               A3CCF2FCFF505572 CRC64;
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01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Urokinase-type plasminogen activator.
                                                                   93.0%; Score 778; DB 4;
99.3%; Pred. No. 2.2e-76;
iive 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             433 AA
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             Glycoprotein, Kinase, Kringle.
SEQUENCE 154 AA; 17305 MW;
                                                                                                                                                                                                                                                                                                                               121 PLVQECMVHDCADG 134
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Best Local Similarity 99.3
Matches 133; Conservative
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Matches 109; Conserv
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Q8MILO;
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59 RGKASIDIMGRPCLPWNSAIVLQQTYHAHRSDALQLGLGKHNYCRNPDNRRPWCYVQVG 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Yano W., Watanabe M.;
"Oryctolagus cuniculus urokinase-type plasminogen activator, mRNA,
complete cds.";
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Gaps

149

89

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67 MGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVGLKPLVQEC 126
                                                                                                                                                                                                                                                                                                                                                                                 69 RPCLPWNSATVLQQTYHAHRSDALQLGCKHNYCRNPDNRRRPWCYVQVGLKPLVQECMV 128
"Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
Nature 420:563-573(2002).
EMBL, AK0544949; BAC35743.1; -.
NON TER 231
SEQÜENCE 231 AA; 25510 MW; 25E8980A682737F2 CRC64:
                                                                                                                                                                                                                                                                                                                                                                                                                90 RPCLAMNAPAVLQKPYNAHRPDAISLGLGKHNYCRNPDNQKRPWCYVQIGLRQFVQECMV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MDRPCLAWNSANVLTKTYHAHRPDALQLGLGKHNYCRNPDHQRRPWCYVQVGLKQLIQEC
                                                                                                                                                                                                                                                                                                                                30 SNCGCQNGGVCVSYKYFSRIRRCSCPRKFQGEHCEIDASKTCYHGNGDSYRGKANTDTKG
                                                                                                                                                                                                                                                                                    9 SNCDCLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYBGNGHFYRGKASTDTMG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRINTS; PRO0722; CHYMOTRYESIN.
Prodom; PRO07395; Kringle; 1.
SMART; SM000130; KR; 1.
PROSITE; PS00021; KRINGLE 1; 1.
PROSITE; PS0001; KRINGLE 1; 1.
PROSITE; PS00134; TRYPSIN_HIS; 1.
Glycoprotein; Hydrolaes; Kinase; Kringle; Protease.
SEQÜENCE 214 AA; 24314 MW; 69975C41C32B0D7E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Urokinase-type plasminogen activator (Fragment).
Oryctolagus cuniculus (Rabbit).
Cryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
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                                                                                                                                                                                  68.0%; Score 569; DB 11; Length 231; 70.4%; Pred. No. 1.4e-53; ive 15; Mismatches 25; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Yin J., Idel, S.,
"Partial mRNA of rabbit uPA.";
Submitted (OCT.1998) to the EMBL/GenBank/DDBJ databases.
--- SIMILARITY: BELONGS TO PEFTIDASE FAMILY SI.
--- SIMILARITY: CONTAINS I KRINGLE DOMAIN.
EMBL, AF097647;
AAD39351.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        214 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR01314; Chymotrypsin.
InterPro; IPR001001; Kringle.
InterPro; IPR001254; Ser_protease_Try.
Pfam; PF00051; Kringle; I.
Pfam; PF00089; trypsin; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1999 (TrEMBLrel. 12, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   129 HDCADGKKPSSPPEE 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  150 HDCSLSKKPSSSVDQ 164
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Best Local Similarity 78.7%
                                                                                                                                                                                                              Local Similarity 70.4
nes 95; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P00749; 1EJN.
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TISSUE=Lung;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEROPS; S01.231
                                                                                                                                                                                         Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              73 PWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVGLKPLVQECMVHDCA 132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13 CLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFYRGKASTDTMGRPCL
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MEDLINE=21071389; PubMed=11204721;

A Balcerzak D., Querenguesser L., Dixon W.T., Baracos V.E.;

Balcerzak D., Querenguesser L., Dixon W.T., Baracos V.E.;

T. "Coordinate expression of matrix-degrading proteinases and their

T. activators and inhibitors in bovine skeletal muscle.";

I. Anim. Sci. 79:94-107(2001)

J. Anim. Sci. 79:94-107(2001)

EMBL; ARH44761; ACNTAINS 1 KRINGLE DOMAIN.

EMBL; ARH44761; ACNTAINS 1 KRINGLE.

R. RSP; P00749; IURK.

R. InterPro; IPR000001; KRINGLE.

R. PRODOM; PD0000395; KRINGLE.

R. PRODOM; PD0000395; KRINGLE.

R. PRODOM; PR000019; KRINGLE.

R. PROSTIE; PS00002; EGF 1; 1.

R. PROSTIE; PS00002; KRINGLE 1; 1.

R. PROSTIE; PS00002; KRINGLE 2; 1.
                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
Bovidae, Bovinae, Bos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse).
Vakaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
VCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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MEDINE=2254683; Dibmed=12466851;
The FANTOM CONSORT; Dibmed=12466851;
the RIKEN Genome Exploration Research Group Phase I & II Team;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 68.8%; Score 576; DB 6; Length 157; 74.8%; Pred. No. 1.6e-54; ive 12; Mismatches 21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 157 157
157 AA; 17858 MW; A768D6C72C1FBFB7 CRC64;
                                                                                                    01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Urokinase plasminogen activator (Fragment).
Bos taurus (Bovine).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QBCGL2;
01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Plasminogen activator (Fragment)
                                                                          157 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Glycoprotein; Kinase; Kringle.
NON TER
157
SEQÜENCE 157 AA; 17858 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                          PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                           rissum=Skeletal muscle;
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                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9913;
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Best Local S
                                                                        Q9TVA8
Q9TVA8;
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Q8C6L2
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Gaps

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01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                            imilar to plasminogen activator, tissue
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                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
TISSUE=Breast tumor;
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Q8SQ23
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                                                                                                                                                                                     01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
Similar to plasminogen activator, tissue.
Homo sapiens (Human).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ch 38.5%; Score 322.5; DB 4; Length 516; 1 Similarity 44.4%; Pred. No. 1.6e-26; 64; Conservative 13; Mismatches 56; Indels 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SWART; SM00020; Tryp_SPC; 1.

PROSITE; P600022; EGF 1; 1.

PROSITE; P600021; KRINGLE 1; 2.

PROSITE; P650040; KRINGLE 2; 2.

PROSITE; P65040; TRYPSIN DOM; 1.

PROSITE; P650134; TRYPSIN DOM; 1.

PROSITE; P650134; TRYPSIN HIS; 1.

PROSITE; P650135; TRYPSIN SER; 1.

EGF-like domain; Glycoprotein; Hydrolase; Kringle; Protease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A STRANSPERSKII;
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
--- SIMILARITY: CCNPAINS 2 KRINGLE DOWAINS.
REBL; BC002795; AAH02795.1; ---
REBL; BC002795; AAH02795.1; ---
RICETPO: PRO06210; EGF 1:--
RICETPO: PRO06210; EGF 1:--
RICETPO: PRO06210; EGF 1:--
RICETPO: PRO06210; Kringle.
RICETPO: PRO0001; Kringle.
REPEM: PRO0008; EGF; 1:--
REPEM: PRO0008; EGF; 1:--
REPEM: PRO0001; KRINGLE.
REPEM: PRO0019; KRINGLE.
REPEM: PRO0019; KRINGLE.
REPEM: REPOON19; KRINGLE.
REPEM: REPOON19; KRINGLE.
REPEM: SMART; SM00118; KRINGLE.
REPEM: SMART; SM00101; EGF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        516 AA; 57370 MW; BAB31901FDC96800 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q91VP2 PRELIMINARY; PRT; 559 AA.
Q91VP2;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
                                                                                                                                                                               516 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         111 PWCYVQVGLKPLVQECMVHDCADG 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PWCYVFKAGKYSSEFCSTPACSEG 165
                                                                                                                                                                               PRT;
|||:|||:|||
61 KVHD-SSGKKPALPP 74
                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
TISSUE=Skin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Serine protease
SEQUENCE 516 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 8
Q91VP2
ID Q91V
AC Q91V
DT 01-DI
DT 01-DI
                                                                                                                      RESULT 7
Q9BU99
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132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 133 RGTWSTAESGAECINWNSSVLSLKPYNARRPNAIKLGLGNHNYCRNPDRDLKPWCYVFKA 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 ELHQVP----SNCDCLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-MR-2003 (TrEMBLrel. 23, Last annotation update)
T-plasminogen activator.
Sus scrofa (Pig).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DR SWART; SMOOLDS, KRINGLE.

BR SWART; SMOOLDS, FRIDE.

BR SWART; SMOOLDS, FRIDE.

BR SWART; SMOOLDS, FRIDE.

BR SWART; SMOOLDS, FRIDE.

BR SWART; SMOOLDS, RR, 2.

BR SWART; SMOOLDS, RR, 2.

BR SWART; SMOOLDS, RR, 2.

BR SCRITE; PROLESS; EGF_1; 1.

BR PROSITE; PROLESS; KRINGLE.

BR PROSITE; PROLESS; KRINGLE.

BR PROSITE; PROLESS; TRYPEIN LDOM; 1.

BROSITE; PROLESS; TRYPEIN LDOM; 1.

BROSITE; PROLESS; TRYPEIN LDOM; 1.

BROSITE; PROLESS; TRYPEIN LDOM; 1.

BROSITE; PROLESS; TRYPEIN LDOM; 1.

BROSITE; PROLESS; TRYPEIN LDOM; 1.

BROSITE; PROLESS; TRYPEIN SER; 1.

BROSITE; PROLESS; TRYPEIN SER; 1.

BROSITE; PROLESS; TRYPEIN SER; 1.

BROSITE; PROLESS; TRYPEIN SER; 1.

BROSITE; PROLESS; TRYPEIN SER; 1.

BROSITE; PROLESS; TRYPEIN SER; 1.

BROSITE; PROLESS; TRYPEIN SER; 1.

BROSITE; PROLESS; TRYPEIN SER; 1.

BROSITE; PROLESS; TRYPEIN SER; 1.

BROSITE; PROLESS; TRYPEIN SER; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match

37.7%; Score 315.5; DB 11; Length 559;
Best Local Similarity 44.5%; Pred. No. 9.8e-26;
Matches 61; Conservative 15; Mismatches 56; Indels 5;
                                                                                                                                                                                                                                                                                                            databases
                                                                                                                                                                                                                                                                 Strausberg R;
Submitted (ULL-2001) to the EMBL/GenBank/DDBJ data)
Submitted (ULL-2001) to the EMBL/GenBank/DDBJ data)
-!- SIMILARITY: EBLONGS TO PEPTIDASE FAMILY SI.
-!- SIMILARITY: CONTAINS 2 KRINGLE DOWAINS.
EMBL; BC011256; AAH11256.1; -.
HSSP; D07061; JAN.
MGD; MGI:97510; Plat.
InterPro; PRR001214; Chymotrypsin.
InterPro; IPR00129; EGF like.
InterPro; IPR000019; Fibrnctni.
InterPro; IPR000010; Kringle.
InterPro; IPR001254; Ser_protease_Try.
Pfam; PF00009; Eff; 1.
Pfam; PF00009; Eff; 1.
Pfam; PF00009; Enl; 1.
Pfam; PF00009; Kringle; 2.
Pfam; PF00009; Kringle; 2.
PRINTS; PR00128; KRINGLE.
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80 HSVPVQSCSEPRČLNGGTCSQALYFSDF-VCQCPEGFVGKRCEVDTRARCYEDRGIGYRG 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5 HQVP-SNCD----CLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFYRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 KASTDIMGRPCLPWNSAIVLQQIYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYV 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                139 TWSTTESGAQCVNWNSSWLALKPYSGRKPNALRLGLGNHNYCRNPDRDTKPWCYV 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     36.0%; Score 301.5; DB 6; Length 564; 48.7%; Pred. No. 3.2e-24; ive 13; Mismatches 41; Indels 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00021; KRINGLE_1; Z.
PROSITE; PS50070; KRINGLE_2; Z.
PROSITE; PS50240; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_HIS; 1.
PROSITE; PS00135; TRYPSIN_SER; 1.
EGF-like domain; Glycoprofein; Hydrolase; Kringle; Protease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Strausberg R.;
Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
-: SIMILARITY: CONTAINS 1 KRINGLE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         564 AA; 62726 MW; 459D8BAC6D4A937C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    517 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL, BC011775; AAH31775.1;
InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001881; EGF_2.
InterPro; IPR00209; EGF_like.
InterPro; IPR00210; IEGF.
InterPro; IPR002010; IEGF.
InterPro; IPR001254; Ser_protease_Try.
Pfam; PF00008; EGF; 2.
                                          InterPro; IPR00083; Fibrnctn1.
InterPro; IPR00081; IEBF.
InterPro; IPR000101; IEBF.
InterPro; IPR00101; Kringle.
InterPro; IPR00101; Kringle.
Pfam; PF00008; EGF; 1.
Pfam; PF00018; fn1; 1.
Pfam; PF00018; Kringle; 2.
Pfam; PF00018; Kringle; 2.
PRINTS; PR00129; CHWOTRYPSIN.
PRODOM; PD00018; KRINGLE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PS01253; FIBRONECTIN_1; 1
                        EGF_like.
Fibrnctnl.
                                                                                                                                                                                                                                                                                                                                                                           Probom, PD000355, SMART; SM00181, EGF; 1.
SMART; SM00058; FN1; 1.
SMART; SM00130; KR; 2.
SMART; SM00020; Tryp SPC; 1.
Thorstore, PS00022; EGF 1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-0CT-2002 (TrEMBLrel. 22, 01-0CT-2002 (TrEMBLrel. 22, 01-MAR-2003 (TrEMBLrel. 23, Hypothetical protein. Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00051; kringle; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 48.7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
TISSUE=Kidney;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00089; t
PRINTS; PR00722;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Serine protease
SEQUENCE 564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q8K0D2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28K0D2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DAY REPORTED TO THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY O
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   59 RGKASTDIMGRPCLPWNSATVLQQTYHAHRSDALQLGLGRCHNYCRNPDNRRRPWCYVQVG 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 ELHQVP-SNCD---CLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFY 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-0CT-2002 (TrEMBLrel. 22, Created)
01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
01-Stoke-type plasminogen activator.
01-Stoke-type plasminogen activator.
01-Stoke-type plasminogen activator.
01-Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
01-02E_TAXID=9986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              37.2%; Score 311.5; DB 6; Length 562; 43.5%; Pred. No. 2.7e-25; tive 15; Mismatches 58; Indels 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00021; KRINGLE 1; 2.
PROSITE; PS50240; KRYPEL 2) 2.
PROSITE; PS50240; TRYPELN DOM; 1.
PROSITE; PS00134; TRYPELN HS; 1.
PROSITE; PS00135; TRYPELN SER; 1.
EGF-like domain; Glycoprotein; Hydrolase; Kringle; Protease;
                                                                                                                           TISSUE Enamel organ;
Ding Y., Xue J., Barrlett J.D.;
Ding Y., Xue J., Barrlett J.D.;
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
PEMBL; AF554605; AAM00297.1;
REMBL; AF554605; AAM00297.1;
RINCEPPO; IPR006210; EGF.
RINCEPPO; IPR006210; IEGF.
RINCEPPO; IPR006210; Kingle.
RINCEPPO; IPR006210; Kingle.
RINCEPPO; IPR006210; Kingle.
RINCEPPO; IPR00031; Kingle.
RPfam; PF00008; EGF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  562 AA; 63668 MW; F9E6B4C77CB101E8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        564 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          119 LKPLVQECMVHDCADGKK 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         196 EKYSPDFCSTPACTKEKE 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SMART; SM00020; Tryp SPc; 1.
PROSITE; PS01022; EGF 1; 1.
PROSITE; PS01186; EGF 2; 1.
PROSITE; PS01253; FIBRONECTIN.
PROSITE; PS00021; KRINGLE 1; 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kringle, 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00039; fn1; 1.
Pfam; PF00051; kringle; 2.
Pfam; PF00089; trypsin; 1.
ProDom; PD000395; Kringle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 43.5 tes 60; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SMART; SM00181; EGF; 1.
SMART; SM00058; FN1; 1.
SMART; SM00130; KR; 2.
                                                                                                      SEQUENCE FROM N.A.
                                   NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Serine protease
SEQUENCE 562 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 10
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Q8MKB1

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Gaps

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FN Type_II
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IPR006209; EGF_like.
IPR000083; Fibrnctn1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              132 A--DGKKPSSPPEE 143
                                                                                                                                                                                                                                                                                                                                                                                277 SAQDVAYPEESPTE 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PF00051; kringle; 1. PF00089; trypsin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR006209;
InterPro; IPR00083;
InterPro; IPR000562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEROPS: S01.211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   fam; PF00008
                                                                                                                                                                                                                      Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                   . 705760
                                                                                                                                                                                                                                                                                                                                                                                                                                       097507
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097507
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                                                                                                                                                                                                                                       174 YWNSHLLLQETYNMFMEDAETHGIAEHNFCRNPDGDHKPWCFVKVNSEKVKWEYCDVTVC 233
                                                                                                                                                                                                                                                                     73 PWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVGLKPLVQE-CMVHDC 131
                                                                                                                                                                                                                         72
                                                                                                                                                                                                                       13 CLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFYRGKASTDTMGRPCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE=96425001; Pubmed=8827452;
Choi-Miura N.H., Tobe T., Sumiya J., Nakano Y., Sano Y., Mazda T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tomita M.; Purification and characterization of a novel hyaluronan-binding protein (PHBP) from human plasma: it has three EGF, a kringle and serine protease domain, similar to hepatocyte growth factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                      SMART; SMUOLOJ; TKY 1.

PROSITE; PRODO22; EGF 1; 3.

PROSITE; PSO1022; EGF 1; 3.

PROSITE; PSO1021; KRINGLE 1; 1.

PROSITE; PSO1021; KRINGLE 2; 1.

PROSITE; PSO1034; TRYPSIN LOM; 1.

PROSITE; PSO1034; TRYPSIN LOM; 1.

PROSITE; PSO1035; TRYPSIN LOM; 1.

PROSITE; PSO1035; TRYPSIN LOM; 1.

PROSITE; PSO1035; TRYPSIN LOM; 1.

PROSITE; PSO1036; TRYPSIN SER; 1.

PROSITE; PSO1036; TRYPSIN SER; 1.

RYDOLPACICAL PROCEASE; SERIE PROCEASE;

KRINGLE; PROLEASE; SERIE PROCEASE;

SEQUENCE 517 AA; 57326 MW; 3855A42035A5EA59 CRC64;
                                                                                                                                                                            31.7%; Score 265; DB 11; Length 517;
41.1%; Pred. No. 2.6e-20;
iive 19; Mismatches 51; Indels
                                                                                                                                                                                                                                                                                                                                                                                                     014520; 000663;
01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
HGF activator like protein (Hyaluronan binding protein 2).
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
Kitamura N.;
Submitted (MAR-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                            560 AA.
                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEROPS; SOI.033; -.
Genew; HGNC:4798; HABP2.
InterPro; IPR001314; Chymotrypsin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Biochem. 119:1157-1165(1996)
           Kringle; 1.
                                                                                                                                                                             Query Match
Best Local Similarity 41.1%
Matches 53; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
TISSUE=Colon, and Kidney;
                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
PRINTS; PRODO18; KRINGLE
           ProDom, PD000395; Kringl
SMART, SM00181; EGF, 3.
SMART, SM00130; KR; 1.
SMART, SM00020; Tryp_SPc
                                                                                                                                                                                                                                                                                                                132 ADGKKPSSP 140
                                                                                                                                                                                                                                                                                                                                      ---PVPDTP 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                      234
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217 YWNSHLLLQENYNMFMEDAETHGIGEHNFCRNPDADEKFWCFIKVTNDKVKWEYCDVSAC 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          159 CQNGATCSRHKRRSKF-TCACPDQFKGKFCEIG-SDDCYVGDGYSYRGKMNRTVNQHACL 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       73 PWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVGLKPLVQE-CWVHDC 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13 CLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFYRGKASTDTMGRPCL 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sus scrofa (Pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
NOSI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 560;
                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PSSO134; TRYPSIN_DOM; 1.
PROSITE; PSSO134; TRYPSIN_BOM; 1.
PROSITE; PSO0135; TRYPSIN_SER; 1.
BGF-11ke domain; Glycoprotein; Hydrolase; Kringle; Protease; Serine procease.
Serine procease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ch 31.5%; Score 263.5; DB 4; Length 1 Similarity 41.0%; Pred. No. 4.1e-20; 55; Conservative 18; Mismatches 56; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUELLY. KINATA T.;
TARADASHI T., KINATA T.;
TARADASHI T., KINATA T.;
"Porcine liver factor XII.";
Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO PEPTIDASF FAMILY S1.
-!- SIMILARITY: CONTAINS 1 KRINGLE DOMAIN.
EMBL; ABO22456; BAA37148.1; -.
HSSP; PO0763; 1DPO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
InterPro; IPR006209; EGF_like.
InterPro; IPR000001; Kringle.
InterPro; IPR0010264; Ser_protease_Try.
Pfam; PF00008; EGF; 3.
Pfam; PF000051; Kringle, 1.
Pfam; PF000151; Kringle, 1.
PRINTS; PR00152; CHYMOTRYPSIN.
PRINTS; PR00191; KRINGLE.
PROSITE; PS00022; EGF_1; 3.
PROSITE; PS01022; EGF_1; 3.
PROSITE; PS01021; KRINGLE.
PROSITE; PS00021; KRINGLE.; 1.
PROSITE; PS00021; KRINGLE.; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ser_protease_Try.
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InterPro; IPR000742; EGF 2.
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5 HOVPSNCDCLNGGTCVSNKYFSNIHW-----CNCPKKFGGQHCEIDKSKTCYEGNGH 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               57 FYRGKASTDIMGRPCLPWNSATVLQOTYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYV 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                290 EYRGVASTAASGLSCLAWNSDLIYQELHVDSVAAAVLLGLGPHAYCRNPDKDERPWCYV 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                239 HTACLSSPCLNGGTC-----HLIVGTGTSVCTCPLGYAGRFCNIVPTEHCFLGNGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17; Gaps
                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 29.9%; Score 250.5; DB 11; Length Best Local Similarity 42.0%; Pred. No. 1.2e-18; Matches 50; Conservative 11; Mismatches 41; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Created)
                                     PRINTS; PRO0722; CHYMOTRYPSIN.
PRINTS; PRO0013; FNTYPEII.
PRINTS; PRO0018; KRINGLE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JAN-1998 (TrEMBLrel. 05, 01-JAN-1998 (TrEMBLrel. 05, 01-MAR-2003 (TrEMBLrel. 23, 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
TISSUE=Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Factor XII.
F12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               035727
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035727
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6 QVPSNCDCLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFYRGKASTD 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical 70.6 kpa protein.
Hypothetical 70.6 kpa protein.
Bux musculus (Mouse).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. (FIETETD=10090;
R PRINTS; PRO0122; CHYMOTRYPSIN.
R PRINTS; PR00013; KNTYEII.
R PRODM; PR000195; KNTMGIE.
R ProDOM; PD000195; KNTMGIE.
R SMART; SM00181; EGF; 2.
R SMART; SM00181; EGF; 2.
R SMART; SM00180; FN1; 1.
R SMART; SM00180; FN2; 1.
R SMART; SM00180; KR; 1.
R SMART; SM00180; KR; 1.
R SMART; SM00180; TYP, SPC; 1.
R PROSITE; PS01186; EGF 2; 1.
R PROSITE; PS01186; EGF 2; 1.
R PROSITE; PS01023; FIBRONECTIN_1; 1.
R PROSITE; PS00021; KRINGLE_1; 1.
R PROSITE; PS00021; KRINGLE_2; 1.
R PROSITE; PS00013; KRINGLE_2; 1.
R PROSITE; PS0013; TRYPSIN_DOM; 1.
R PROSITE; PS0013; TRYPSIN_DOM; 1.
R PROSITE; PS0013; TRYPSIN_HIS; 1.
R PROSITE; PS0013; TRYPSIN_HIS; 1.
R PROSITE; PS0013; TRYPSIN_HIS; 1.
R PROSITE; PS0013; TRYPSIN_HIS; 1.
R PROSITE; PS0013; TRYPSIN_HIS; 1.
R PROSITE; PS0013; TRYPSIN_HIS; 1.
R PROSITE; PS0013; TRYPSIN_HIS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30.8%; Score 258; DB 6; Length 616; 39.0%; Pred. No. 1.8e-19; Live 15; Mismatches 58; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Strausberg R.;
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
-!- SIMILARITY: COUTAINS 1 KRINGLE DOMAIN.
EMBL BEOLOGYFG, ACH19376.1; -.
HSSP; PO0761; 1AN1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    616 AA; 68012 MW; 4C5FE3D71EBBD1A9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                653 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001314; Chymotrypsin.
InterPro; IPR006209; BGF_1;ke.
InterPro; IPR0006319; Fibrnctn1.
InterPro; IPR000562; FN Type_II.
InterPro; IPR006210; IEGF.
InterPro; IPR001204; Ser_protease_Try.
Pfam; PF000009; EGF; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        125 ECMVHDCAD-GKKP----SSPPE 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              289 YCRLARCQAPIGEAPPILTPTQSPSE 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PF00040; fn2; 1.
PF00051; kringle; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best local Similarity 39.0%
Matches 57, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PF00039; fn1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
TISSUE=Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Serine protease
SEQUENCE 616 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          240 RW----TVEATYRNMTEKQALSWGLGHHAFCRNPDNDTRPWCFVWSGDRLSWDYGGLEQC 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          73 PWNSATVLQQTY-HAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVGLKPLVQECMVHDC 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13 CLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFYRGKASTDTMGRPCL 72
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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                R SMART; SM001033; ALLINGTE; 1.

R SMART; SM001059; FN1; 1.

SMART; SM00059; FN2; 1.

SMART; SM00020; TN2p, 5Pc; 1.

SMART; SM00020; TN2p, 5Pc; 1.

R PROSITE; PS00122; EGF_1; 2.

R PROSITE; PS00123; FIBRONECTIN 1; 1.

R PROSITE; PS00023; FIBRONECTIN 2; 1.

R PROSITE; PS00021; KRINGLE; 1.

R PROSITE; PS00034; TRYPSIN H15; 1.

R PROSITE; PS00134; TRYPSIN H15; 1.

R PROSITE; PS00135; TRYPSIN H15; 1.

R PROSITE; PS00135; TRYPSIN H15; 1.

R PROSITE; PS00136; TRYPSIN H15; 1.

R PROSITE; PS00136; TRYPSIN H15; 1.

R PROSITE; PS00136; TRYPSIN H15; 1.

R PROSITE; PS00136; TRYPSIN H15; 1.

R PROSITE; PS00136; TRYPSIN H15; 1.

R PROSITE; PS00136; TRYPSIN H15; 1.

R PROSITE; PS00136; TRYPSIN H15; 1.

R PROSITE; PS00136; TRYPSIN H15; 1.

R PROSITE; PS00136; TRYPSIN H15; 1.

R PROSITE; PS00136; TRYPSIN H15; 1.

R PROSITE; PS00136; TRYPSIN H15; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 29.9%; Score 250; DB 11; Length 597; Best Local Similarity 36.6%; Pred. No. 1.3e-18; Matches 52; Conservative 16; Mismatches 54; Indels 20;
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No. Dou D.;

A Dou D.;

A Dou D.;

I "A brain-type plasminogen activator.";

Submitted (APR-2000) to the EMBL/Geneank/DDBJ databases.

-:- SIMILARITY: BELONGS TO PEPTIDASE FAMILY SI.

-:- SIMILARITY: CONTAINS I KRINGLE DOWAIN.

R HSSP; PO0750; 1PK2.

R HSSP; PO0750; 1PK2.

R InterPro; 1PR0010314; Chymotrypsin.

R InterPro; 1PR000083; Fibrnctni.

R InterPro; 1PR000083; Fibrnctni.

R InterPro; 1PR000083; Fibrnctni.

R InterPro; 1PR000081; Kringle.

R Pfam; PF00089; fin; 1.

R Pfam; PF00089; trypsin; 1.

R Pfam; PF00089; Kringle; 1.

R PRINTS; PR00125; KRINGLE.

R PRINTS; PR00125; KRINGLE.

R PRINTS; RN00185; KRINGLE.

R SMART; SM00180; KR; 1.

R SMART; SM00180; KR; 1.

R SMART; SM00120; Tryp_SPC; 1.
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Neonatal thrombolytic agent alpha-form (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            132 -----ADGKKPSSPP 141
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                                                                                   ProDom; PD000995; FN Type_II; 1. ProDom; PD000395; Kringle; 1.
PRINTS; PR00013; FNTYPEII.
PRINTS; PR00018; KRINGLE.
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183 CLHGGRCLE---VEGHRLCHCPVGYTGPFCDVDTKASCYDGRGLSYRGLARTTLSGAPCO 239
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                                                                                                                                                                                                                                                                                  Gaps
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Wada H., Nishioka J., Nakatani K., Kasai Y., Abe Y., Nobori T
"Molecular chracterization of coaggulation factor XII-Mie.";
Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.

EMBL, AB09845; BAC23095.1; -.

SEQUENCE 615 AA; 67735 MW; 030508870A0C7EDB CRC64;
PROSITE, PSO0021, KRINGLE 1; 1.
PROSITE, PSO0021, KRINGLE 2; 1.
PROSITE, PSO0034, TRYPSIN_DOM, 1.
PROSITE, PSO0134, TRYPSIN_DSK, 1.
PROSITE, PSO0135, TRYPSIN_SER, 1.
Glycoprocein, Hydrolase, Kringle, Protease, Serine protease.
NON TER 395 A8, 44123 MW; 3FBD4A2F0B7CIIC8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match. 27.8%; Score 233; DB 4; Length 615; Best Local Similarity 42.3%; Pred. No. 9.2e-17; Matches 44; Conservative 12; Mismatches 40; Indels
                                                                                                                                                                                                                              Length 395,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        73 PWNSATVLOOTY-HAHRSDALQLGLGKHNYCRNPDNRRRPWCYV 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          240 PWAS----EATYRNVTAEQARNWGLGGHAFCRNPDNDIRPWCFV 279
                                                                                                                                                                                                                                                                             49; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Dou D.;
"Production of kringle fragment.";
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
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01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Plasminogen/activator kringle.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
                                                                                                                                                                                                                           Query Match 27.8%; Score 233; DB 4; Best Local Similarity 41.2%; Pred. No. 5.7e-17; Matches 47; Conservative 12; Mismatches 49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      90 AA
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01-WAR-2003 (TrEMBLrel. 23, Last seq
01-WAR-2003 (TrEMBLrel. 23, Last ann
Coagulation factor XII-Mie.
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Q8IZZS;
01-MAR-2003 (
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23 HPBLSB----CFTVNGRDYRGTVSQAGPEGTPCLYWNQTT---QHLYNAQSDPDGELGLGNH 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  41 HCEIDKSKTCYEGNGHFYRGKAS-TDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKH
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MEDLINE=20538710; PubMed=11083926;
Ip F.C., Glass D.G., Gles D.R.; Cheung J., Lai K.O., Fu A.K.,
Yancopoulos G.D., In Y.;
"Cloning and characterization of muscle-specific kinase in chicken.";
Mol. Cell. Neurosci. 16:661-673(2000).
12 WCYVFKAGKYISEFCSTPACTKVAEEDGDCYTGNGLAYRGTRSRTKSGFSCLPWNPVFLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gallus gallus (Chicken).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Archosauria, Aves, Neognathae, Galliformes, Phasianidae, Phasianinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE=22308873; PubMed=12421700;
Davidson G., Mao B., Del Barco Barrantes I., Niehrs C.;
"Kremen proteins interact with Dickkopf1 to regulate anteroposterior
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Xenopus laevis (African clawed frog).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae;
                                                           81 QQTYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVGLKPLVQECMVHDC 131
                                                                                                       . Match 20.8%; Score 174; DB 13; Length 421; Local Similarity 47.4%; Pred. No. 1.5e-10; les 36; Conservative 6; Mismatches 28; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 13; Length 947;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CNS patterning.";
Development 129:5587-5596(2002).
EMBL; AY:50813; AAN64661.1; -.
SEQUENCE 421 AA; 46274 MW; 74D04DB1682CD15F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OL-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Muscle-specific receptor tyrosine kinase MuSK.
                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                       421 AA
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                                                                                                                                                                                                                                                                                                                                   Created)
                                                                                                                                                                                                                                                                       PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            78 NYCRNPDADVOPWCYV 93
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01-MAR-2003 (TrEMBLrel. 23,
01-MAR-2003 (TrEMBLrel. 23,
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NCBI_TaxID=9031;
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01-MAR-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ogatus gatius (Ultromi).
Ebkaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
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                                                                                                                                                                                                                                                                                                                                                               Score 218.5; DB 4; Length 90;
Pred. No. 4.2e-16;
5; Mismatches 36; Indels
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PROSITE; PS50070; KRINGLE_2; 2.
PROSITE; PS50240; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_HIS; 1.
Glycoprotein; Hydrolase; Kringle; Protease; Serine protease.
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36.9%; Pred. No. 1.9e-13;
tive 11; Mismatches 50; Indels
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                                                                                              PEAM, PF00051, Kringle; 1.
PRINTS; PR00018; KRINGLE.
PRODOM; PD000395, Kringle; 1.
PROSITE; PS00021; KRINGLE 1; 1.
PROSITE; PS00021; KRINGLE 2; 1.
PROSITE; PS00070; KRINGLE 2; 1.
SEQUENCE 90 AA; 9804 MW; A33887F9FDF4C7B1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1996 (TrEMBLrel. 01, Last sequence update) 01-MAR-2003 (TrEMBLrel. 23, Last annotation update) Tissue-type plasminogen activator (Fragment).
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         .!- SIMILARITY: CONTAINS 1 KRINGLE DOMAIN.
SMBL; AF282882; AAM52248.1; -.
InterPro; IPR000001; Kringle.
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HSSP; P00756; IRTF
HSSPS; S01.232;
INTERPRO; IPR000001; Kringle.
INTERPRO; IPR001254; Ser_protease_Try.
Pfam; PF00089; trypsin; 1
PRINTS; PR00018; KRINGLE.
ProDom; PD000395; KRINGLE.
SMART; SM00130; KR; 1:
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                                                                                                                                                                                                                                                                                                                                                                     26.1%;
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Gallus gallus (Chicken)
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Best Local Similarity
Matches 41; Conserva'
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Matches 41; Conserv
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SEQUENCE
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6; Gaps

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64 TDTMGRPCLPWNSATVLQQTYHAHR-----SDALQLGLGKHNYCRNP-DNRRRPWC 113
                                                                                                                                                                                                                                                               479 VTASGIPCOKWS-----DOAPHLHRRTPQVFPELSDA-----ENYCRNPGGENERPWC 526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 74 WNSAT----VLOQTYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQV-----GL 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30 WC----NCPKKFGGQHCEIDKSK------TCYEGNGHFYRGKASTDIMGRPCLP 73
                                                                                         4 LHQVPSNCDCLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFYRGKAS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1996 (TrEMBLrel. 23, Last annotation update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Growth factor Livertine.

Kenopus laevis (African clawed frog).

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Amphibiae; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R InterPro; IPR00001; Kringle.
R InterPro; IPR000001; Kringle.
R InterPro; IPR000001; Kringle.
R InterPro; IPR003046; Pan app.
R InterPro; IPR003066; Prochrombin.
R InterPro; IPR003066; Prochrombin.
R InterPro; IPR003056; Prochrombin.
R Pfam; PF00051; Kringle; 4.
R Pfam; PF00069; trypsin; 1.
R Pfam; PR00089; trypsin; 1.
R RPINTS; PR00125; CHYMOTRYPSIN.
R RRINTS; PR00125; CHYMOTRYPSIN.
R RRINTS; PR001295; Kringle; 4.
R SMART; SM00403; KR; 1.
R SMART; SM00403; PAN AP; 1.
R SMART; SM00020; KRINGLE 1; 4.
R RAFET; SM00020; KRINGLE 1; 4.
R ROSITE; PS00020; KRINGLE 1; 4.
R ROSITE; PS00020; KRINGLE 1; 4.
R ROSITE; PS00040; KRINGLE 1; 4.
R ROSITE; PS00404; TRYPSIN DOM; 1.
R ROSITE; PS04040; TRYPSIN DOM; 1.
R ROSITE; PS05040; TRYPSIN DOM; 1.
R ROSITE; PS05040; TRYPSIN DOM; 1.
R ROSITE; PS05040; TRYPSIN DOM; 1.
R ROSITE; PS05040; TRYPSIN DOM; 1.
R ROSITE; PS05040; TRYPSIN DOM; 1.
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19.8%; Score 166; DB 13; Length 716;
Best Local Similarity 31.1%; Pred. No. 1.9e-09;
Matches 42; Conservative 11; Mismatches 40; Indels 4;
      Pred. No. 3.5e-10;
; Mismatches 36; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SECUENCE FROM N.A.

Ruiz i Altaba A., Thery C.;

Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.

-1- SIMILARITY: CONTAINS 4 KRINGLE DOMAINS.

EMBL; U57455; AAB52574.1; --
HSSP; P00747; ICEA.
                                                                                                                                                                                                                                                                                                                      114 YVQVGLKPLV--QECMVHDCADG-----KKPSS-----PP 141
                                                                                                                                                                                                                                                                                                                                                                              527 YTK---DPSVTWEYCSVSPCGDASLSLGTRKPNGETQNLPP 564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              716 AA
31.1%; Pre
tive 15;
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      Best Local Similarity 31.1
Matches 50; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 22
Q91691
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211 NRTPENFPCKN----LDENYCRNPDGETAPWCYTTNSEVRWEHCQIPSCESSPITTEYLD 266
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. Prite Shepherd S.R., Coffman K.T., Resnick D., Chan R., Kisker O., Polkman J., Maters D.J.; "Angiostatin is Detectable in the Urine of Dogs with Spontaneous Bone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5 HOVPSNCDCLNGGTCVSNKYFSN----IHWC-NCPKKFGGQHCEIDKSKT-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rattus norvegicus (Rat).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 359;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: CONTAINS 4 KRINGLE DOMAINS.
EMBL; AY069985; AALS8519.1; -.
InterPro; IPRO00001; Kringle.
InterPro; IPR003966; Prothrombin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bangert K., Johnsen A.H., Thorsen S.;
"Rat plasminogen: cDNA and gene structure.";
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  359 359
359 AA; 41172 MW; 776D35F4AB0BDD9E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2003 (TrEMBLrel. 23, Last annotation update)
Plasminogen protein precursor (EC 3.4.21.7).
PLASMINOGEN.
                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19.8%; Score 165.5; DB 6; 29.0%; Pred. No. 1e-09; tive 13; Mismatches 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      812 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          320 HFPEAGL-TMNYCRNPDADKSPWCY 343
                                                                                                                                                                                         Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PEAM; PF00051; Kringle; 4.
PRINTS; PR00019; KRINGLE.
PRINTS; PR010019; KRINGLE.
ProDom; PD000395; Kringle; 4.
SMART; SM0130; KR; 4.
PROSITE; PS00071; KRINGLE_1; 4.
PROSITE; PS00070; KRINGLE_2; 4.
                                                                                                                                                                         01-MAR-2002 (TrEMBLrel. 20, 01-MAR-2002 (TrEMBLrel. 20, 01-MAR-2003 (TrEMBLrel. 23,
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                                                                                            PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                   Plasminogen (Fragment)
Canis familiaris (Dog)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
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TISSUE=Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9615;
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NON TER
SEQUENCE
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RESULT 23
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                                                                                                                                          SOUR REPRESENTATION OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PRO
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, Aoki S., Kitajima K., Funakoshi H., Takahashi T.,
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InterPro; IPR000024; Fz domain.
InterPro; IPR003098; Ig_dc.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR000001; Kringle.
Fam; PF001392; Fz; I.
Fam; PF00047; ig; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PRO0018; KRINGLE.
Probom; PD000395; Kringle; 1.
SMART; SM00408; IGC2; 1.
SMART; SM00130; KR; 1.
PROSTTE; PS50038; FZ; 1.
PROSTTE; PS50038; IG LIKE; 1.
PROSTTE; PS500021; KRINGLE 1; 1.
PROSITE; PS50070; KRINGLE 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                      100 NYCRNPDNRRRPWCYV 115
                                                                                                                                                                                                                                                                                                                                                                                                                                              80 NYCRNPDGDVSPWCYI 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
TISSUE=Muscle,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 26
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KT Teceptor Site for plasminogen "Y receptor Site for plasminogen";

L. SIMILARITY: CONTAINS 5 KRINGLE DOMAINS.

TREMEL; AJ24649; CAB46614.1;

TREMEL; AJ24649; CAB46614.1;

TREMEL; AJ24649; CAB46614.1;

TREMEL; AJ24649; CAB46614.1;

TREPPO: IPRO001314; Chymotrypsin.

DR InterPro: IPRO0014; Chymotrypsin.

DR InterPro: IPRO03609; Pan app.

DR InterPro: IPRO01554; Ser_Drotase_Try.

DR InterPro: IPRO01401; Sometotropin.

DR PRINTS; PRO051; Kringle; 5.

DR PERM: PRO0051; Kringle; 5.

DR PRINTS; PRO0158; KRINGLE.

DR PRINTS; PRO0168; KRINGLE.

DR PRINTS; PRO01695; KRINGLE.

DR PRINTS; PRO01695; KRINGLE.

DR PRINTS; PRO01695; KRINGLE.

DR PRINTS; PRO01695; KRINGLE.

DR PRINTS; PRO01695; KRINGLE.

DR PRINTS; PRO01695; KRINGLE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                308 NRTPENFPCKN----LEENYCRNPDGETAPWCYTTDSQLRWEYCEIPSCGSSVSPDQSDS 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  364 SVLPEQTPVVQECYQGNGKSYRGTSSTINTGKKCQSW-----VSMTPHSHSKTPANFPDA 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    95 GLGKHNYCRNPDN-RRRPWCYVQVGLKPLV--QECMVHDCAD------GKKPSSP 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5 HOVPSNCDCLNGGTCVSNKYFSN----IHWC-NCPKKFGGQHCEI------DKS-- 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                48 -----KTCYEGNGHFYRGKASTDIMGRPCLPWNSAIVLQQIYHAHRSDALQL--- 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19.8%; Score 165.5; DB 11; Length 812; 27.8%; Pred. No. 2.5e-09; tive 22; Mismatches 51; Indels 57; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                             Glycoprotein; Hydrolase; Kringle; Protease; Serine protease; Signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Xenopus laevis (African clawed frog).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE 812 AA; 90535 MW; 8C703C51410EBC9E CRC64;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PLASMINOGEN
                                                                                                                                                                                                                                                                                                                        SMART; SM00130; KR; 4.

SMART; SM00473; PAN AP; 1.

RNART; SM00020; Tryp_SPC; 1.

RNOSITE; PS00021; KRINGLE 1; 5.

PROSITE; PS0070; KRINGLE 2; 5.

PROSITE; PS00138; SOMATOTROPIN 2; 1.

PROSITE; PS00134; TRYPSIN HIS; 1.

PROSITE; PS00135; TRYPSIN HIS; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    [1] SEQUENCE FROM N.A.
MEDLINE=21167372; PubMed=11267660;
                        TISSUE=Liver;
MEDLINE=91250378; PubMed=1645711;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 27.8%
Matches 50; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
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22 CSDSFHSECYTVNGADYRGTQNQTSLDGGKPCLFWNE--TPQHPYNTLKYPNGEGGLGEH 79
42 CEIDKSKTCYEGNGHFYRGKASTDTM--GRPCLPWNSATVLQQTYHAHRSDALQLGLGKH
                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Merazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                      Length 452;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-UNN-2001 (TrEMBLrel. 17, Created)
01-UNN-2001 (TrEMBLrel. 17, Last sequence update)
01-MNR-2003 (TrEMBLrel. 23, Last annotation update)
Similar to receptor tyrosine kinase-like orphan receptor 1.
                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
19.0%; Score 159; DB 13; Length 4
Best Local Similarity 40.8%; Pred. No. 6.7e-09;
Matches 31; Conservative 9; Mismatches 32; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Strausberg R.;
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
-! SIMILARITY: CONTAINS 1 KRINGLE DOMAIN.
EMBL; BCO06374; AAH06374.1; -.
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454 AA
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InterPro; IPR0010001; Kringle.
InterPro; IPR001254; Ser protease_Try.
Pfam; PF00051; Kringle; 2.
Pfam; PF00089; trypsin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      93 QLG--LGKHNYCRNPDNRRR-PWCY 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      351 RFPELNGGHSYCRNPGNOKEAPWCF 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Apolipoprotein a (Fragment).
BABAPOA.
                                                                                                                                                                                                                    Query Match
Best Local Similarity 29./*
Best Local Similarity 29./*
Conservative
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                   SEQUENCE FROM N.A.
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01-JUN-1998 (
01-MAR-2003 (
                                                                                                                                                                                                 SEQUENCE
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046506
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  236 DETSSVPKPRDLCRDECEVLENVLČQTEXIFARSNPMILMRLKLPNČEDLPQPESPEAAN 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 NELHQVP-----PKKFGGQH 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C------EIDKSKTCYEGNGHFYRGKASTDTMGRPCLPWNSATVLQQTYHAHRSDAL 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.

STRAIN=C57BL/6J; TISSUE=Adipose tissue;

STRAIN=22354683; PubMed=12466851;

The FANTOM Consortium Research Group Phase I & II Team;

the RIKEN Genome Exploration Research Group Phase I & II Team;

"Analysis of the mouse transcriptome based on functional annotation of 60,70 full-length cDNss.";

Nature 420:563-573 (2002).

EMBL; AKO80896; BAC38068.1; -.

SEQUENCE 937 AA; 104118 MW; CB440323CA66EC28 CRC64;
                                                                                                                            2 NELHQVP-----PKKFGGQH
                                                                                                                                                            236 DETSSVPKPRDLCRDECEILENVLCQTEYIFARSNPMILMRLKLPNCEDLPQPESPEAAN
                                                                                                                                                                                                 C-----BIDKSKTCYEGNGHFYRGKASTDTMGRPCLPWNSATVLQQTYHAHRSDAL
                                                                                        37; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 37; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
Glycoprotein; Immunoglobulin domain; Kinase; Kringle; Receptor SEQUENCE 393 AA; 43825 MW; 1F93DCBBBBF53855 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 18.9%; Score 158.5; DB 11; Length 937; Best Local Similarity 29.7%; Pred. No. 1.7e-08; Matches 43; Conservative 14; Mismatches 51; Indels 37;
                                                   Query Match
18.9%; Score 158.5; DB 4; Length 393;
Best Local Similarity 29.7%; Pred. No. 6.5e-09;
Matches 43; Conservative 14; Mismatches 51; Indels 37
                                                                                                                                                                                                                                                                                                                                                                                                                               01-WAR-2003 (TrEMBLrel. 23, Created)
01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
01-WAR-2003 (TrEMBLrel. 23, Last annotation update)
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                937 AA
                                                                                                                                                                                                                                                                  QLG--LGKHNYCRNPDNRRR-PWCY 114
                                                                                                                                                                                                                                                                                           93 QLG--LGKHNYCRNPDNRRR-PWCY 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       351 RFPELNGGHSYCRNPGNOKEAPWCF 375
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01-MAR-2003 (TrEMBLrel. 23, Last seq
01-MAR-2003 (TrEMBLrel. 23, Last ann
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=10090;
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Q8BNP9
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296 CIRIGIPMADPINKNHKCYNSTGVDYRGTVSVTKSGRQCQPWNS-----QYPHTHSFTAL 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 NELHQVP-----PKKFGGQHCVSNKYFS-----NIHWCNC-----PKKFGGQH 41
STRAIN=CS7BL/6J; TISSUE=Adipose tissue;
MEDLINE=22354683; PubMed=12466851;
The FANTOM Consortium.
The FANTOM Consortium.
The RIKEN Genome Exploration Research Group Phase I & II Team;
The Manalysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
Mature 420:563-5731(2002).
EMBL; AK049369; BAC33714.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            236 DETSSVPKPRDLCRDECEVLENVLCQTEYIFARSNPMILMRLKLPNCEDLPQPESPEAAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      42 C------EIDKSKTCYEGNGHFYRGKASTDTMGRPCLPWNSATVLQQTYHAHRSDAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 37; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cox L.A., Jett C., Hixson J.E., "Molecular Basis of the Apolipoprotein (a) Null Phenotype: A Splice Site Mutation is Associated with Deletion of a Single Exon in a Null
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Papio hamadryas (Hamadryas baboon).
Sukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Papio.
                                                                                                                                                                                                                                                                                                                                                                                                               DB 11; Length 937;
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DR PRINTS; PR000122; CHYMOTRYPSIN.
PRINTS; PR0001395; KRINGLE.
R PCDDom; PD0001395; KRINGLE.
R PS0001395; KR1, 2.
SWART; SM00130; TRYP_SPC: 1.
R PROSITE; PS50021; KRINGLE 1; 2.
R PROSITE; PS50040; KRINGLE 2; 2.
R PROSITE; PS50040; TRYPSIN_DOM; 1.
R PROSITE; PS00135; TRYPSIN_DOM; 1.
R Qlycoprotein; Hydrolase; Kringle; Lipoprotein; Protease; 4 Serine protease.
I NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                           18.9%; Score 158.5; DB 11; Length
29.7%; Pred. No. 1.7e-08;
ive 14; Mismatches 51; Indels
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-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
-!- SIMILARITY: CONTAINS 2 KRINGLE DOMAINS.
EMBL, AF029691; AAB97886.1; -
                                                                                                                                                                                                                                                                                                                                 937 AA; 104088 MW; D6F2D84E67D03C69 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (TrEMBLrel. 06, Created)
(TrEMBLrel. 06, Last sequence update)
(TrEMBLrel. 23, Last annotation update)
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50 CYEGNGHFYRGKASTDIMGRPCLPWNSAIVLQ--QIYHAHRSDALQLGLGKHNYCRNPDN 107
                                                                                                                                                                                                                                                                                                                                                                                        102 CYHGDGQSYRGSFSTTVTGRTCQSHSSMTPHQHKRTPENHPNDGLTM-----NYCRNPDA 156
                                                                                                     18.9%; Score 158; DB 6; Length 454;
39.8%; Pred. No. 8.6e-09;
tive 10; Mismatches 31; Indels 12; Gaps
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18.8%; Score 157; DB 4; Length 113;
Best Local Similarity 34.8%; Pred. No. 2.4e-09;
Matches 39; Conservative 13; Mismatches 36; Indels 24; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
OGOSTEL 181705; PubMed=11285247;
OGOSTEL A. Kraft H.G., Ehnholm C., Utermann G.;
Single nucleotide polymorphisms in exons of the apo(a) kringles IV types 6 to 10 domain affect Lp(a) plasma concentrations and have different patterns in Africans and Caucasians.";
Hum. Mol. Genet. 10:815-824(2001)
-: SIMILARITY: CONTAINS I KRINGIE DOMAIN.
EMBL; AF156663; AAF03680:1; --
EMBL; AF156663; AAF03680:1; --
HSSP; POOTAT, IPW.
HSSP; POOTAT, IPW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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113 AA; 12685 MW; F3D65681D9B5253A CRC64;
50041 MW; 974E30744C187B2F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-WAR-2003 (TrEMBLrel. 23, Last annotation update)
Apolipoprotein(a) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           113 AA
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Search completed: December 3, 2003, 14:43:00 Job time : 18.5948 secs

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32, Appli
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100.0%; Pred. No. 1.7e-76;
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US-10-237-866-12
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US-10-880-503-6
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US-10-193-658-145
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US-09-981-451-14
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APPLICANT: HIGAZI, Abd Al-Roof
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: TISSUE CONTRACTABILITY
FILE REFERENCE: 9596-331
CURRENT APPLICATION NUMBER: US/09/880,503
CURRENT FILING DATE: 2001-06-13
PRIOR FILING DATE: 2001-06-13
PRIOR FILING DATE: 2000-06-20
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PATCHIN VET: 2.1
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TYPE: PRT
ORGANISM: Homo sapiens
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837
1 SNELHQVPSNCDCLNGGTCV.....QECMVHDCADGKKPSSPPEE 143
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Copyright (c) 1993 - 2003 Compugen Ltd.
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US-10-171-311-149

US-10-171-61-149

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US-10-18-18-12

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No.
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KASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVGLK 120
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APPLICANT: Severin, Jean M.
APPLICANT: Bedalji, Rohinton
APPLICANT: Gohnson Jr., Robert W.
APPLICANT: Holzman, Thomas F.
TILE OF INVENTION: HIGHLY CRYSTALLINE URCKINASE
FILE REFERENCE: 6310.US.Pl
CURRENT APPLICATION NUMBER: US/09/264,468B
PRIOR PRING DATE: 1999-03-05
PRIOR FILING DATE: 1999-03-06
PRIOR FILING DATE: 1998-03-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100.0%; Pred. No. 5.5e-76;
Matches 143; Conservative 0; Mismatches 0;
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APPLICANT: Berger, Allison
APPLICANT: Guillemette, Tracy L.
APPLICANT: Kamackar, Shubhangi
APPLICANT: Schlegel, Robert
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SOFTWARE: FastSEQ for Windows Version 4.0
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LOCATION: (1)...(20)
OTHER INFORMATION: Leader sequence
NAME/KEY: VARIANT
LOCATION: (279)...(279)
OTHER INFORMATION: Xaa = any amino acid
NAME/KEY: VARIANT
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CTHER INFORMATION: Xaa = any amino acid
US-09-264-468B-1
                                                                                                           121 PLVOECMVHDCADGKKPSSPPEE 143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 161, Application US/10301822 ; Publication No. US20030148410A1 ; GENERAL INFORMATION:
                                                                                                                                                                                                                Sequence 1, Application US/09264468B
Patent No. US20020106775A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                              APPLICANT: Wang, Jieyi
APPLICANT: Neraber, Vicki L
APPLICANT: Henkin, Jack
APPLICANT: Smith, Richard A.
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ORGANISM: Homo sapiens
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                                                            Sequence 3, Application US/09880503
Patent No. US20020131964A1
GENERAL INFORMATION:
APPLICANT: CINES, Douglas B
APPLICANT: CINES, Douglas B
APPLICANT: HIGAZI, Abd Al-Roof
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING MUSCLE CELL AND
FILE REFERENCE: 9596-331
CURRENT APPLICATION NUMBER: US/09/880,503
CURRENT FILING DATE: 2001-06-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 KASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVGLK 120
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100.0%; Pred. No. 5.2e-76;
ative 0; Mismatches 0;
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100.0%; Score 837; DB 15;
Best Local Similarity 100.0%; Pred. No. 4.2e-76;
Matches 143; Conservative 0; Mismatches 0;
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PRIOR FILING DATE: 2000-66-20
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin Ver. 2.1
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Best Local Similarity 100.0
Matches 143; Conservative
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US-10-106-698-6266
                               RESULT 2
US-10-106-698-6266
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US-10-076-421-2
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                                                                APPLICANT: INITIONAL GENES, COMPOSITIONS, KITS, AND
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION OF COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR
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APPLICANT: Davies, Michael J
APPLICANT: Davies, Michael J
APPLICANT: Fish, Paul V
APPLICANT: Fish, Paul V
APPLICANT: Huggins, Jonathan P
APPLICANT: McIncosh, Fraser S
APPLICANT: McIncosh, Fraser S
APPLICANT: Occleston, Nicholas L
TILLE OF INVENTION: Composition
FILE PERERENE: 2002-04-25
FILE PERERENE: 2002-04-25
PRIOR APPLICATION NUMBER: US/09/726,295
PRIOR PILING DATE: 2000-11-30
PRIOR FILING DATE: 1999-12-29
NUMBER OF SEQ ID NOS: 60
SOFTWARE: PATENTIN VET: 2.2
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Monahan, John E.
Thibodeau, Stephen N.
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CORGANISM: Homo Sapiens
US-10-301-822-161
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1 SNELHQVPSNCDCLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFYRG

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81. XASTDIMGRPCLPMNSAIVLQQIYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVGLK 140
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                                                                                 61 KASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVGLK 120
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21 SNELHQVPSNCDCLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFYRG 80
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TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, REVENTION, AND THERAPY
TITLE OF INVENTION: OF CERVICAL CANCER
TITLE REFERENCE: MRI-035
CURRENT APPLICATION NUMBER: US/10/171,311
CURRENT FILING DATE: 2002-06-12
PRIOR FILING DATE: 2001-06-13
PRIOR APPLICATION NUMBER: US 60/298,159
PRIOR APPLICATION NUMBER: US 60/298,159
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                                                                                                                                                                                                                                                                                                                                                                                          RESULT 7
US-10-076-421-2
Sequence 2, Application US/10076421
Publication No. US20020193304A1
GENERAL INFORMATION:
GENERAL INFORMATION:
JAPPLICANT: WADA, MANBU
JAPPLICANT: WADA, NANBU
JAPPLICANT: WADA, NANBU
JAPPLICANT: WADA, NANBU
JAPPLICANT: WADA, NANBU
JAPPLICANT: WADA, NANBU
JAPPLICANT: WADA, NANBER: US/10/076,421
CURRENT APPLICATION NUMBER: US/205-05-17
PRIOR FILING DATE: 2001-02-20
PRIOR FILING DATE: 2001-02-20
PRIOR FILING DATE: 2001-02-30
PRIOR FILING DATE: 2001-06-19
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PATENTIN VET. 2.1
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, Publication No. US20030087270A1
, GENERAL INFORMATION:
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APPLICANT: Zhao, Xumei
APPLICANT: Monahan, John
APPLICANT: Kamatkar, Shubhangi
APPLICANT: Gante, Karen
APPLICANT: Gannavarapu, Manjula
APPLICANT: Hoersh. Sehaetin
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98.8%; Score 827; DB 12;
99.3%; Pred. No. 5.3e-75;
tive 0; Mismatches 1;
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Pred, No. 8.7e-76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Mismatches
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                                                                                            ; Sequence 149, Application US/10247671; Publication No. US20030194721A1; GENERAL INFORMATION:
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, Sequence 2, Application US/10407821
; Publication No. US20030219386A1
; GENERAL INFORMATION:
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Best Local Similarity 99.3
Matches 142; Conservative
                                                                                                                                                                  APPLICANT: Mikita, Thomas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Homo sapiens
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Best Local Similarity
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: W.Y TOT
APPLICANT: L1, Jinan
FILE REFERENCE: 3810/14577-US3
CURRENT FILING DATE: 2002-07-10
PRIOR APPLICATION NUMBER: US/10/193,656
CURRENT FILING DATE: 2001-07-10
PRIOR FILING DATE: 2001-07-10
PRIOR FILING DATE: 2001-07-10
PRIOR FILING DATE: 2001-07-10
PRIOR FILING DATE: 2001-07-10
PRIOR FILING DATE: 2001-07-10
PRIOR FILING DATE: 2001-07-13
SOFTWARE: PATENTING DATE: 2001-07-13
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                                                                                                                                                                                                                                                           100.0%; Score 837; DB 15;
100.0%; Pred. No. 5.5e-76;
tive 0; Mismatches 0;
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DATABASE ACCESSION NUMBER: Genbank / P00749;
DATABASE ENTRY DATE: 1986-07-21
RELEVANT RESIDUES: (1)..(431)
US-10-193-656-4
PRIOR FILING DATE: 2001-06-13
PRIOR APPLICATION NUMBER: US 60/335,936
PRIOR FILING DATE: 2001-11-14
NUMBER OF SEQ ID NOS: 238
SOFTWARE: PSECSEQ for Windows Version 4.0
SEQ ID NO 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            141 PLVQECMVHDCADGKKPSSPPEE 163
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                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.
Matches 143; Conservative
                                                                                                                                                                    TYPE: PRT
ORGANISM: Homo sapiens
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APPLICAMT: IDELL.
TITLE OF INVENTION: INTRAPLEURAL SINGLE-CHAIN UROKINASE ALONE OR COMPLEXED
TITLE OF INVENTION: TO ITS SOLUBLE RECEPTOR PROTECTS AGAINST PLEURAL
TITLE OF INVENTION: TO ITS SOLUBLE RECEPTOR PROTECTS AGAINST PLEURAL
TITLE OF INVENTION: ADHESIONS IN TETRACYCLINE-INDUCED PLEURITIS IN RABBITS
FILE REFERENCE: UTSN: 0.2105
CURRENT APPLICATION NUMBER: US/10/407, 821
CURRENT FILING DATE: 2003-04-04
PRIOR FILING DATE: 2002-09-27
PRIOR FILING DATE: 2002-09-27
PRIOR FILING DATE: 2002-09-05
NUMBER OF SEQ ID NOS: 3
SOFTWARE: PATENTIN Ver: 2.1
SEQ ID NO S: 5
SEQ ID NOS: 4
SEQ ID NOS: 4
SEQ ID NOS: 5
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APPLICANT: Shiffman, Dov
APPLICANT: Porter, Gordon, J.
APPLICANT: Raser, Matthew R.
APPLICANT: Kaser, Matthew R.
TITLE OF INVENTION: GENES EXPRESSED IN TREATED FOAM CELLS
FILE REFERENCE: PA-0050 US
CURRENT APPLICATION NUMBER: US/10/247,671
CURRENT FILING DATE: 2002-09-18
PRIOR PILING DATE: 2001-09-19
NUMBER OF SEQ ID NOS: 186
SOTWARE: PERL PROGram
SEQ ID NO 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ) NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20030194721A1 1453334CD1
US-10-247-671-149
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LENGTH: 138 amino acids
TYPE: amino acid
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COMPUTER READABLE FORM:
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INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
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Sequence 4, Application US/09880503
Barent No. US20020131964A1
GENERAL INFORMATION:
APPLICANT: CINES, Douglas B
APPLICANT: HIGAZI, Abd Al-Roof
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING MUSCLE CELL AND
TITLE OF INVENTION: TISSUE CONTRACTABILITY
FILE REFERENCE: 9596-331
CURRENT FILING DATE: 2001-06-13
PRIOR APPLICATION NUMBER: US/09/880,503
CURRENT FILING DATE: 2000-06-20
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: NOVEL BIOLOGICALLY ACTIVE POLYPEPTIDES,
PREPARATION THEREOF AND PHARMACEUTICAL COMPOSITION
CONTAINING SAID POLYPEPTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVGLK 120
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                                                                           KASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVGLK 120
                                                                                                   SNELHQVPSNCDCLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDXSKTCYEGNGHFYRG 60
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   SNELHQVPSNCDCLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFYRG 60
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100.0%; Pred. No. 4.1e-72;
tive 0; Mismatches 0;
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Rhone-Poulenc Rorer Inc.
STREET: 500 Arcola Road, 3C43
CITY: Collegeville
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Guitton, Jean-Dominique
Jung, Gerard
Yeh, Patrice
                                                                                                                                                   121 PLVQECMVHDCADGKKPSSPPEE 143
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Patent No. US20020151011A1
GENERAL INFORMATION:
APPLICANT: Fleer, Reinhard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 PLVQECMVHDCADGK 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 135; Conservative
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ORGANISM: Homo sapiens
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COUNTRY: U
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US-09-984-186-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO 4
LENGTH: 135
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PREPARATION THEREOF AND PHARMACEUTICAL COMPOSITION CONTAINING SAID POLYPEPTIDES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64 KASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVGLK 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 SNELHQVPSNCDCLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFYRG
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Guitton, Jean-Dominique
Jung, Gerard
Yeh, Patrice
TILE OF INVENTION: NOVEL BIOLOGICALLY ACTIVE POLYPEPTIDES,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 138;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRILING AFFLICATION NUMBER: US/08/797,689
FILING DATE: 31-JAN-1997
APPLICATION NUMBER: US 08/256,927
FILING DATE: 28-UUL-1994
APPLICATION NUMBER: FR 92/01064
FILING DATE: 31-JAN-1992
APPLICATION NUMBER: PCT/FR93/00085
FILING DATE: 28-JAN-1993
ATTOREY/AGENT INFORMATION:
REGISTRATION NUMBER: P-38,619
                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: ST92006-US TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: Rhone-Poulenc Rorer Inc. STREET: 500 Arcola Road, 3C43 CITY: Collegeville COUNTE: PA
                                                                         CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/984,186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear MOLECULE TYPE: protein ; SEQUENCE DESCRIPTION: SEQ ID NO: 12: US-09-984-186-12
COMPUTER: Macintosh
OPERATING SYSTEM: System 7.1
SOFTWARE: Word 5.1 (PatentIn)
                                                                                                                      FILING DATE: 29-Oct-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (610) 454-3839
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Publication No. US20030022308A1
GENERAL INFORMATION:
APPLICANT: Fleer, Reinhard
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KASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVGLK 120
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Guitton, Jean-Dominique
Jung, Gerard
Yeh, Patrice
TITLE OF INVENTION: NOVEL BIOLOGICALLY ACTIVE POLYPEPTIDES,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 138;
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100.0%; Pred. No. 4.2e-72;
iive 0; Mismatches 0;
                OPERATING SYSTEM: System 7.1
SOFTWARE: Word 5.1 (Patentin)
CURRENT APPLICATION DATA:
CLASSIFICATION NUMBER: US/10/237,708
FILING DATE: 10-Sep-2002
CLASSIFICATION: «UNKNOWN»
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/797,689
FILING DATE: 31-JAN-1997
APPLICATION NUMBER: US 08/256,927
FILING DATE: 28-JUL-1994
APPLICATION NUMBER: FR 92/01064
FILING DATE: 31-JAN-1993
FILING DATE: 28-JAN-1993
                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Smith Ph.D., Julie K.
REGISTRATION NUMBER: P.38,619
REFERENCE/DOCKET NUMBER: ST92006-US
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STREET: 500 Arcola Road, 3C43
CITY: Collegeville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (610) 454-3839
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Publication No. US20030036171A1
GENERAL INFORMATION:
APPLICANT: Fleer, Reinhard
                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 138 amino acids
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MEDIUM TYPE: Floppy
  COMPUTER: Macintosh
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           amino acid
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Best Local Similarity 100.
Matches 135; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 138;
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100.0%; Pred. No. 4.2e-72;
ive 0; Mismatches 0;
                                                                                                                                                                                                                       FILING DATE: 31-JAN-1997
APPLICATION NUMBER: US 08/256,927
FILING DATE: 28-JUL-1994
APPLICATION NUMBER: FR 92/01064
FILING DATE: 31-JAN-1992
FILING DATE: 28-JAN-1993
                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INPORMATION:
NAME: Smith Ph.D., Julie K.
REGISTRATION NUMBER: P-38,619
REFERENCE/DOCKET NUMBER: ST92006-US
TELECOMMUNICATION INFORMATION:
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STREET: 500 Arcola Road, 3C43
CITY: Collegeville
                     COMPUTER: Macintosh
OPERAITING SYSTEM: System 7.1
SOFTWARE: Word 5.1 (Patentin)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/237,667
FILING DATE: 10-Sep-2002
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/797,689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 12:

US-10-237-667-12
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Guitton, Jean-Dominique
Jung, Gerard
Yeh, Patrice
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Publication No. US2030036170A1
GENEAL INFORMATION:
APPLICANT: Fleer, Reinhard
MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 138 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   454-3808
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INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
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COMPUTER READABLE FORM:
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Best Local Similarity 100.
Matches 135; Conservative
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Pournier, Alain
Guitton, Jean-Dominique
Jung, Gerard
Yeh, Patrice
Yeh, Patrice
TITLE OF INVENTION: NOVEL BIOLOGICALLY ACTIVE POLYPEPTIDES,
CONTAINING SAID POLYPEPTIDES
CONTAINING SAID POLYPEPTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 KASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVGLK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 SNELHQVPSNCDCLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFYRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 SNELHQVPSNCDCLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFYRG
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                                                                   FILING DATE: 10-Sep-2002
CLASSIFICATION: «Unknown»
PRIOR APPLICATION LOUR CONFIDENCE CLASSIFICATION NUMBER: US/08/797,689
FILING DATE: 31-JAN-1997
APPLICATION NUMBER: US 08/256,927
FILING DATE: 31-JAN-1994
APPLICATION NUMBER: ER 92/01064
FILING DATE: 31-JAN-1992
APPLICATION NUMBER: PCT/FR93/00085
FILING DATE: 32-JAN-1993
ATTORNEY AGENT INFORMATION:
NAME: Smith Ph.D., Julie K.
REGISTRATION NUMBER: P.38,619
REGISTRATION NUMBER: P.38,619
TELECOMMUNICATION INFORMATION:
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ADDRESSEE: Rhone-Poulenc Rorer Inc.
STREET: 500 Arcola Road, 3C43
CITY: Collegeville
STATE: PA
  SOFTWARE: Word 5.1 (Patentin)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/237,871
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-10-237-871-12
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OPERATING SYSTEM: System 7.1
SOFTWARE: Word 5.1 (PatentIn)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (610) 454-3839
TELEFAX: (610) 454-3808
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
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/ Publication No. US2030082747A1
// GENERAL INFORMATION:
APPLICANT: Fleer, Reinhard
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 138 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 PLVQECMVHDCADGK 135
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Guitton, Jean-Dominique
Jung, Gerard
Yeh, Patrice
Yeh, Patrice
TITLE OF INVENTION: PREPARATION THEREOF AND PHARMACEUTICAL COMPOSITION
CONTAINING SAID POLYPEPTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  64 KASTDIMGRPCLPWNSATVLQQIYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVGLK 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 KASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNRRPWCYVQVGLK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 SNELHQVPSNCDCLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFYRG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 SNELHQVPSNCDCLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFYRG 63
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                                                                                                                                               PRIOR CHASSITECATION DATA:

APPLICATION NUMBER: US/08/797,689
FILING DATE: 31-JAN-1997
APPLICATION NUMBER: US 08/256,927
FILING DATE: 28-UU-1994
APPLICATION NUMBER: FF 92/01064
FILING DATE: 31-JAN-1992
APPLICATION NUMBER: PCT/FR93/00085
FILING DATE: 28-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: SMICH Ph. D., UNLIE K.
REGISTRATION NUMBER: P-38,619
REFERENCE/DOCKET NUMBER: ST92006-US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rhone-Poulenc Rorer Inc.
STREET: 500 Arcola Road, 3C43
CITY: Collegeville
STATE: PA
COUNTRY: USA
OPERATING SYSTEM: System 7.1
SOFTWARE: Word 5.1 (PatentIn)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/237,866
FILING DATE: 10.5ep-2002
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: Macintosh
OPERATING SYSTEM: System 7.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
TELEPHONE: (610) 454-3839
TELEFAX: (610) 454-3808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 12, Application US/10237871
Publication No. US20030036172A1
GENERAL INFORMATION:
APPLICANT: Fleer, Reinhard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM: / MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 138 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
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Sequence 9, Application US/09880503

Patent No. US20020131964A1

GENERAL INFORMATION:
APPLICANT: CINES, Douglas B

APPLICANT: HIGAZI, Abd Al-Roof

TILLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING MUSCLE CELL AND

TILLE REFERENCE; 9596-331

CURRENT FILING DATE: 2001-06-13

PRIOR PELICATION NUMBER: US/09/880,503

CURRENT FILING DATE: 2000-06-20

NUMBER OF SEQ ID NOS: 18

SEQ ID NO 9

LENGTH: 96
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; Patent No. US20020133964A1
; GENERAL INFORMATION:
    GENERAL INFORMATION:
    APPLICANT: GINES, Douglas B
; APPLICANT: HIGAZI, Abd Al-Roof
    TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING MUSCLE CELL AND
    TITLE OF INVENTION: TISSUE CONTRACTABILITY
    TILE PERERENCE: 9596-331
    CURRENT APPLICATION NUMBER: US/09/880,503
    CURRENT APPLICATION NUMBER: US 60/212,847
    PRIOR APPLICATION NUMBER: US 60/212,847
    PRIOR FILING DATE: 2000-06-20
    NUMBER OF SEQ ID NOS: 18
    SOFTWARE: Patentin Ver. 2.1
    SEQ ID NO 1
    LENGTH: 88
                                                                                  KASTDIMGRPCLPWNSAIVLQQIYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVGLK 120
                                                                                                                 61 KASTDIMGRPCLPWNSATVLQQIYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVGLK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               48 KTCYEGNGHPYRGKASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDN 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 KTCYEGNGHFYRGKASIDIMGRPCLPWNSAIVLQQIYHAHRSDALQLGLGKHNYCRNPDN 60
                               1 SNELHQVPSNCDCLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFYRG 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 88;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 RRRPWCYVQVGLKPLVQECMVHDCADGKKPSSPPEE 96
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ORGANISM: Homo sapiens
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Betent No. US20020131964A1
GENERAL INFORMATION:
APPLICANT: CINES, Douglas B
APPLICANT: HIGAZI, Abd Al-Roof
TITLE OF INVENTION: TOMPOSITIONS AND METHODS FOR MODULATING MUSCLE CELL AND
TITLE OF INVENTION: TISSUE CONTRACTABILITY
FILE REPERENCE: 9596-331
CURRENT APPLICATION NUMBER: US/09/880,503
CURRENT FILING DATE: 2001-06-13
PRIOR APPLICATION NUMBER: US 60/212,847
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 SNELHQVPSNCDCLNGGTCVSNKYFSNIHWCNCPKKFGQQHCEIDKSKTCYEGNGHFYRG 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 KASTDTWGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVGLK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               64 KASTDIMGRPCLPWNSATVLQQIYHAHRSDALQLGLGGGHNYCRNPDNRRRPWCYVQVGLK 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           O Similarity 100.0%; Pred. No. 4.2e-72; 35; Conservative 0; Mismatches 0;
                                                                                          PRIOR PERIORITION DATA:

APPLICATION DATA:

APPLICATION NUMBER: US/08/797,689

FILING DATE: 31-JAN-1997

APPLICATION NUMBER: US 08/256,927

PILING DATE: 28-JUL-1994

APPLICATION NUMBER: FR 92/01064

FILING DATE: 31-JAN-1992

APPLICATION NUMBER: PCT/FR93/00085

FILING DATE: 28-JAN-1993

ATTORNEY/AGINT INPORMATION:

NAME: Smith Ph.D., Julie K.

REGISTRATION NUMBER: P-38,619

REFERENCE/DOCKET NUMBER: ST92006-US

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELEPHONE: (610) 454-3898
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/237,624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
TOPOLOGY: linear
;
MOLECULE TYPE: protein
;
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-10-237-624-12
                                                   FILING DATE: 10-Sep-2002
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 138 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 12: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 PLVQECMVHDCADGK 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      124 PLVQECMVHDCADGK 138
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Best Local Similarity 100.0
Matches 135; Conservative
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ID NO 6
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59 RGKASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVG 118
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                                                                                                                                                                                                                                                                                                                    3 ELHQVP-SNCD---CLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFY 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        136 RGTWSTAESGAECTNWNSSALAQKPYSGRRPDAIRLGLGNHNYCRNPDRDSKPWCYVFKA 195
                                                                                                                                                                                                                                                                                                                                                                                42 OCHSVPVKSCSEPRCFNGGTCOQALYFSDF-VCQCPEGFAGKCCEIDTRATCYEDQGISY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 ELHQVP-SNCD---CLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFY
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                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 7, Application US/09969271

Batent No. US20020098179A1

GENERAL INFORMATION:
APPLICANT: Pfizer Limited (GB and EP (GB) only)

TITLE OF INVENTION: Pharmaceutical Combinations

TILE REPERENCE: PCS10951APME
CURRENT APPLICATION NUMBER: US/09/969,271

PRIOR APPLICATION NUMBER: US/09/969,271

PRIOR APPLICATION NUMBER: GB 0025473.0

PRIOR FILING DATE: 2001-10-01

NUMBER OF SEQ ID NOS: 7

SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                        ; Score 328.5; DB 11; Length
; Pred. No. 8.7e-25;
14; Mismatches 54; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          54; Indels
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Patent No. US20020156263A1
GENERAL INFORMATION:
APPLICANT: Chen, Huei-Mei
TITLE OF INVENTION: GENES EXPRESSED IN BREAST CANCER
FILE.REFERENCE: PA-0037 P
CURRENT APPLICATION NUMBER: US/09/974,298
CURRENT FILING DATE: 2001-10-04
PRIOR PELICATION NUMBER: 60/238,331
PRIOR FILING DATE: 2000-05-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
39.2%; Score 328.5; DB 9
Best Local Similarity 46.3%; Pred. No. 9.3e-25;
Matches 63; Conservative 14; Mismatches 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         119 LKPLVQECMVHDCADG 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     161 GKYSSEFCSTPACSEG 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           119 LKPLVQECMVHDCADG 134
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                                                                                                                                                                                        Query Match
Best Local Similarity 46.3%;
Matches 63; Conservative 1.
                                                        TYPE: PRT
ORGANISM: Homo sapiens
US-09-987-455-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Homo sapiens
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US-09-974-298-145
SEQ ID NO 19
LENGTH: 527
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US-09-969-271-7
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APPLICANT: Manosroi, Jiradej
APPLICANT: Manosroi, Jiradej
APPLICANT: Manosroi, Jiradej
APPLICANT: Tayapiwatana, Chatchai
APPLICANT: Goetz, Friedrich
APPLICANT: Werner, Rolf-Guenther
TITLE OF INVENTION: Methods for Large Scale Protein Production in Prokaryotes
FILE OF INVENTION: WIMBER: US/09/987,457
CURRENT APPLICATION NUMBER: US/09/987,457
CURRENT FILING DATE: 2001-11-14
PRIOR FILING DATE: 2001-11-14
PRIOR FILING DATE: 2001-11-14
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PATENTION OF 1: 14
NUMBER OF SEQ ID NOS: 18
ESEQ ID NOS: 18
ESEQ ID NOS: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               42 QCHSVPVKSCSEPRCFNGGTCQQALYFSDF-VCQCPEGFAGKCCEIDTRATCYEDQGISY 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              59 RGKASTDIMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVG 118
                                    1 KTCYEGNGHFYRGKASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKGHNYCRNPDN 60
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APPLICANT: Jiradej Manosroi
APPLICANT: Jiradej Manosroi
APPLICANT: Jiradej Manosroi
APPLICANT: Chatchal Tayapiwatana
APPLICANT: Chatchal Tayapiwatana
APPLICANT: Chatchal Tayapiwatana
APPLICANT: Chatchal Tayapiwatana
APPLICANT: Chatchal Tayapiwatana
APPLICANT: CAST.
APPLICANT: Rolf-Guenther Werner
TITLE OF INVENTION: DNA-Derived tpA or K2S Molecules
TITLE OF INVENTION: DNA-Derived tpA or K2S Molecules
TITLE OF INVENTION: DNA-Derived tpA or K2S Molecules
CURRENT APPLICATION NUMBER: 60/20/997,455
CURRENT FILING DATE: 2001-11-14
PRIOR FILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-02-16
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PRIOR FILING DATE: 2001-02-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 39.2%; Score 328.5; DB 1 Best Local Similarity 46.3%; Pred. No. 8.7e-25; Matches 63; Conservative 14; Mismatches 54
                                                                                                                        108 RRRPWCYVQVGLKPLVQECMVHDCADGK 135
                                                                                                                                                                                 61 RRRPWCYVQVGLKPLVQECMVHDCADGK 88
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                                                                                                                                                                                                                                                                                                                                           Sequence 18, Application US/09987457
Publication No. US20030013150A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              119 LKPLVQECMVHDCADG 134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; ORGANISM: Homo sapiens (tPA)
US-09-987-457-18
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ZIP: 20036
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US-10-349-543-5
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Publication No. US20030199016A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
FILE REPERENCE: P1788R1
CURRENT APPLICATION NUMBER: US/09/703,695
PRIOR APPLICATION NUMBER: US/09/703,695
PRIOR APPLICATION NUMBER: US 60/163,607
PRIOR FILING DATE: 2000-11-01
PRIOR FILING DATE: 2000-11-01
PRIOR FILING DATE: 1999-11-04
NUMBER OF SEQ ID NOS: 4
                                                                                                                                                                                                                                                                                         3 ELHQVP-SNCD---CLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFY
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دي
                                                                                                                                                                                                          39.2%; Score 328.5; DB 10; Length 562; 46.3%; Pred. No. 9.3e-25; Live 14; Mismatches 54; Indels 5;
                                                                                                                 ; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20020156263A1 1001470CD1
US-09-974-298-145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              54; Indels
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39.2%; Score 328.5; DB 1:
Best Local Similarity 46.3%; Pred. No. 9.3e-25;
Matches 63; Conservative 14; Mismatches 54
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                                                                                                                                                                                                                                                                                                                                                                                                                                                119 LKPLVQECMVHDCADG 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      196 GKYSSEFCSTPACSEG 211
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                                                                                                                                                                                                                                                    63; Conservative
NUMBER OF SEQ ID NOS: 194
SOFTWARE: PERL Program
                                                                          TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                               Query Match
Best Local Similarity
                                     SEQ ID NO 145
LENGTH: 562
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Matches
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59 RGKASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVG 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Varga, Janos
TITLE OF INVENTION: CYCLIC PEPTIDES THAT BIND TO
                                                                                                                                                                                                                                                                                                                                                                                                Length 562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
OF INVENTION: NOVEL DRUG TARGETS FOR ARTHRITIS
                                                                                                                                                                                                                                                                                                                                                                                                    DB 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: RADER, FISHMAN & GRAUER
STREET: 1233 20TH STREET NW, SUITE 501
CITY: WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                 .3e-25;
                                                                                                                                                                                                                                                                                        DATABASE ACCESSION NUMBER: GenBank / P00750; DATABASE ENTRY DATE: 1986-07-21; RELEVANT RESIDUES: (1)..(562)
                                                                                                                                                                                                                                                                                                                                                                                                                                     14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/285,783
FILING DATE: 05-Apr-1999
ATTORNEY/AGENT INFORMATION:
           39.2%; Score 328.5; 46.3%; Pred. No. 9.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/10/349,543
FILING DATE: 22-Jan-2003
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: LIVNAT, SHMUEL
REGISTRATION NUMBER: 33,949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 5, Application US/10349543
Publication No. US20030166514A1
GENERAL INFORMATION:
APPLICANT: Jones, Terence R.
Haney, David N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    119 LKPLVQECMVHDCADG 134
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                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 46.3%
nes 63; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
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NS-09-880-503-7

Sequence 7, Application US/0980503

Sequence 7, Application US/0980503

Sequence 7, Application US/0980503

Sequence 7, Application US/0980503

PAPELICANT: CINES, Douglas B

APPLICANT: CINES, Douglas B

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING MUSCLE CELL AND

TITLE OF INVENTION: TISSUE CONTRACTABILITY

TITLE OF INVENTION: TISSUE CONTRACTABILITY

TITLE OF INVENTION: TISSUE CONTRACTABILITY

CURRENT APPLICATION NUMBER: US/09/880,503

CURRENT FILING DATE: 2001-06-13

FRIOR FILING DATE: 2000-06-20

NUMBER OF SEQ ID NOS: 18

SEQ ID NO 7

LENGTH: 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2. Application US/09880503

### Sequence 2. Application US/09880503

### Sequence 2. Application US/09880503

### Sequence 2. Application US/09880503

### Sequence 2. Application US/09880503

### SPELICANT: CINES, Douglas B

### APPLICANT: HIGAZI, Abd Al-Roof

### TITLE OF INVENTION: TISSUE CONTRACTABILITY

### TITLE OF INVENTION: TISSUE CONTRACTABILITY

### TITLE OF INVENTION: TISSUE CONTRACTABILITY

### CURRENT APPLICATION NUMBER: US/09/880,503

### CURRENT APPLICATION NUMBER: US 60/212,847

### PRIOR FILING DATE: 2000-06-20

### NUMBER OF SEQ ID NOS: 18

### SCOFTWARE: PATENT US: 2.1

### SEQ ID NO 2
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34.4%; Score 288; DB 10; Length 323;
Best Local Similarity 100.0%; Pred. No. 6e-21;
Matches 48; Conservative 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 SNELHQVPSNCDCLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSK 48
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 49;
REFERENCE/DOCKET NUMBER: ANG-001/DIV (80144-0007)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 955-8787
TELEFAX: (202) 955-3751
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 SNELHQVPSNCDCLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                              FEATURE:
NAME/KEY: Disulfide-bond
LOCATION: group(11..19, 13..31, 33..42)
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-349-543-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match 35.0%; Score 293; DB 12; Best Local Similarity 100.0%; Pred. No. 2.4e-22; Matches 49; Conservative 0; Mismatches 0;
                                                                                                                                                                                  LENGTH: 49 amino acids
                                                                                                                                                                                                        TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-503-7
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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.	sin - protein search, using sw model December 3, 2003, 14:34:58 , Search time 7.39655 Seconds (without alignments) 1859.261 Million cell updates/sec	US-09-880-503-8 score: 837 1 SNELHQVPSNCDCLNGGTCVQECMVHDCADGKKPSSPPEE 143	table: BLOSUM62 Gapop 10.0 , Gapext 0.5	j: 283308 segs, 96168682 residues	umber of hits satisfying chosen parameters: 283308	DB seq length: 0 DB seq length: 2000000000	ocessing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries	B: PIR 76:* 1: Dix1:* 2: Dix2:* 3: Dix3:* 4: Dix4:*	No. is greater derive	ich Length DB ID	837 100.0 431 1 UKHU u-plasmino	74.7 442 1 UKPG u-plasminogen ac	05 72,3 433 1 JN0560 u-plasminogen ac 92 70 7 432 1 S18932	569 68.0 433 1 UMS u-plasminogen ac	35.5 40.1 477 1 A34369 t-plasminogen ac 35.5 40.1 477 2 JS0598	.5 40.0 434 1 A35005 u-plasminogen ac	28.5 39.2 291 2 138098 t-plasminogen ac	28.5 39.2 562 1 UKHUT t-plasminogen ac	325 38.8 559 1 A35029 t-plasminogen ac 15.5 37.7 559 1 A29941	.5 37.1 477 2 USO597 t-plasminogen ac	268 32.0 603 2 S28941 coagulation fact	.5 31.5 560 1 JC4795 plasma hyaluronan	62 31.3 655 1 A46666 33 27.8 615 1 KFHU12 coagulation fact	23 26.6 394 2 JSD600 t-plasminogen	1/ 23:3 2 343281 69 20.2 685 1 A48289 neurotrophic rec	63 19.5 460 2 B61545 plasmin (EC 3.4. .5 19.4 4548 1 S00657	161 19.2 1420 2 A32869 apolipoprotein(a) 160 191 123 2 C61545	159.5 19.1 810 2 830848 plasmin (5C 3.4.21 159 19 1 7 861545 plasmin (5C 3.4.21
	л - п	cor	able	arched:	0	8 sed 8 sed	SS 1.	Database :	Pred. No. score gre and is de	Scor	83	625.	9 1	י י י	335	334.	328.	328	3 32 4 315.	310.	26	263.	23	1 22	3 16	4 162.	16	. 62 . 7

plasmin (EC 3.4.21	plasmin (EC 3.4.21	plasmin (EC 3.4.21	plasmin (EC 3.4.21	plasmin (EC 3.4.21	plasmin (EC 3.4.21	plasmin (EC 3.4.21	macrophage-stimula	plasmin (EC 3.4.21	neurotrophic recep	macrophage-stimula	apolipoprotein(a)	hypothetical prote	macrophage-stimula	hepatocyte growth
PLBO	PLHU	PLPG	PLMS	A60140	146260	A40522	A47136	A61545	B45082	A40332	T18518	T18840	JC5061	JH0579
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812	810	790	812	89	810	169	711	455	943	716	2869	806	716	728
19.0	18.7	18.5	18.5	18.4	18.3	18.2	17.9	17.8	17.7	17.6	17.6	17.5	17.4	17.3
159	156.5	155	155	154	153.5	152.5	150	149	148	147.5	147	146.5	145.5	144.5
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ALIGNMENTS

	RESULT 1 ITMHI
	u-plasminogen activator (EC 3.4.21.73) precursor [validated] - human N;Alternate names: cellular plasminogen activator; urokinase; urokinase-type plasminog. N;Contains: urokinase-type plasminogen activator chain A; urokinase-type plasminogen a:
	C;Species: Homo sapiens (man) C;Species: 17-Dec-1982 #sequence_revision 04-Dec-1986 #text_change 15-Sep-2000 C;Date: 17-Dec-1982 #sequence_revision 04-Dec-1986 #text_change 15-Sep-2000 C;Accession: A00931; 152209; 4710102; A37561; 138102; 865783; A37562; A37564; A
	A.R.C.C.D. A.; Gindall, C.; VIII. (1985) G.; Debasio, G.; Boase, S.; Blasi, F.; A. Mucleic Acids Res. 13, 2759-2771, 1985 A;Tffle: The human urokinase-plasminogen activator gene and its promoter. A;Reference number: A00931; MUID:85215647; PMID:2987867
	A;Accession: A00931 A;Molecule type: DNA A;Residues: 1-431 <ric> A;Cross-references: GB:X02419; NID:g37601; PIDN:CAA26268.1; PID:g1834524 A;Cross-references: the authors translated the codon ATG for residue 214 as Ile</ric>
-	R;Nagamine, Y.; Pearson, D.; Grattan, M. Biochem. Biophys. Res. Commun. 132, 563-569, 1985 A+24ter: Exon-intron boundary-s-liding in the generation of two mRNAs coding for porcin A Reference number: 152209; MUID:86050639; PMID:3933505
	A;Accession: 152209 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA A;Begidnog: 145-151 - AMA;
	A; CETAGES TEFERENCES: 1910, 1871-1918, MID: 9340174; PIDN: AAA61257.1; PID: 9340175 R: Magai, M.; Hiramatsu, R.; Kaneda, T.; Hayasuke, N.; Arimura, H.; Nishida, M.; Suyama Gene 36, 183.1982.1982 1982
	A; Reference number: JT0102, MUID:86056954, PMID:2415429 A; Accession: JT0102 A; MOlecule type: mRNA
	A; KUSIQUES: 1-Z13, 1', Z15-431 «NACZ. A; Cross-references: GB: K03226; NID: G340155; PIDN: AAC97138.1; PID: G340158; GB: D00244; N R; Verde, P.; Stoppelli, M.P.; Galefi, P.; Di Nocera, P.; Blasi, F. Proc. Natl., Acad., Sci. U.S.A. 81, 4727-4731, 1984
	A;Title: Identification and primary sequence of an unspliced human urokinase poly(A) + A;Reference number: A37561, MUID:84272706, PMID:6589620 A;Accession: A37561 A;Accession: A37561 A;MOID:84778706 A;MOID:84787A
,	A;Residues: 66-431 <ver> A;Cross-references: GB:D00244; NID:g220138 R;Gacobs, P.; Cravador, A.; Loriau, R.; Brockly, F.; Colau, B.; Chuchana, P.; van Else</ver>
	DNA 1, 137-146, 1989 A/Title: Molecular cloning, sequencing, and expression in Escherichia coli of human pr A/Aiterance number: 138102; MUID:85203359; PMID:3888571 A/Accession: 138102 A/Status: preliminary
	A.Wolecule type: mRNA A.Residues: 1-150,'W',152-213,'I',215-385,'C',387-429,'V',431 <jac> A,Cross-references: EMBL:X02760; NID:g35297; PIDN:CAA26535.1; PID:g35298</jac>

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A/Residues: 21-10, X'.32, X', 34-38, X',40-43 <KEN>
A/Rebani, S.A.; Desjardins, J.; Bell, A, W'; Banville, D.; Mazar, A.; Henkin, J.; Goltzm Biochem. Biophys Res Commun. 173, 1058-1064, 1990
A/Reference number: A36697; MuID: 91097529; PMID: 2125213
A/Residues: 21-34 <RAB>
A/Residues: 21-34 <RAB>
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A/Reference number: A51255; PDB: 11DD
A/Reference number: A61255; PDB: 11DD
A/Reference number: A44375; MuID: 93003110; PMID: 1327118
A/Reference number: A44375; MuID: 93003110; PMID: 1327118
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A/Reference number: A6822; PDB: 11RK
A/Reference number: A66822; PDB: 11RK
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A/Reference 
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A;Title: Characterization of single chain urokinase-type plasminogen activator with a nd A;Reference number: S65783; MUID:96186279; PMID:8652631
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A; Mesidues: 158-410 <57E.

B; Residues: 158-410 <57E.

B; Residues: 158-410 <57E.

Biochem. Biophys. Res. Commun. 171, 401-406, 1990

A; Title: Carbohydrate composition and presence of a fucose-protein linkage in recombinan

A; Reference number: A35689; MUID: 90365737; PMID: 2393398
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A, Pathway: fibrinolysis
C, Superfamily: urokinase-type plasminogen activator; EGF homology; kringle homology; try
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A;Molecule type: protein
A;Molecule type: protein
A;Molecule type: protein
A;Molecule type: protein
B;Steffens, G.J.; Gunzler, W.A.; Otting, F.; Frankus, E.; Flohe, L.
R;Steffens, G.J.; Gunzler, W.A.; Otting, F.; Frankus, E.; Flohe, L.
A;Title: Z. Physiol. Chem. 383, 1043-1058, 1982
A;Title: The complete amino acid sequence of low molecular mass urokinase from human
A;Reference number: A37564; MUID:83055099; PMID:6754572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Accession: A37562
A;Molecule type: protein
A;Residues: 21-177 cGIN>
B;Schaller, J.; Nick, H.; Rickli, E.E.; Gillessen, D.; Lergier, W.; Studer, R.O.
Bicchem. 125, 251-257, 1982
A;Title: Human low-molecular-weight urinary urokinase. Partial characterization and A;Reference number: A37563; MUID:83003608; PMID:6749491
                                                                                                                                                                              A; Accession: S65783
A; Status: preliminary
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 21-140, L', 142-213, 'I', 215-431 < YOS>
A; Cross-references: EMBL:D11143; NID:g1311467; PIDN:BAA01919.1; PID:g1199928
A; Cross-references: EMBL:D11143; NID:g1311467; PIDN:BAA01919.1; PID:g1199928
B; Gunzler, W.A.; Steffens, G.J.; Otting, F.; Kim, S.M.A.; Frankus, E.; Flohe, L.
Hoppe-Seyler's Z. Physiol. Chem, 363, 1155-1165, 1982
A; Title: The primary structure of high molecular mass urokinase from human urine.
A; Reference number: A37562; MUID:83055084; PMID:6754569
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A;Introns: 19/3; 29/1; 65/1; 123/2; 154/1; 227/2; 277/1; 324/1; 373/3
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u-plasminogen activator (BC 3.4.21.73) precursor - yellow baboon
C,Species: Papio cynocephalus, Papio hamadryas cynocephalus (yellow baboon)
C,Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 18-Jun-1999
C,Accession: S14687, S08651
R,Au, Y.P.T.; Wang, T.W.; Clowes, A.W.
Nucleic Acids Res. 18, 311, 1990
A,Title: Nucleotide and deduced amino acid sequences of baboon urokinase-type plasmino
A,Reference number: S14687, MUID:90287734; PMID:211376
A,Accession: S14687
A,Accession: S14687
A,Modecule type: mRNA
A,Residues: 1.433 AUV.
A,Residues: 1.433 AUV.
A,Coss-references: EMEL:X51935; NID:938130; PIDN:CAA36200.1; PID:938131
C,Superfamily: urokinase-type plasminogen activator; EGF homology; kringle homology; C,Keywords: glycoprotein, heterodimer; hydrolase; kringle; serine proteinase
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F;178-421/Domain: signal sequence #status predicted
F;223,274,378/Active site: Hs, Asp, Ser #status predicted
F;223,274,378/Active site: Hs, Asp, Ser #status predicted
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F; 31-62/Domain: kringle homology <KGR>
F; 31-62/Domain: kringle homology or KGR>
F; 31-79-431/Product: urokinase-type plasminogen activator chain B #status experimental <F; 31-39, 33-51, 53-62, 70-151, 91-133, 122-146, 168-299, 209-225, 217-288, 313-382, 345-361, 372-F; 31-39, 33-51, 53-62, 70-151, 91-133, 122-146, 168-299, 209-225, 217-288, 313-382, 345-361, 372-F; 38/Binding site: carbohydrate (Thr.) (covalent) #status experimental F; 2224, 275, 376/Active site: His, Asp, Ser #status experimental
F; 322/Binding site: carbohydrate (Asn) (covalent) #status experimental
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 100.0%; Score 837; DB 1; Length 4 Best Local Similarity 100.0%; Pred. No. 9.3e-68; Matches 143; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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4; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tch 90.5%; Score 757.5; al Similarity 92.3%; Pred. No. 1.30 132; Conservative 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PLVQECMVHDCADGKKPSSPPEE 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 141 PLVQECMVHDCADGKKPSSPPEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 PLVQECMVHDCADGKKPSSPPEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QRVQECMVHNCADGKKPSSPPEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   140
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u-plasminogen activator (EC 3.4.21.73) precursor - rat
NATerantae names activator activator, urokinase-type; urinary plasminogen activator
C;Species: Rattus norvegicus (Norway rat)
C;Date: 18-Oct-1989 #sequence_revision 10-Feb-1995 #text_change 18-Jun-1999
R;Rabbani, S.4.
R;Rabbani, S.A.
submitted to the EMBL Data Library, April 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C,Superfamily: urokinase-type plasminogen activator; EGF homology; kringle homology; t; C,Superfamily: urokinase-type plasminogen activator; EGF homology; kringle; serine proteinase (F,1-19/Domain: signal sequence #status predicted <SIG> (F,1-13/Domain: signal sequence #status predicted <SIG> (F,1-17/Product: urokinase-type plasminogen activator chain A #status predicted <ACH> (F,31-62/Domain: EGF homology <EGF> (F,0-151/Domain: kringle homology <ERG> (F,109-432/Product: urokinase-type plasminogen activator chain B #status predicted <BCH: (F,179-420/Domain: trypsin homology <ERY> (F,168-300,210-226,218-289,314-383,346-362,373-401/Disulfide bonds: #status predicted (F,225,276,377/Active site: His, Asp, Ser #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rikagno, P.; Cassano, S.; Degen, J.; Kessler, C.; Blasi, F.; Rossi, G.
FEBS Lett. 306, 193-198, 1992
A.fitle: The receptor for the plasminogen activator of urokinase type is up-regulated
A.Reference number: IS3472; MUID:92339549; PMID:1321734
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Modecule type: mRNA
A; Residues: 1-15, H'. 17-23, 'G', 25-331,'N', 333-432 cRAB>
A; Residues: 1-15, H'. 17-23, 'G', 25-331,'N', 333-432 cRAB>
A; Cross-references: BMEL: X6551; NID: 957456; PIDN: CAA46601.1; PID: 957457
A; Experimental source: tissue kidney, N.P.; Phillips, S.M.; Ramshaw, I.A.; Kefford, R.F.
Cancer Res. 52, 2489-2496, 1992
A; Title: Transcriptional and posttranscriptional activation of urokinase plasminogen
A; Reference number: 160186; MUID: 92233409; PMID: 1568219
                        F;181-433/Product: plāsminogen āctivator chain B #status predicted <MA2>
F;181-421/Domain: trypsin homology <TRY3
F;170-301,211-227,219-290,315-384,347-363,374-402/Disulfide bonds: #status predicted
F;226,277,378/Active site: His, Asp, Ser #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           81 RGXANRDLSGRPCLAWDSPTVLLXMYHAHRSDAIQLGLGKHNYCRNPDNQRRPWCYVQIG 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RGKASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                      21 SNEVHKESGESNCGCLNGGKCVTYKYFSNIQRCSCPKKFQGEHCEIDTSKTCYQGNGHSY
                                                                                                                                                                                                                                                                                                                                                                          1 SNELHQV--PSNCDCLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFY
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A;Cross-references: EMBL:X66907; NID:g396200; PIDN:CAA47356.1; PID:g938279
                                                                                                                                                                                                                                                                                                 Gaps
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A,Residues: 1-432 <RES>
A,Cross-references: EMEL:X63434; NID:957465; PIDN:CAA45028.1; PID:957466
A,Experimental source: strain Fischer 344; tissue mammary
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0
                                                                                                                                                                                                                     DB 1; Length 433;
6.2e-47;
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                                                                                                                                                                                                                                                                                                 24; Indels
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; Pred. No. 9.1e-46;
10; Mismatches 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                             Best Local Similarity 72.4%; Pred. No. 6.2e
Matches 105; Conservative 14; Mismatches
                                                                                                                                                                                                                         Score 605;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                141 LKQFVQFCMVQDCSVGKSPSSPREK 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    119 LKPLVQECMVHDCADGKKPSSPPEE 143
F;72-153/Domain: kringle homology <KRG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 70.7%;
75.6%;
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Best Local Similarity 75.6:
Matches 102; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Reference number: S24604
A;Accession: S24604
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A/Residues: 1-433 «KRA)
A/Residues: 1-433 «KRA)
A/Residues: 1-433 «KRA)
A/Residues: 1-433 «KRA)
A/Residues: 1-430 «KRA)
A/Residues: 1-430 «KRA)
C/Superfemnly: urokinase-type plasminogen activator; EGF homology; kringle homology; tr
C/Reywords: glycoprotein; heterodimer; hydrolase; kringle; serine proteinase
E/1-10/Domain: signal sequence #status predicted cSGS>
E/21-179/Product: plasminogen activator chain A #status predicted «MAl>
E/21-179/Product: urokinase-type plasminogen activator chain A #status predicted cACH>
E/33-64/Domain: EGF homology «EGF>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ajintrons: 19/3; 31/1; 67/1; 125/2; 165/1; 238/2; 288/1; 335/1; 384/3
C; Superfamily: urokinase-type plasminogen activator; EGF homology; kringle homology; tr
C; Keywords: glycoproctein; heterodimer; hydrolase; kringle; serine proteinase
F;1-20/Domain: signal sequence #status predicted <SIGs
F;1-188/Product: urokinase-type plasminogen activator chain A #status predicted <ACH>F;33-64/Domain: EGF homology <EGF>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      F;72-153/Domain: kringle homology kRG>
F;190-442/Product: urokinase-type plasminogen activator chain B #status predicted
F;190-430/Domain: trypsin homology kTRY>
F;190-430/Domain: trypsin homology kTRY>
F;152/Binding site: carbohydrate (Govalent) #status predicted
F;179-310, 220-226, 228-299, 324-393, 386-372, 383-411/Disulfide bonds: #status predict
F;235, 286, 387/Active site: His, Asp, Ser #status predicted
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Gene 125, 177-183, 1993
                                                                                                                                                                                                                                                                                         C;Accession: A00932
R;Magamine, Y.; Pearson, D.; Altus, M.S.; Reich, E.
Nucleic Acids Res. 12, 9525-9541, 1984
A;Title: cDNA and gene nucleotide sequence of porcine plasminogen activator.
A;Reference number: A00932; MUID:85087954; PMID:6096832
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C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 16-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 SNELHQV -- PSNCDCLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SHELHQESGASNCGCLNGGKCVSYKYFSNIQRCSCPKKFQGEHCEIDTSQTCFEGNGHSY
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                                                                                                                                        -plasminogen activator (EC 3.4.21.73) precursor - pig
Alternate names: uPA
Species: Sus scrofa domestica (domestic pig)
Date: 04-Dec-1986 #sequence_revision 17-Mar-1987 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19; Indels
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submitted to the Protein Sequence Database, December 1986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                73.4%; Score 625.5; DB 1
73.4%; Pred. No. 9.1e-49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LKOLVOECMVPNCSGGESHRPAYDGKNPFSTPEK 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Reference number: A37566
A;Contents: annotation; correction to residue 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     u-plasminogen activator (EC 3.4.21.73) precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A,Molecule type: DNA
A,Residues: 1-240,'H',242-442 <NAG1>
A,Experimental source: kidney cell line LLC-PK1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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Best Local Similarity
Matches 113; Conserv
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A;Title: Isolation, characterization, and cDNA cloning of a vampire bat salivary plasmi
A;Reference number: A34369; MUID:90036867; PMID:2509450
                                                                                                                                                                                                                                                                                                                                                                                                                                F;128-209/Domain: kringle homology «KRG»
F;226-471/Domain: trypsin homology «TRX»
F;27-72,70-79,87-89,92.109,111-120,128-209,149-191,180-204,214-345,257-273,265-334,359-
F;272,321,428/Active site: His, Asp, Ser #status predicted
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F.128-209/Domain: Kringle homology <KRG>
F.128-219/Domain: Kringle homology <KRG>
F.228-2109/Domain: Kringle homology <FRYS>
F.228-2109/Domain: Lrypsin homology <FRYS>
F.42-72,70-79,87-98,92-109,111-120,128-209,149-191,180-204,214-345,257-273,265-334,359-8718S,398/Binding site: carbohydrate (Asn) (covalent) #status predicted
F.225-226/Cleavage site: His-Ser (plasmin) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KiKraetzschmar, J.; Haendler, B.; Langer, G.; Boidol, W.; Bringmann, P.; Alagon, A.; Gene 105, 229-237, 1991
A.Title: The plasminogen activator family from the salivary gland of the vampire bat A;Reference number: JS0597; MUD:92039036; PMID:1937019
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: mRNA
A; Residues: 1-477 «KRA»
A; Residues: 1-477 «KRA»
A; Costales: 1-477 «KRA»
A; Costales: 1-477 «KRA»
C; Superfamily: Lissue plasminogen activator; EGF homology; fibronectin type I repeat
C; Keywords: fibrinolysis; glycoprotein; hydrolase; kringle; serine proteinase
F; 1-2.10 Domain: aignal sequence #status predicted «SIG»
F; 22-36, Domain: propeptide #status predicted «PRO»
F; 37-477/Product: plasminogen activator alpha-2 #status predicted «PLA»
F; 42-9/Domain: fibronectin type I repeat homology «1FA»
                                                                                                                                                                                                                     repeat
                                                                                                                                                                       A,Cross-references: CB:J05082, NID:g166080, PIDN:AAA31596.1, PID:g166081
C;Superfamily: tissue plasminogen activator; EGF homology; fibronectin type I ocknoweds: fibrinolysis; glycoprotein; hydrolase; kringle, serine proteinase F;1-21/Domain: signal sequence #status predicted <SIG> F;22-36/Domain: propeptide #status predicted <PRO> F;3-37/Product: plasminogen activator #status predicted <PRO> F;4-79-Product: plasminogen activator #status predicted <PLA> F;4-79-Domain: fibronectin type I repeat homology <FF> F;87-120/Domain: EGF homology <EGF> ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RGKASTDIMGRPCLPWNSAIVLQOIYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVG 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N,Alternate names: tissue plasminogen activator
C;Species: Desmodus rotundus (common vampire bat)
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 16-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QCHTVPVKSCSELRCFNGGTCWQAASFSDF-VCQCPKGYTGKQCEVDTHATCYKDQGVTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ELHQVP----SNCDCLNGGTCVSNKYFSN1HWCNCPKKFGGQHCE1DKSKTCYEGNGHFY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             78 QCHTVPVKSCSELRCFNGGTCWQAASFSDF-VCQCPKGYTGKQCEVDTHATCYKDQGVTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 ELHQVP----SNCDCLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ..
S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    272,321,428/Active site: His, Asp, Ser #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        t-plasminogen activator (EC 3.4.21.68) alpha-2 precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            40.1%; Score 335.5; DB 2;
46.3%; Pred. No. 1e-22;
iive 17; Mismatches 50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 46.3%; Pred. No. 1e-22;
Matches 62; Conservative 17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   119 LKPLVQECMVHDCA 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SKFILEFCSVPVCS 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          62; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
Matches 62; Conserv
                                                                                                                         A;Molecule type: mRNA
A;Residues: 1-477 <GAR>
                                                                                               A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            t-plasminogen activator (BC 3.4.21.68) precursor - false vampire bat (Megaderma lyra) C;Species: Megaderma lyra C;Species: Megaderma lyra C;Species: Megaderma lyra C;Date: lo-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999 C;Accession: A34369 R;Gardell, S.J.; Duong, L.T.; Diehl, R.E.; York, J.D.; Hare, T.R.; Register, R.B.; Jacob
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Residues: 1-433 cDEG>
A; Cross-references: GB:M17922; NID:g202296; PIDN:AAA40539.1; PID:g202297
A; Cross-references: GB:M17922; NID:g202296; PIDN:AAA40539.1; PID:g202297
B; Belln, D.; Vassalli, J.D.; Combepine, C.; Godeau, F.; Nagamine, Y.; Reich, E.; Kocher, Eur. J. Blochem. 148, 225-232, 1985
A; Title: Cloning, nucleotide sequencing and expression of cDNAs encoding mouse urokinase A; Reference number: A24615; MUID:85179474; PMID:2985383
                                                                                                                                                             89 RPCLAWNSPAVLQQIYNAHRSDALSLGLGKHNYCRNPDNQRRPWCYVQIGLKQFVQECMV 148
                                                                                                                         RPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVGLKPLVQECMV 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     69 RPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVGLKPLVQECMV 128
                                                           88
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   69
                                                                                                                                                                                                                                                                                                                                                                                                                                                          u-plasminogen activator (EC 3.4.21.73) precursor - mouse
C;Species: Mus musculus (house mouse)
C;Dacession: 30-Sep-1987 #text_change 18-Jun-1999
C;Accession: A29420; A24615
R;Degen, S.J.F.; Heckel, J.L.; Reich, E.; Degen, J.L.
Biochemistry 26, 8270-8279, 1987
A;Title: The mutrine urokinase-type plasminogen activator gene.
A;Reference number: A29420; MUID:88163489; PMID:2831940
                                    SNCGCQNGGVCVSYXYFSSIRRCSCPKKFKGEHCEIDTSKTCYHGNGQSYRGKANTDTKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9 SNCDCLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFYRGKASTDTMG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30 SNCGCQNGGVCVSYKYFSRIRRCSCPRKFQGEHCEIDASKTCYHGNGDSYRGKANTDTKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         90 RPCLAWNAPAVLQKPYNAHRPDAISLGLGKHNYCRNPDNQKRPWCYVQIGLRQFVQECWV
   SNCDCLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFYRGKASTDTMG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;Molecule type: mRNA
;Residues: 1-433 <BEL>
;Cross-references: GB:X02389; NID:955127; PIDN:CAA26231.1; PID:955128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ..
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Pred. No. 1.1e-43;
5; Mismatches 25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         68.08;
                                                                                                                                                                                                                                               HDCADGKKPSSPPEE 143
                                                                                                                                                                                                                                                                                                       149 ODČSLSKKPŠŠTVDO 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HDCADGKKPSSPPEE 143
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Best Local Similarity
Matches 95; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Accession: A29420
Molecule type: DNA
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                                                                                                                         69
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F)180-425/Domain: trypsin homology <TRY>
F)180-425/Domain: trypsin homology <TRY>
F)41-52,46-63,65-74,82-163,103-145,134-158,168-299,211-227,219-288,313-388/Disulfide br
F)139,352/Shidhing site: carbohydrate (5,8n) (covalent) #status predicted
F)179-180/Cleavage site: His-Ser (plasmin) #status predicted
F)226,275,382/Active site: His, Asp, Ser #status predicted
F)345-361,378-406/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N,Alternate names: tissue plasminogen activator
C;Species: Desmodus rotundus (common vampire bat)
C;Dates: 11-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 16-Jul-1999
C;Accession: JSO599
R;Kraetzschmar, J:; Haendler, B:; Langer, G:; Boidol, W.; Bringmann, P.; Alagon, A.;
Gene 105, 229-237, 1391
A;Title: The plasminogen activator family from the salivary gland of the vampire bat
A;Reference number: JSO597; MUID:92039036; PMID:1937019
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A;Cross-references: GB:M63989; NID:g166076; PIDN:AAA31594.1; PID:g166077
A;Cross-references: GB:M63989; NID:g166076; PIDN:AAA31594.1; PID:g166077
C;Superfamily: Lissue plasminogen activator; EGF homology; fibronectin type I repeat C;Superfamily: Lissue plasminogen activator; EGF homology; fibronectin type I repeat C;Superfamily: Lissue plasminogen activator predicted «SIG»
F;22-36/Domain: signal sequence #status predicted «PRO»
F;37-431/Product: plasminogen activator beta #status predicted «PLA»
F;41-74/Domain: EGF homology «KRG»
F;82-163/Domain: Kringle homology «KRG»
C;Keywords: alternative splicing; fibrinolysis; glycoprotein; kringle
F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-32/Domain: propeptide #status predicted <PRO>
F;34-20/Pomain: propeptide #status predicted <PRO>
F;31-291/Product: t-plaaminogen activator, inactive endothelial splice form #status |
F;41-78/Domain: fibronectin type I repeat homology <IFA>
F;86-119/Domain: EGF homology <EGF>
F;215-208/Domain: Kringle homology %KRL>
F;215-294/Domain: kringle homology #status atypical <KR2>
F;215-294/Domain: kringle homology #status atypical <KR2>
F;41-71,69-78,86-97,91-108,110-119,127-208,148-190,179-203/Disulfide bonds: #status |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RGKASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVG 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  136 RGTWSTAESGAECTNWNSSALAQNAYSGRRPDAIRLGLGNHNYCRNPDRDSKPWCYVFKA 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              69 RPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVGLKPLVQECMV 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OCHSVPVKSCSEPRCFNGGTCQQALYFSDF-VCQCPEGFAGKCCEIDTRATCYEDQGISY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SNCDCLNGGTCVSNKYFSNIHWCNCPKKFGGOHCEIDKSKTCYEGNGHFYRGKASTDTMG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          t-plasminogen activator (EC 3.4.21.68) beta precursor - common vampire bat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                       ch 39.2%; Score 328.5; DB 2; Length 291; I Similarity 46.3%; Pred. No. 2.9e-22; 63; Conservative 13; Mismatches 55; Indels 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 431;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LKPLVQECMVHDCADG 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GKYSSEFCSTPACSEG 211
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Best Local Similarity
Matches 59; Conserv
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Matches 6
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C'Superfamily: urokinase-type plasminogen activator; EGF homology; kringle homology; try

C'Reywords : glycoprotein; heterodimer; hydrolase; kringle; serine proteinase

E) 21-11/Domain: signal sequence #status predicted <81G->
E) 22-17/Product: urokinase-type plasminogen activator chain A #status predicted <ACH->
E) 46-71/Domain: EGF homology <EGF->
E) 79-158/Domain: kringle homology <ERG->
E) 173-428/Product: urokinase-type plasminogen activator chain B #status predicted <BCH->
E) 173-426/Domain: trypsin homology <ERG->
E) 13-46/Domain: trypsin homology <ERG->
E) 13-46/Domain: trypsin homology <ERG->
E) 13-46/Domain: trypsin homology <ERG->
E) 13-46/Domain: trypsin homology <ERG->
E) 162-296, 202-218, 210-285, 210-379, 342-358, 369-397/Disulfide bonds: #status predicted
E) 217, 272, 373/Active site: His, Asp, Ser #status predicted
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C.Species: Homo sapiens (mān)
C.Spate: 17-May-1996 #sequence_revision 17-May-1996 #text_change 22-Jun-1999
C.Spacession: 138098; Soll678
R.Siebert, P.D.; Fong, K.
R.Siebert, P.D.; Fong, K.
R.Voleitc Acids Res 18, 1086, 1990
A.Title: Variant tissue type plasmingen activator (PLAT) cDNA obtained from human endot A.Reference.number: 138098; MUID:90192128; PMID:1969145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      prd
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A; Molecule type: mRNA
A; Residucs: 1-291 <SIE
A; Cross-references: EMBL:X13097; NID:g35282; PIDN:CAA31489.1; PID:g35283
C; Comment: For the main splice form, see PIR:UKHUT. This form probably does not have
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Introns: 24/3, 39/1, 85/1, 122/1, 180/2, 211/1, 268/2
C;Superfamily: tissue plasminogen activator; EGF homology; fibronectin type I repeat
                                         RGKASTDIMGRPCLPWNSAIVLQQIYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVG 118
                                                                                95
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   t-plasminogen activator precursor, inactive endothelial splice form - human N;Alternate names: tissue plasminogen activator
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Species: Gallus gallus (chicken)
:Date: 20-Jul-1990 #sequence_revision 20-Jul-1990 #text_change 16-Jul-1999
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Residues: 1-434 <LES>
Cross-references: GB:J05187; NID:g212858; PIDN:AAA49131.1; PID:g212859
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C,Accession: A35005
R;Lealie, N.D.; Kessler, C.A.; Bell, S.M.; Degen, J.L.
J. Biol. Chem. 265, 1339-1344, 1990
A;Tile: The chicken urokinase-type plasminogen activator gene.
A,Reference number: A35005; MUID:90110185; PMID:2295632
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54.2%; Pred. No. 1.2e-22;
vative 14; Mismatches 30;
                                                                                                                                                                                                                                                                                                                                                                                                                               plasminogen activator (EC 3.4.21.73) precursor Alternate names: uPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: GDB:119496; OMIM:173370
A;Map position: Sp12-8p12
A;Introns: 24/3; 39/1; 85/1; 122/1; 180/2;
                                                                                                                                                                               LKPLVQECMVHDCA 132
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Best Local Similarity
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A;Residues: 33-45;311-320 cPDH-
A;Residues: 33-45;311-320 cPDH-
A;Residues: 31-45;311-320 cPDH-
A;Experimental source: uterus
A;Residues: 31-45;311-320 cPDH-
A;Experimental source: uterus
A;Contee: in the uterus, cleavage of the activation peptide may also occur after 38-Gln
R;van Zonneveld, A.J.; Veerman, H.; Pannekoek, H.
J. Biol. Chem. 261, 14214-14218, 1986
A;Reference number: A3756;7; MUID: 97033611; PMID: 3021732
A;Contents: annotation; fibrin binding site
B;Verheijen, J.H.; Caspers, M.P.M.; Chang G.T.G.; de Munk, G.A.W.; Pouwels, P.H.; Engr
R;Verheijen, J.H.; Caspers, M.P.M.; Chang Site
A;Title: Involvement of finger domain and kringle 2 domain of tissue-type plasminogen A;Reference number: A37568; MUID: 87161-81; PMID: 3030730
A;Contents: annotation; fibrin binding site
A;Contents: annotation; identification and pharmacokinetic properties of human tissue-type
A;Contents: annotation; novel forms of expressed recombinant t-PA
R;Harris, T.J.R.; Patel, T.; Marston, F.A.O.; Little, S.; Emtage, J.S.; Opdenakker, G.
Mol. Biol. Med. 3, 279-292, 1986
A;Title: Cloning of cDNA coding for human tissue-type plasminogen activator and its ex;
A;Reference number: A54645; MUID: 86284200; PMID: 3090401
A;Reference number: A54645; MUID: 86284200; PMID: 3090401
                                                                                                               RiPohl, G.; Kaplan, L.; Einarsson, M.; Wallen, P.; Jornvall, H.
PEBS Lett. 168, 29-32, 1984
A;Tis Lett. Differences between uterine and melanoma forms of tissue plasminogen activato.
A;Reference number: A91322; MUID:84158956; PMID:6538514
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A;Cross-references: GB:M11890; NID:g339837; PIDN:AAA61213.1; PID:g339839
C;Comment: Cleavage by plasmin or trypsin produces two chains held together by a singl C;Comment: C-PA converts plasminogen to plasmin by hydrolyzing a single Arg-Val bond. C;Comment: t-PA binds chain A of fibrin by kringle 2 and the fibronectin type I repeat C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: GB:M18182; NID:g340176; PIDN:AAA36800.1; PID:g340177
R;Fisher, R.; Waller, E.K.; Grossi, G.; Thompson, D.; Tizard, R.; Schleuning, W.D.
D. Bioll Chem. 260, 11223-11230, 1988
A;Title: Isolation and characterization of the human tissue-type plasminogen activator A;Reference number: 155232; MUID:85289338; PMID:3161893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          F;311-562/Product: t-plasminogen activator chain B #status experimental <BCH>
F;311-556/Domain: trypsin homology <TRY>
F;41-71,69-78,86-97,91-108,110-119,127-208,148-190,179-203,215-296;236-278,267-291,299
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A.Introns: 24/3; 39/1; 85/1; 122/1; 180/2; 211/1; 268/2; 297/1; 362/2; 408/1; 455/3; 5
A.Introns: 24/3; 39/1; 85/1; 122/1; 180/2; 211/1; 268/2; 297/1; 362/2; 408/1; 455/3; 5
A.Introns: 24/3; 39/1; 85/1; 122/1; 180/2; 211/1; 268/2; 297/1; 362/2; 408/1; 455/3; 5
C.Superfamily: tissue plasminogen activatos; Edr homology; fibronectin type I repeat homology and sequence #status predicted and activatos; F12-23/Domain: signal sequence #status predicted and activatos; F33-562/product: t-plasminogen activatos chain A #status experimental and activatos; A.3-562/Product: t-plasminogen activatos chain A #status experimental and activatos; F86-119/Domain: Edr homology activatos; A. F86-119/Domain: Edr homology activatos; A. F86-119/Domain: Activatos; A. F86-119/Domain: Activatos; A. F87-208/Domain: Actingle homology activatos; A. F87-208/Domain: Actingle homology activatos; A. F87-208/Domain: Actingle homology activatos; A. F87-208/Domain: Actingle homology activatos; A. F87-208/Domain: Actingle homology activatos; A. F87-208/Domain: Actingle homology activatos; A. F87-208/Domain: Actingle homology activatos; A. F87-208/Domain: Actingle homology activatos; A. F87-208/Domain: Actingle homology activatos; A. F87-208/Domain: Actingle homology activatos; A. F87-208/Domain: Actingle homology activatos; A. F87-208/Domain: Actingle homology activatos; A. F87-208/Domain: Actingle homology activatos; A. F87-208/Domain: Actingle homology activatos; A. F87-208/Domain: Actingle homology activatos; A. F87-208/Domain: Actingle homology activatos; A. F87-208/Domain: Actingle homology activatos; A. F87-208/Domain: Actingle homology activatos; A. F87-208/Domain: Actingle homology activatos; A. F87-208/Domain: Actingle homology activatos; A. F87-208/Domain: Actingle homology activatos; A. F87-208/Domain: Actingle homology activatos; A. F87-208/Domain: Actingle homology activatos; Actingle homology activatos; Actingle homology activatos; Actingle homology activatos; Actingle homology actingle homology actingle homolo
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A; Residues: 1-562 < HAR>
A; Cross-references: GBH.MISS18; NID:g190031; PIDN:AAA60111.1; PID:g190032
A; Note: parts of this sequence were confirmed by peptide sequencing
R; Reddy, V.B.; Garramone, A.J.; Sasak, H.; Wei, C.
DNA 6, 461-472, 1987
A; Affle: Expression of human uterine tissue-type plasminogen activator in mouse cells
A; Reference number: 160110; MUID:88054470; PMID:2824147
                                                              active
                               residues 36-562,
H.
number: A90488; MUID:85000468; PMID:6431976
annotation; melanoma cells, partial sequence of :
Kaplan, L.; Einarsson, M.; Wallen, P.; Jornvall,
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A;Molecule type: DNA
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A;Cross-references: GDB:119496; OMIM:173370
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A;Molecule type: mRNA
A;Residues: 1-562 <RES>
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                                                                                                                                                                                                                                                                                                                                                            A;Accession: A91322
                                                                                                         L-plasminogen activator (EC 3.4.21.68) precursor [validated] - human
N;Alternate names: L-PA; tissue plasminogen activator
C;Species: Homo sapiens (man)
C;Date: 14-Nov-1983 #sequence revision 14-Nov-1983 #text change 08-Dec-2000
C;Accession: A94004; A23529; ŪTO562; A93293; S02125; A91343; A93951; A91322; A54645; I66
R;Ny, T.; Elgh, F.; Lund, B.
Proc. Natl. Acad. Sci. U.S.A. 81, S355-S359, 1984
A;Title: The structure of the human tissue-type plasminogen activator gene: correlation
A;Reference number: A94004; MUID:84298137; PMID:6089198
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A; Residues: 1-562 < PEN>
A; Residues: 1-562 < PEN>
A; Residues: 1-562 < PEN>
A; Cross-references: GB:100141
A; Experimental source: melanoma cells
A; Experimental source: melanoma cells
B; Sasaki, H.; Saito, Y.; Hayashi, M.; Otsuka, K.; Niwa, M.
Nucleic Acids Res: 16, 5695, 1988
A; Title: Nucleotide sequence of the tissue-type plasminogen activator cDNA from human fe
A; Reference number: S02125; MUID:882652579; PMID:3133640
A; Accession: S02125
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A,Residues: 31-562 <ITRA
A,Residues: 31-562 <ITRA
A,Cross-references: DDBJ:D01096; NID:g220128; PIDN:BAA00881.1; PID:g441174
A,Experimental source: embryonic lung fibroblast IMR-90 cells
A;Note: part of this sequence, including the amino end of the mature protein, was confir
B,Fennica, D.; Halmes, W.E.; Kohr, W.J.; Harkins, R.N.; Vehar, G.A.; Ward, C.A.; Bennett
Nature 301, 214-221, 1983
A,Fitle: Cloning and expression of human tissue-type plasminogen activator cDNA in Esche
A,Reference number: A93293; MUID:83115262; PMID:6337343
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Molecule type: mRNA

Molecule type: mRNA

Molecule type: mRNA

Molecule type: mRNA

Molecule type: mRNA

Molecule type: mRNA

Molecule type: mRNA

Molecule type: mRNA

Molecule type: Molecule tetal lung cells

Molecule type type: Molecule the type plasminogen

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Molecule type: Molecule type plasminogen

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Molecule type: Molecule type plasminogen
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A; Residues: 1-38, G', 86-433,'E', 435-562 < KAG>
A; Residues: 1-38, G', 86-433,'E', 435-562 ells; ATCC 138
R; Edlund, T.; Ny, T.; Ranby, M.; Heden, L.O.; Palm, G.; Holmgren, E.; Josephson, S.
Proc. Natl. Acad. Sci. U.S.A. 80, 349-352, 1983
A; Title: Isolation of cDNA sequences coding for a part of human tissue plasminogen activ
A; Reference number: A93951, MUID:83169656; PMID:6572897
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A,Residues: 1-562 <DBS.
A,Cross-references: GB:KO3021; NID:G339817; PIDN:AAA98809.1; PID:G339818
A,Cross-references: GB:KO3021; NID:G339817; PIDN:AAA98809.1; PID:G339818
R;Itagaki, Y.; Yasuda, H.; Morinaga T.; Mitsuda, S.; Higashio, K.
Agric. Biol. Chem. S5, 1222-1232, 1991
A,Tille: Purification and characterization of tissue plasminogen activator secreted by
A,Reference number: JT0562; MUID:91291340; PMID:1368681
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Residues: 251-358 <EDL>
Residues: 251-358 <EDL>
Faxperimental source: melanoma cells
Fobl, G.; Kallstrom, M.; Bergsdorf, N.; Wallen, P.; Jornvall, H.
iochemistry 23, 3701-3707, 1984
Title: Tissue plasminogen activator: peptide analyses confirm an indirectly derived
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A Residues: 1-562 < NNTA
A Residues: 1-562 < NNTA
A Cross-reference GB:L00141
A Note: the codon given for residue 93 (ACC) is inconsis
R:Friezner Degen, S.U.; Rajput, B.; Reich, E.
J. Biol. Chem. 251, 6972-6985, 1986
A/Itle: The human tissue plasminogen activator gene.
A,Reference number: A23529; MUID:86196143; PMID:3009482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Accession: A23529
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us-09-880-503-8.rpr

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Fig. 259/Domain: Dispute #status predicted <PRO>Fig. 259/Product: t-plasminogen activator #status predicted <PRO>Fig. 259/Product: t-plasminogen activator #status predicted <PRO>Fig. 259/Product: t-plasminogen activator chain A #status predicted <ACH>Fig. 269/Product: t-plasminogen activator chain A #status predicted <ACH>Fig. 750-700main: fibronectin type I repeat homology <IFI>Fig. 200/Domain: EGF homology <IFI>Fig. 200/Domain: Kringle homology <IFI>Fig. 200/Domain: Kringle homology <IRI>Fig. 200-559/Product: t-plasminogen activator chain B #status predicted <BCH>Fig. 309-553/Domain: trypsin homology <IRI>Fig. 200-553/Domain: trypsin homology <IRI>Fig. 200-553/Pomain: trypsin homology <IRI>Fig. 309-553/Pomain: trypsin homology <IRI>Fig. 309-553/Pomain: trypsin homology <IRI>Fig. 309-553/Pomain: trypsin homology <IRI = Fig. 309-553/Pomain: trypsin homology <IRI = Fig. 309-553/Pomain: trypsin homology <IRI = Fig. 309-553/Pomain: trypsin homology <IRI = Fig. 309-553/Pomain: trypsin homology <IRI = Fig. 309-553/Pomain: trypsin homology <IRI = Fig. 309-553/Pomain: trypsin homology <IRI = Fig. 309-553/Pomain: trypsin homology <IRI = Fig. 309-553/Pomain: trypsin homology <IRI = Fig. 309-553/Pomain: trypsin homology <IRI = Fig. 309-553/Pomain: trypsin homology <IRI = Fig. 309-50/Pomain: trypsin homology <IRI = Fig. 309-50/Pomain: trypsin homology <IRI = Fig. 309-50/Pomain: trypsin homology <IRI = Fig. 309-50/Pomain: trypsin homology <IRI = Fig. 309-50/Pomain: trypsin homology <IRI = Fig. 309-50/Pomain: trypsin homology <IRI = Fig. 309-50/Pomain: trypsin homology <IRI = Fig. 309-50/Pomain: trypsin homology <IRI = Fig. 309-50/Pomain: trypsin homology <IRI = Fig. 309-50/Pomain: trypsin homology <IRI = Fig. 309-50/Pomain: trypsin homology <IRI = Fig. 309-50/Pomain: trypsin homology <IRI = Fig. 309-50/Pomain: trypsin homology <IRI = Fig. 309-50/Pomain: trypsin homology <IRI = Fig. 309-50/Pomain: trypsin homology <IRI = Fig. 309-50/Pomain: trypsin homology <IRI = Fig. 309-50/Pomain: trypsin homology <IRI = Fig. 309-50/Poma
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A;Residues: 33-37, X',39-40 <LIW>
C;Superfamily: tissue plasminogen activator; EGF homology; fibronectin type I :
C;Keywords: fibrinolysis; glycoprotein; hydrolase; kringle; serine proteinase
F;l-17/Domain: signal sequence #status predicted <SIG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     59 RGKASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVG 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   133 RGTWSTAENGAECINWNSSALSQKPYSARRPNAIKLGLGNHNYCRNPDRDVKFWCYVFKA 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     58

    common vampire bat

                                                                                                                                                                                                                                                                                                                                                                                        C,Species: Mus musculus (house mouse)
C,Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C,Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C,Accession: A29941; S48205; S48206
R;Rickles, R.J.; Darrow, A.L.; Strickland, S.
A;Biol. Chem. 263, 1563-1569, 1988
A;Title: Molecular cloning of complementary DNA to mouse tissue plasminogen
A;Reference number: A29941; MUID:88087303; PMID:2826484
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A,Molecule type: mRNA
A,Residues: 1-559 <RIC>
A,Cross-references: GB:J03520, NID:g202109; PIDN:AAA40470.1; PID:g202110
A,Cross-references: GB:J03520, NID:g202109; PIDN:AAA40470.1; PID:g202110
R;Lijnen, H.R.; van Hoef, B.; Beelen, V.; Collen, D.
Eur. J. Biochem. 224, 863-811, 1994
A;Title: Characterization of the murine plasma fibrinolytic system.
A;Reference number: S48202; MUID:95010076; PMID:7523120
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                                                                                                                                                                                                                                                                                                                                                               t-plasminogen activator (EC 3.4.21.68) precursor - mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   t-plasminogen activator (EC 3.4.21.68) alpha-1 precursor N'Alternate names: tissue plasminogen activator C'Species: Desmodus rotundus (common vampire bat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26;
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44.5%; Pred. No. 7.4e-21;
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                                                                                                                                                                     193 GKYTTEFCSTPAC----PKGPTED 212
                                                                                  LKPLVQECMVHDCADGKKPSSPPEE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A, Molecule type: protein
A, Residues: 33-37,'X',39-40 <LIJ>
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A; Residues: 309-316 <LI2>
A; Accession: S48206
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      t-plasminogen activator (EC 3.4.21.68) precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: A35029; A31597
R;Feng, P.; Ohlsson, M.; Ny, T.
A;End, P.; Ohlsson, M.; Ny, T.
A;Title: The structure of the TATA-less rat tissue-type plasminogen activator gene. Spec
A;Reference number: A35029; MUID:90130448; PMID:2105315
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;309-559/Product: Lrypsin homology <TRY>
;309-65/Jomain: trypsin homology <TRY>
;309-65/Jomain: trypsin homology <TRY>
;309-68,66-75,83-94,88-105,107-116,1124-205,145-187,176-200,213-294,234-276,265-289,297-,3149,481/Binding site: carbohydrate (Asn) (covalent) #status predicted
;308-309/Cleavage site: Arg-Ile (plasmin, trypsin) #status predicted
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A;Molecule type: DNA
A;Residues: 1-559 <FEN>
A;Cross-references: GB:M31197; NID:g207429; PIDN:AAA42261.1; PID:g207431; GB:J05226
F;152,483/Binding site: carbohydrate (Asn) (covalent) #status experimental F;219/Binding site: carbohydrate (Asn) (covalent) (partial) #status experimental $7.310-311/Cleavage site: Arg-Ile (plasmin, trypsin) #status experimental F;357,406/Active site: His, Asp #status predicted F;513/Active site: Ser #status experimental
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RGKASTDIMGRPCLPWNSAIVLQQIYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVG 118
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A,Cross-references: GB:M23697, NID:9530159, PIDN:AAA1812.1; PID:9530160
A;Cross-references: GB:M23697, NID:9530159, PIDN:AAA1812.1; PID:9530160
C;Superfamily: tissue plasminogen activator; EGF homology; fibronectin type I C;Keywords: fibrinolysis: glycoprotein; hydrolase; kringle, serine proteinase F;1-17/Domain: signal sequence #status predicted <SIG>F;1-27/Domain: propeptide #status predicted <PRO>F;30-559/Product: t-plasminogen activator #status predicted <MAT>F;30-559/Product: t-plasminogen activator chain A #status predicted <ACH>F;38-75/Domain: fibronectin type I repeat homology <1Fl>
                                                                                                                                                                                                                                                                                                                                                                                                    3 ELHQVP-SNCD---CLNGGTCVSNKYFSNIHWCNCPKKFGGQHCBIDKSKTCYEGNGHFY 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28
                                                                                                                                                                                                                                                                                                                                                                                                                                                  BLHQVP----SNCDCLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OCHSVPVRSCSEPRCFNGGTCQQALYFSDF-VCQCPDGFVGKRCDIDTRATCFEGQGITY
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                                                                                                                                                                                                                                                                                                                              Gaps
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15, Mismatches 56, Indels
                                                                                                                                                                                                                                           Length
                                                                                                                                                                                                                                                                                                                      Indels
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                                                                                                                                                                                                                                   ; Score 328.5; DB 1;
; Pred. No. 5e-22;
14; Mismatches 54;
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F;124-205/Domain: kringle homology <KR1>
F;213-294/Domain: kringle homology <KR2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;Ny, T.; Leonardsson, G.; Hsueh, A.J.W.
DNA 7. 671-677, 1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LKPLVQECMVHDCADG 134
                                                                                                                                                                                                                                   39.2%;
46.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         196 GKYSSEFCSTPACSEG 211
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Best Local Similarity 44.1%,
Matches 64, Conservative
                                                                                                                                                                                                                                                                                1 Similarity 46.3% 63; Conservative
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Best Local S
Matches 63
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plasma hyaluronan-binding protein precursor - mouse
C;Species: Mus musculus (house mouse)
C;Species: 11.Mar-1998 #sequence_revision 11-Mar-1998 #text_change 16-Jul-1999
C;Accession: JC5878
R;Hashimoto, K.; Tobe, T.; Sumiya, J.; Saguchi, K.; Sano, Y.; Nakano, Y.; Choi-Miura, 1
Biol. Pharm. Bill. 20, 1127-1130, 1997
A;Title: Cloning of the cDNA for a mouse homologue of human PHBP: A novel hyaluronan-b.
A;Reference number: JC5878; MUID:98065239; PMID:9401717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A.Residues: 1-558 «HAS»
C.Comment: This protein acts as serine protease.
C.Superfamily: plasma hyaluronan-binding protein; EGF homology; kringle homology; tryp:
F.1-23/Domain: signal sequence #status predicted <SIG»
F.24-311/Product: plasma hyaluronan-binding protein large chain #status predicted <MAT:
F.75-106/Domain: EGF homology <EG1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            F;113-145/Domain: EGF homology <EG2>
F;112-185/Domain: EGF homology <EG3>
F;192-274/Domain: kringle homology <KR1>
F;312-556/Product: plasma hyaluronan-binding protein small chain #status predicted <MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Richol-Miura, N.H.; Tobe, T.; Sumiya, J.; Nakano, Y.; Sano, Y.; Mazda, T.; Tomita, M. J. Biochem. 119, 1157-1165, 1996
A; Fitle: Purification and characterization of a novel hyaluronan-binding protein (PHBP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A)Gene: GDB:HABP2, HABP, PHBP, HGFAL
A,Cross-references: GDB:4573962
C,Complex: a disulfide-bonded heterodimer of chains produced from the same precursor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          73 PWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVGLKPLVQE-CMVHDC 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Molecule type: mRNA
A;Residues: 1-560 <CHO>
A;Cross-references: GB:S83182; NID:g1836158; PIDN:AAB46909.1; PID:g1836159
A;Experimental source: plasma
A;Note: parts of this sequence, including the amino ends of the mature chains,
C;Genetics:
   73 PWNSATVLQQTYHAHRSD-ALQLGLGKHNYCRNPDNRRRPWCYVQVGLKPLVQECMVHDC 131
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N;Alternate names: hepatocyte growth factor activator-like protein; PHBP
N;Contains: serine proteinase (BC 3.4.21,.)
C;Species: Homo sapiens (man)
C;Date: 15-Oct-1995 #sequence_revision 16-Aug-1996 #text_change 19-Jul-2002
C;Accession: JC4795
                                                                        239 RWAS----EATYRNMTAEQALRRGLGHHTFCRNPDNDTRPWCFVWMGNRLSWEYCDLAQC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          157 CQNGGVCSRHRRRSRF-TCACPDQXKGKFCEIGPD-DCYVGDGYSYRGKVSKTVNQNPCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           215 YWNSHLLLQETYNMFMEDAETHGIAEHNFCRNPDGDHKPWCFVKVNSEKVKWEYCDVTVC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13 CLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFYRGKASTDTMGRPCL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31.7%; Score 265; DB 2;
41.1%; Pred. No. 2.5e-16;
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                                                                                                                                                 132 ADGKKPSSPPEE 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           53; Conservative
                                                                                                                                                                                                                  295 QYPPQPTATPHD 306
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Afgreeable: 1977 < KRA
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Afgreeable: 1977 < KRA
Afgreeable: 1977 < KRA
Afgreeable: 1977 < KRA
Afgreeable: 1977 < KRA
Cross-references: GB maninogen activator; EGF homology; fibronectin type I repeat hom C; Keywords: fibrinolysis; glycoprotein; hydrolase; kringle; serine proteinase
C; Keywords: fibrinolysis; glycoprotein; hydrolase; kringle; serine proteinase
F; 12-3-5/Domain: propeptide #status predicted < FRO
F; 12-3-5/Domain: fibronectin type I repeat homology < KRO
F; 12-3-29/Domain: EGF homology < KRO
F; 12-3-29/Domain: kringle homology < KRO
F; 12-3-29/Domain: kringle homology < KRO
F; 12-3-29/Domain: kringle homology < KRO
F; 12-3-29/Domain: kringle homology < KRO
F; 12-3-26/Cleaváge site: asrbohydrate (Asn) (covalent) #status predicted
F; 12-2-26/Cleaváge site: His-Ser (plasmin) #status predicted
F; 12-2-26/Cleaváge site: His-Ser (plasmin) #status predicted
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Semba, U.; Yamamoto, T.; Kunisada, T.; Shibuya, Y.; Tanase, S.; Kambara, T.; Okabe, H.
Lochim. Biophys. Acta 1159, 113-121, 1992
Title: Primary structure of guinea-pig Hageman factor: sequence around the cleavage si
Reference number: S28941; MUID:93003367; PMID:1390917
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Superfamily: coagulation factor XII; EGF homology; fibronectin type I repeat homology;
Keywords: hydrolase; serine proteinase
                                                                                                                                             bat
                          R;Kraetzschmar, J.; Haendler, B.; Langer, G.; Boidol, W.; Bringmann, P.; Alagon, Gene 105, 229-237, 1991.
A;Title: The plasminogen activator family from the salivary gland of the vampire A;Reference number: JS0597; MUID:92039036; PMID:1937019
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVGLK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5 HQVPSN-CD---CLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFYRG 60
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31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 16-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               coagulation factor XIIa (EC 3.4.21.38) - guinea pig (fragment)
N;Alternate names: Hageman factor
C;Species: Cavia porcellus (guinea pig)
C;Date: 25-Feb-1994 #sequence_revision 03-Aug-1995 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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80
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    32.0%; Score 268; DB 2; Length 603; 38.6%; Pred. No. 1.4e-16; Live 21; Mismatches 52; Indels
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134-169/Domain: fibronectin type I repeat homology <FB1>
177-208/Domain: EgF homology <FBF>
216-294/Domain: kringle homology <FRGS
216-294/Domain: kringle homology <
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 38.6%
Matches 51, Conservative
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Matches 60; Conservative
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A;Molecule type: mRNA
A;Residues: 1-603 <SEM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Accession: S28941
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C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 27-Nov-1895 #sequence revision 30-Jun-1991 #text_change 08-Dec-2000
C;Accession. A29411; A26814; A20819; A20191; A22248; A21037
R;Cool, D.E.; MacGillavray, R.T.A.
J. Biol. Chem. 262, 13662-13673, 1987
J. Biol. Chem. 262, 13662-13673, 1987
A;Title: Characterization of the human blood coagulation factor XII gene. Intron/exon (A;Reference number: A29411; MUID:88007593; PMID:2888762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Accession: A25191
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Redidues: 146-378, GG, 380-615 <QUE>
A; Cross-references: GB:M13147; NID:g180360; PIDN:AAA70224.1; PID:g180361
B; McMullen, B.A.; Fujikawa, K.
B; McMullen, B.A.; Fujikawa, K.
B; Biol. Chem. 260, 5328-5341, 1985
A; Title: Amino acid sequence of the heavy chain of human alpha-factor XIIa (activated.)
A; Reference number: A22248; MUID:85182674; PMID:3886654
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A)Cross-references: GB M31315; NID:g182291; PIDN:AAA70225.1; PID:g182292
R)Crool, D.E.; Edgell, C.J.S.; Louie, G.V.; Zoller, M.J.; Brayer, G.D.; MacGillivray, R.Crool, Chem. 260, 1366-13676, 1985
A)Title: Chem. 260, 1366-13676, 1985
A)Title: Characterization of human blood coagulation factor XII cDNA. Prediction of the A;Reference number: A00930; MUID:86033830; PMID:3877053
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R.Harris, R.J.; Ling, V.T.; Spellman, M.W.
J. Biol. Chem. 267, 5103-5107, 1992
A.Hitle. O-linked fucose is present in the first epidermal growth factor domain of fact A,Reference number: A44606; MUID:92184750; PMID:1544894
A;Contents: annotation; carbohydrate binding site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
A; Molecule type: DNA
A; Molecule type: DNA
A; Cross-references cCOON
A; Cross-references GB: Worlda, S.; Galeffi, P.; Fantoni, A.; Cortese, R.
R; Tripodi, M.; Citarella, F.; Guida, S.; Galeffi, P.; Fantoni, A.; Cortese, R.
Nucleic Acids Res. 14, 3146, 1986
A; Title: CDNA sequence coding for human coaqulation factor XII (Hageman).
A; Reference number: A26814; MUID: 86176794; PMID: 3754331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              for human factor XII (Hageman factor) PMID:3011063
                                                                                                                                                                                                                                                   FYRGKASTDIMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQ 116
                                                                                                                                                                                                                                                                                                                              293 GYRGVÁSTSASGLSCLAWNSDLLYQELHVDSVGAÁALLGLGPHAYCRNPDNDERPWCYVV 352
                                                                                                                                                                         242 HTACLSSPCLNGGTC-----HLIVATGTTVCACPPGFAGRLCNIEPDERCFLGNGT
                                                                                               S HOVPSNCDCLNGGTCVSNKYFSNIHW------CNCPKKFGGQHCEIDKSKTCYEGNGH
                        Gaps
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A/Residues: 14-332,'S',334-615 <CC2>
A/Residues: 14-332,'S',334-615 <CC2>
A/Cross-references: GBM11723; NID:g180358; PIDN:AAA51986.1; PID:g180359
R/Cross-references: GBM11723; NID:g180358; PIDN:AAA51986.1; PID:g180359
R/Cue, B.G.; Davie, EW
Biochemistry 25, 1525-1528, 1986
A/Title: Characterization of a cDNA coding for human factor XII (Hageman A/Reference number: A25191; MUID:86216049; PMID:3011063
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     coagulation factor XIIa (EC 3.4.21.38) precursor [validated] - human N.Alternate names: Hageman factor (activated)
                        30;
                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                -----ADGKKPSSP 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       353 KDSALSWEYCRLEACESLTRVQLSPDLLATLPEPASP 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Accession: A22248
Molecule type: protein
Residues: 20-379 <MCM>
Fullikawa, K. McMullan, B.A.
Biol. Chem. 258, 10224-10933, 1983
Title: Amino acid sequence of human beta-factor XIIa.
Reference number: A21037; MUD:83291041; PMID:6604055
                    57
                    Mismatches
                    12;
                                                                                                                                                                                                                                                                                                                                                                                                            117 VGLKPLVQECMVHDC-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Molecule type: protein;Residues: 354-362;373-615 <FUJ>
                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A, Accession: A26814
A, Molecule type: mRNA
A, Residues: 4-615 <TRI>
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                    58;
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                    Matches
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C;Superfamily: plasma hyaluronan-binding protein; EGF homology; Kringle nomology; cryps, C;Keywords: chondroitin sulfate protegalycan; glycoprotein; hyaluronic acid; hydrolase; F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-313/Product: plasma hyaluronan-binding protein, 50K chain #status predicted <50K>
F;24-313/Product: plasma hyaluronan-binding protein, 50K chain #status predicted <50K>
F;115-147/Domain: EGF homology <EG2>
F;115-147/Domain: EGF homology <EG2>
F;154-187/Domain: EGF homology <EG2>
F;154-187/Domain: EGF homology <EG2>
F;154-187/Domain: EGF homology <EG2>
F;164-187/Domain: EGF homology <EG3>
F;164-187/Domain: EGF homology <EG3>
F;164-207/Domain: trypsin homology <EG3>
F;164-207/Binding site: carbohydrate (Asn) (covalent) #status predicted F;54,207/Binding site: carbohydrate (Asn) (covalent) #status predicted F;362,405,509/Active site: His, Asp, Ser #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Accession: A46688
!/Miyazawa, K.; Shimomura, T.; Kitamura, A.; Kondo, J.; Morimoto, Y.; Kitamura, N.
T. Biol. Chem. 268, 10024-10028, 1993
!/Title: Molecular cloning and sequence analysis of the cDNA for a human serine protease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       F;408-641/Domain: trypsin homology <TRY>
F;40,48,290,468,492,546/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;164-175,169-186,188-197,202-230,228-237,245-256,250-267,269-278,286-367,307-349,338-36
F;447,497,598/Active site: His, Asp, Ser #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pathway: tissue repair and regeneration

Superfamily: coagulation factor XII; ESF homology; fibronectin type I repeat homology;

Keywords: glycoprotein; hydrolase; kringle; liver; plasma; serine proteinase

11-34/Domain: signal sequence #status predicted <SIG>

1108-148/Domain: Eibronectin type II repeat homology <1F2>

1245-273/Domain: EGF homology <EG2>

1245-273/Domain: EGF homology <EG2>

1286-367/Domain: kringle homology <KRG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cross-references: DDBJ:D14012; NID:g219680; PIDN:BAA03113.1; PID:g219681; Experimental source: liver (mRNA); serum (protein); Note: sequence extracted from NCBI backbone (NCBIN:131227, NCBIP:131228); Note: parts of the sequence, including the amino ends of the heavy and light chains,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .373-407/Product: hepatocyte growth factor activator light chain #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Description: activates hepatocyte growth factor by specific proteolytic cleavage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hepatocyte growth factor activator (EC 3.4.21.-) precursor [validated] - human C;Species: Homo sapiens (man)
C;Date: 21-Sep-1993 #sequence_revision 25-Aug-1995 #text_change 08-Dec-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    217 YWNSHLLLQENYNMFWEDAETHGIGEHNFCRNPDADEKPWCFIKVTNDKVKWEYCDVSAC 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CONGATCSRHKRRSKF-TCACPDQFKGKFCEIG-SDDCYVGDGYSYRGKMNRTVNQHACL 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              73 PWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVGLKPLVQE-CMVHDC 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13 CLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFYRGKASTDTMGRPCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31.5%; Score 263.5; DB 1; Length 560; 41.0%; Pred. No. 3.4e-16; ive 18; Mismatches 56; Indels 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 655;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 262; DB 1;
Pred. No. 5.3e-16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31.3%;
36.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               132 A--DGKKPSSPPEE 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SAQDVAYPEESPTE 290
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A;Cross-references: GDB:9954514
A;Map position: 4p16-4p16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 41.0%
Matches 55; Conservative
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Best Local Similarity
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Objective factor XIIa (EC 3.4.21.38) precursor - bovine (fragment)

Natternate names: Hageman factor (activated)
Cispecies: Bos primigenius taurus (cattle)
Cispecies: Bos primigenius taurus (cattle)
Cidate: 10-Apr-1995 #sequence_revision 22-Apr-1995 #text_change 21-Jan-2000
CiAccession: S45281; A61329
Rishbuya, Y. Semba, U.; Okabe, H.; Kambara, T.; Yamamoto, T.
Biochim. Biophys. Acta 1206, 63-70, 1994
A;Title: Primary structure of bovine Hageman factor (blood coagulation factor XII): con A;Reference number: S45281; MUID: 94242782; PMID: 8186251
A;Accession: S45281
A;Molecule type: mRNA
A;Residues: 1-593 - S4HI>
A;Residues: 1-593 - S4HI>
A;Residues: 1-593 - S4HI>
A;Residues: 1-593 - S4HI>
A;Note: the authors translated the codon GAG for residue 23 as Val, GAG for residue 203 as Phe, GTG for residue 203 as Phe, GTG for residue 286 as (is, and ATC for residue 505 as Leu
R;Pujikawa, K; Walsh, K.A.; Davie, E.W.
Biochemistry 16, 2270-2278, 1977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Riwilson, C.; Goberdhan, D.C.I.; Steller, H. Proc. Natl. Acad. Sci. U.S.A. 90, 7109-7113, 1993
A.Title: Dror, a potential neurotrophic receptor gene, encodes a Drosophila homolog of A;Reference number: A48289; MID:9348222; PMID:8394009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   homology; fibronectin type I repeat homologs; glycoprotein; hydrolase; monomer; plasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OVCRTNPCLNGDSCLOAE -- GHRLCRCAPSFAGRLCDVDLKASCYDDRDRGLSYRGMAG 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                64 TDTMGRPCLPWNSATVLQQTY-HAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVGLKPL 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TILSGAPCQSWAS----BATYWNVTAEQVLNWGLGDHAFCRNPDNDTRPWCFIWKGDRLS 278
                                      A;Title: Isolation and characterization of bovine factor XII (Hageman factor) A;Reference number: A61329; MUID:77182112; PMID:861210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N;Alternate names: trk-related receptor
N;Contains: protein-tyrosine kinase (EC 2.7.1.112)
C;Species: Drosophila melanogaster
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 17-Nov-2000
C;Accession: A48289
DKSKTCYEGNGHFYRGKASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6 QVPSNCDCLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYE--GNGHFYRGKAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 58; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A.Molecule type: protein
M.Residues: 10-16, X'.18-19,525-550 «FUJ»
C.Superfamily: coagulation factor XII; EGF homology; fibro
C.Keywords: blood coagulation; fibrinolysis; glycoprotein;
F.37-78/Domain: fibronectin type II repeat homology «IF2»
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         F;88-120/Domain: EGF homology REGP.
F;125-160/Domain: Eibronectin type I repeat homology «FB1»
F;207-287/Domain: kringle homology «RGP»
F;350-287/Domain: trypsin homology «TRV»
F;350-287/Domain: trypsin homology «TRV»
F;541/Active site: Ser #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25.9%; Score 217; DB 2; 35.7%; Pred. No. 5.4e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15; Mismatches
                                                                                                                            PDNRRRPWCYVQVGLKPLVQECMVHDCA 132
                                                                                                                                                                                       127
                                                                                                                                                                                    PDGASKPWCYVIKARKFTSESCSVPVCS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Accession: A61329
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Best Local Simil
Matches 46; C
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A;Title: The plasminogen activator family from the salivary gland of the vampire bat Des A;Reference number: JS0597; MUID:92039036; PMID:1937019
A;Accession: JS0600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cross-references: GB:M63990; NID:g166078; PIDN:AAA31595.1; PID:g166079; Note: the authors translated the codon ATC for residue 75 as Thr.

Note: the authors translated the codon ATC for residue 75 as Thr.

Superfamily: tissue plasminosen activator; EGF homology; fibronectin type I repeat hom the codon and the codon and the codon and the codon and the codon and the codon and the codon and the codon and the codon and the codon and the codon activator gamma #status predicted <PLO>

12.1 Domain: propeptide #status predicted <PRO>
13.1 AFP roduct: plasminosen activator gamma #status predicted <PLO>
145.126/Domain: kringle homology <RRG>
145.126/Domain: trypsin homology <RRG>
145.126.56-109 $97-121,131-26.174-190.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Pathway: blood coagulation; fibrinolysis

S;Superfamily: coagulation factor XII; EGF homology; fibronectin type I repeat homology;
C;Superfamily: coagulation; fibrinolysis; glycoprotein; hydrolase; kringle; plasma; s
F;1-19/Domain: signal sequence #status predicted <SIG>
F;2-0-372,373-615/Product: coagulation factor XIIa, alpha form #status experimental <AI2>
F;47-88/Domain: fibronectin type II repeat homology <FE2>
F;98-130/Domain: EGF homology <EG1>
                                                    A,Map position: 5q34-5qter
A;Introns: 19/3; 39/1; 72/2; 96/1; 133/1; 177/1; 212/1; 267/2; 340/1; 417/2; 463/1; 511/
C;Complex: factor XII, prekallikrein, and HMW kininogen form a complex bound to anionic
C;Function:
                                                                                                                                                                                    A; Description: factor XIIa catalyzes the proteolytic activation of plasminogen, plasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1.09/Binding site: carbohydrate (Thr) (covalent) #status experimental 4.749,433/Binding site: carbohydrate (Asn) (covalent) #steatus experimental 1.299,305,328,329,337/Binding site: carbohydrate (Thr) (covalent) #status predicted 1.308/Binding site: carbohydrate (Ser) (covalent) #status predicted
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Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 16-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           common vampire bat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1; Length 615;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           240 PWAS----EATYRNVTAEQARNWGLGGHAFCRNPDNDIRPWCFV 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       73 PWNSATVLQQTY-HAHRSDALQLGLGKHNYCRNPDNRRRPWCYV 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13; Mismatches 36; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           412,461,563/Active site: His, Asp, Ser #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27.8%; Score 233; DB 1; 42.3%; Pred. No. 2e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              42.3%; Pred. nv.
                        A; Cross-references: GDB:119892; OMIM:234000
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Best Local Similarity 44.3<sup>†</sup>
Matches 39, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 27.8
Best Local Similarity 42.3
Matches 44; Conservative
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A; Molecule type: protein
A; Molecule type: protein
A; Residues: 20-21, 'P',23-34;177-179, 'N',181-186,'T',188-196,'DKG',200;292-314,'W',316-
X',4936-4401 <EAT>
X',4956-4401 <EAT>
A; Glarke, J.G.; Lindahl, G.E.; Liu, A.C.; Zysow, B.R.; Meer, K.; Schwartz,
Proc. Natl. Acad. Sci. U.S.A. 90, 1369-1373, 1993
A; Title: S control regions of the apolipoprotein(a) gene and members of the related p
A; Reference number: A47277; MUID:93165698; PMID:7679504
                                                                                                                                                                                                                                                                                                                                                                                                                                      apoprotein(a) (EC 3.4.21.-) precursor [validated] - human N;Alternate names: apolipoprotein(a); lipoprotein(a) chain apo(a) (c)Species: Homo sapiens (man) (c)Species: Homo sapiens (man) (c)Date: 30-Jun-1989 #sequence revision 30-Jun-1989 #text change 08-Dec-2000 (c)Accession: S00657; A28017; A47277; I60906; A47233; I52415; I65286 (M.; Schoclession: J.W.; Tomlinson, J.E.; Kuang, W.J.; Eaton, D.L.; Chen, E.Y.; Fless, G.M.; Scholle: CDNA sequence of human apolipoprotein(a) is homologous to plasminogen.
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A;Molecule type: DNA
A;Residues: 1-16 < RES.
A;Cross-references: GB:L07899; NID:g967973; PID:g967974
A;Cross-references: GB:L07899; NID:g967973; PID:g967974
B;Malgaretti, N.; Acquati, F.; Magnaghi, P.; Bruno, L.; Pontoglio, M.; Rocchi, M.; Sac, Proc. Natl. Acad. Sci. U.S.A. 89, 11584-11588, 1992
A;Title: Characterization by yeast artificial chromosome cloning of the linked apolipo A;Reference number: A47233; MUID:93087573; PMID:1454851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R,Ichinose, A.
Biochemistry 31, 3113-3118, 1992
Biochemistry 31, 3113-3118, 1992
A;Title: Multiple members of the plasminogen-apolipoprotein(a) gene family associated A;Title: Multiple member: I52415; MUID:92207924; PMID:1554698
A;Accession: I52415.
78
                                                                                                                                                                   SYPNAGLTM-----NYCRNPDADKSPWCYT---TDPRVRWEFCNLKKAPQAPSVENPPE 129
                                                                                                    86 AHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVGLKPLV--QECMVHDCADGKKPSSPPE 142
20 KKLAGRSVEDCAAKCE-EEAQDCYHGNGQGYRGTSSTTVTGRKCQSWSSMIPHRHQKTPE
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A;Note: apo(a) gene 1 (nomenclature of reference 152415)
A;Accession: A4733
A;Accession: A4733
A;Accession: A7789: DNA
A;Residues: 1-16 <RE5>
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A;Note: apo(a) gene 1 (nomenclature of reference I52415)
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A;Molecule type: DNA
A;Residues: 1-16 <RE2>
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A, Residues: 1-16 <RE3>
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C;Superfamily: Drosophila neurotrophic receptor ror; kringle homology; protein kinase ho
C;Superfamily: Drosophila neurotrophic receptor ror; kringle homology; protein; tyros
C;Keywords: ATP; glycoprotein; kringle; phosphotransferase; transmembrane protein; tyros
F;237-310/Domain: kringle homology «KRG»
F;314-338/Domain: transmembrane #status predicted «TM1»
F;408-677/Domain: protein kinase homology «KIN»
F;416-424/Region: protein kinase ATP-binding motif
F;45,63,129,144,250/Binding site: carbohydrate (Asn) (covalent) #status predicted
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**Superfamily: plasmin; kringle homology; plasminogen_related protein precursor homology; Superfamily: plasmin; kringle homology; plasmin; kringle; plasmin; protein proteinase; Z***
**Keywords: fibrinolysis; glycoprotein; hydrolase; kringle; plasm; serine proteinase; Z***
**1-37,38-117,118-460/Product: plasminogen (fragments) #status experimental <APT>
**1-37/Domain: activation peptide (fragment) #status experimental <APT>
**1-37/Domain: kringle homology <KR4>
**1-118/Domain: kringle homology <KR4>
**1-118/Domain: kringle homology <KR4>
**1-118/Domain: kringle homology <KR4>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62
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Cibace: 28-0ct-1994 #sequence_revision 01-Nov-1996 #text_change 17-Mar-1999
Cipacession: B61545, 2000
Rischaller, J.; Rickli, E.E.
Enzyme 40, 63-69, 1988
A;Ttle: Structural aspects of the plasminogen of various species.
A;Reference number: A61545, MUID:89005015; PMID:3168975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 ELHQVPSNCDCLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFYRGKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           212 DCQKLPQHKDCLSLGITI--------EVDKTENCYWEDGSTYRGVA
                                                                                                                                                                                        A; Cross-references: GB: L20297; NID: 9348103; PIDN: AAA 28860.1; PID: 9348104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 685;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19.5%; Score 163; DB 2; Length 460; 33.6%; Pred. No. 3e-07; Live 16; Mismatches 43; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Molecule type: protein
Residues: 1-37;38-117 <SCH>
/Schaller, U.; Straub, C.; Kaempfer, U.; Rickli, E.E.
octein Seq. Data Anal. 5, 21-25, 1992
/fitle: Complete anino acid sequence of ovine miniplasminogen.
/Reference number: S28200; MUID:93149995; PMID:1492092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        118-460/Product: miniplasminogen #status experimental <MIN>132-211/Domain: kringle homology <KR5>
226-460/Domain: plasmin chain B #status experimental <BCH>231-453/Domain: trypsin homology <TRY>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 F;231-453/Domain: trypsin nowolvyy .....
F;272,315,410/Active site: His, Asp, Ser #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20.2%; Score 169; DB 1;
28.8%; Pred. No. 1.2e-07;
iive 27; Mismatches 35;

    sheep (fragments)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Alternate names: plasminogen; Contains: miniplasminogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 28.83
Matches 38, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            301 IIELČDIPKĆÁĎ 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             122 LVQECMVHDCAD 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                         A;Molecule type: mRNA
A;Residues: 1-685 <WIL>
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Best Local Similarity
Matches 40; Conserv
                                               preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Accession: B61545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Accession: S28200
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63

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Query Match

ઠે g us-09-880-503-8.rpr

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RESULT 27
C6145
plasming C6 3.4.21.7) precursor - goat (fragments)
NyAternate names: plasminogen
C;Species: Capra aegagrus hircus (domestic goat)
C;Species: Capra aegagrus hircus (domestic goat)
C;Species: Capra aegagrus hircus (domestic goat)
C;Accession: C61545
R;Schaller, J; Rickli, E.E.
Enzyme 40, 63.469, 1988
A;Title: Structural aspects of the plasminogen of various species.
A;Reference number: A61545; MUD:89005015; PMID:3168975
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1.123 <SCH>
C;Superfamily: plasmin; kringle homology; plasminogen-related protein precursor homolc C;Keyword8: hydrolase; serine proteinase
F;41-118/Domain: kringle homology <KR4>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C,Accession: B32869, B33848

R;Tomlinson, J.E.; McLean, J.W.; Lawn, R.M.

J. Biol. Chem. 264, 5957-5965, 1989

A;Title: Rhesus monkey apolipoprotein(a). Sequence, evolution, and sites of synthesis.

A;Reference number: A32869; MUID:89174660; PMID:2925643
    A;Accession: A32869
A;Accession: A32869
A;Accession: A32869
A;Accession: Winny
A;Reaiduces: 1-1420 c7004
A;Cross-references: GB:J04635; NID:g342072; PIDN:AA36833.1; PID:g342073
C;Superfamily: apolipoprotein(a); kringle homology; trypsin homology
C;Keywords: hydrolase; kringle; lipid binding; lipoprotein; serine proteinase
F;50-127/Domain: kringle homology cKR1>
F;10-127/Domain: kringle homology cKR2>
F;32-469/Domain: kringle homology cKR3>
F;32-469/Domain: kringle homology cKR3>
F;32-65-83/Domain: kringle homology cKR3>
F;26-803/Domain: kringle homology cKR3>
F;26-803/Domain: kringle homology cKR3>
F;34-1031/Domain: kringle homology cKR3>
F;1068-1145/Domain: kringle homology cKR3>
F;1068-1145/Domain: kringle homology cKR3>
F;1068-1143/Domain: kringle homology cKR1>
F;1191-1413/Domain: kringle homology cKR1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1068 CYHGNGQSYRGTFSTTVTGRTCQSWSSMTPHQHKRTPENHPNDDLTM-----NYCRNPDA 1122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       50 CYEGNGHFYRGKASTDTMGRPCLPWNSATVLQ--QTYHAHRSDALQLGLGKHNYCRNPDN 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20 KKLAGRSVEDCAAKCE-EEAQDCYHGNGQSYRGTSSTTVTGRKCQSWSSMIPHRHQKTPE 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     plasmin (EC 3.4.21.7) precursor - rhesus macaque
C:Species: Macaca mulatta (rhesus macaque)
C:Pate: 31-Mar-1999 #sequence_revision 31-Mar-1989 #text_change 22-Jun-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                35 KKFGGQ-----HCEIDKSKTCYEGNGHFYRGKASTDTMGRPCLPWNSATV--LQQTYH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   86 AHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVGLKPLV--QECMVHDCAD 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      35; Indels 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 1420;
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19.1%; Score 160; DB 2; Length 123;
Best Local Similarity 34.5%; Pred. No. 1.8e-07;
Matches 38; Conservative 17; Mismatches 35; Indels ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19.2%; Score 161; DB 2;
40.9%; Pred. No. 1.2e-06;
tive 9; Mismatches 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1123 DIGPWCFT---MDPSVRREYCNLIRCSD 1147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           108 RRRPWCYVQVGLKPLVQE--CMVHDCAD 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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les 36; Conserv
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genes closely linked on chromosome 6 are identical in the first coding
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C;Species: Macaca mulatta (rhesus macaque)
C;Species: Macaca mulatta (rhesus macaque)
C;Accession: A32869; A30848
R;Tominson, J.E.; McLean, J.W.; Lawn, R.M.
J. Biol. Chem. 264, 9597-5965, 1989
A;Title: Rhesus monkey apolipoprotein(a). Sequence, evolution, and sites of synthesis. A;Reference number: A32869; MUID:89174660; PMID:2925643
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             70 PCLPWNSAIVLQQIYHAHRSDALQLGLGXHNYCRNPDNRRRPWCYVQVGLKPLV--QECM 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    69
                                                                             C;Superfamily: apolipoprotein(a); kringle homology; trypsin homology
C;Keywords: hydrolase; kringle; lipid binding; lipoprotein; serine proteinase
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-4548/Product: apolipoprotein(a) #status experimental <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27 NIHW--CN---CP-----KKFGGQHCEIDKSKT---CYEGNGHFYRGKASTDTMGR
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33.1%; Pred. No. 2.4e-06;
ive 12; Mismatches 46;
                                                                                                                                                                                                                     F/28-105/Domain: kringle homology «KR1»
F/28-105/Domain: kringle homology «KR2»
F/28-105/Domain: kringle homology «KR2»
F/28-105/Domain: kringle homology «KR2»
F/28-105/Domain: kringle homology «KR2»
F/28-503/Domain: kringle homology «KR5»
F/28-903/Domain: kringle homology «KR5»
F/28-1017/Domain: kringle homology «KR5»
F/28-1017/Domain: kringle homology «KR2»
F/28-1017/Domain: kringle homology «KR2»
F/28-1017/Domain: kringle homology «KR2»
F/28-1017/Domain: kringle homology «KR1»
F/28-105-1017/Domain: kringle homology «KR1»
F/28-105-100-Momain: kringle homology «KR1»
F/28-105-105-Domain: kringle homology «KR1»
F/28-105-105-Domain: kringle homology «KR1»
F/28-105-105-Domain: kringle homology «KR2»
F/28-105-105-Domain: kringle homology «KR2»
F/28-106-215/Domain: kringle homology «KR2»
F/28-106-215/Domain: kringle homology «KR2»
F/28-22-249/Domain: kringle homology «KR2»
F/28-22-249/Domain: kringle homology «KR2»
F/28-28-28-Domain: kringle homology «KR2»
F/28-28-28-Domain: kringle homology «KR2»
F/28-28-28-Domain: kringle homology «KR2»
F/28-28-28-Domain: kringle homology «KR2»
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F/28-28-28-Domain: kringle homology «KR3»
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F/28-28-28-Domain: kringle homology «KR3»
F/28-28-28-Domain: kringle homology «KR3»
F/28-28-28-Domain: kringle hom
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Matches 41, Conserv
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A32869
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A;Accession: S45046
A;Molecule type: mRNA
A;Residues: 1-812 < RERA
A;Residues: 1-812 < RERA
A;Residues: 1-812 < RERA
A;Cross-references: EMBL:X79402; NID:g494962; PIDN:CAA55939.1; PID:g494963
A;Experimental source: liver
A;Note: it is uncertain whether Met-1 or Met-8 is the initiator
Bix: J: Moser, P.W.; Dannegger-Muller, G.A.K.; Rosselet, S.J.; Kampfer, U.; Ri:
Bur. J: Blochem. 149, 267-278, 1985
A;Titler, Complete anino acid sequence of bovine plasminogen. Comparison with human pla
A;Reference number: A25835; WUID:85203906; PMID:3846532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A, Molecule type: mRNA
A, Residues: 706-743, 'R', 745-812 <MAL>
A, Residues: 706-743, 'R', 745-812 <MAL>
A, Crose-references: GB. R702955; ND: 9163551; PIDN: AAA30714.1; PID: 9163552
R, Brunisholz, R.A.; Lerch, P.G.; Schaller, J.; Rickli, E.E.; Lergier, W.; Manneberg, M. Bur. J. Biochem. 114, 465-470, 1981
Bur. J. Biochem. 114, 465-470, 1981
A, Title: Comparison of the primary structure of the N-terminal CNBr fragments of human A, Reference number: S03735; MUID: 81212097; PMID: 7238497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C:Superfamily: plasmin; kringle homology; plasminogen-related protein precursor homologic (Superfamily: plasmin; kringle; plasmin; hydrolase; kidney; kringle; plasmin; E;1-26/Domain: signal sequence #status predicted <SIG>
F;8-103/Domain: plasminogen-related protein precursor homology <PLPH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Description: dissolves the fibrin of blood clots; acts as a proteolytic factor in a ns the walls of the graafian follicle; also activates the urokinase-type plasminogen a A;Pathway: fibrinolysis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fig. 2012/Product: plasminogen #status experimental <PRO>
Fig. 2012/Product: plasminogen #status experimental <PRO>
Fig. 2013/Domain: activation peptide #status experimental <APT>
Fig. 4812/Product: plasmin chain A #status experimental <ART>
Fig. 188/Domain: kringle homology 
Fig. 202-269/Domain: kringle homology 
Fig. 202-269/Domain: kringle homology 
Fig. 202-269/Domain: kringle homology 
Fig. 384 461/Domain: kringle homology 
Fig. 384 461/Domain: kringle homology 
Fig. 384 4812/Domain: kringle homology 
Fig. 384 812/Domain: trypsin homology 
Fig. 384 805/Domain: trypsin homology 
Fig. 384 806/Domain: trypsin homology 
Fig. 384 806/Domain: trypsin homology 
Fig. 384 806/Domain: trypsin homology 
Fig. 386 806/Domain: trypsin homology 
Fig. 387 806 Fig. 387 3110-188 3131-171, 159-183, 192-269, 195-323, 213-252, 241-264, 282-359, 303-342, 200-200
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    #text_change 18-Jun-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           315 NRTPENFPCKNLEENYCRNPNGEKAPWCYTTN--SEVRWEYCTIPS-----CESSPLST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  --CYEGNGHFYRGKASTDTMGRPCLPWNSATVLQQTYHAH---RS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5 HQVPSNCDCLN-------GGTCVSNKYPSNIHW--CNCPKKFGGQHCEIDKSKT
                                                                                                                                                                        the bovine plasminogen cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             90 DALQLGLGKHNYCRNPDNRRRPWCYVQVGLKPLV--QECMVHDCADGKK--PSSP 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             F,315/Binding site: carbohydrate (Asn) (covalent) #status experimental F;365/Binding site: carbohydrate (Ser) (covalent) #status experimental F;624,667,762/Active site: His, Asp, Ser #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19.0%; Score 159; DB 1; Length 812; 28.0%; Pred. No. 1.1e-06; ive 15; Mismatches 55; Indels
A;Status: translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    49; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A,Molecule type: protein
A,Residues: 27-83 <BRU>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C; Function:
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                                                                                                       A, Residues: 1-810 < TOM>
A, Residues: 1-810 < TOM>
A, Residues: 1-810 < TOM>
A, Cross-references: GB.J04697; NID:g342272; PIDN:AAA36901.1; PID:g342273
A, Cross-references: GB.J04697; NID:g342272; PIDN:AAA36901.1; PID:g342273
A, Cross-references: GB.J04697; NID:g342272; PIDN:AAA36901.1; PID:g342273
C, Superfamily: plasmin; kringle homology; plasminogen-related protein precursor homology criming endence #status predicted <SIG>
F).196/Domain: signal sequence #status predicted <SIG>
F).103-181/Domain: kringle homology <KR1>
F).103-181/Domain: kringle homology <KR2>
F).262/Domain: kringle homology <KR4>
F).517-454/Domain: kringle homology <KR4>
F).581-803/Domain: kringle homology <KR5>
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F).581-803/Domain: kringle homology <RR5>
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F).581-803/
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A;Molecule type: protein
A;Molecule type: protein
A;Molecule type: protein
C;Superfamily: plasmin; kringle homology; plasminogen-related protein precursor homology
C;Keywords: hydrolase; serine proteinase
F;37-114/Domain: kringle homology <KR4>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NPDADKGPWCFTTDPSVRWEYCNLKKCSGTEGSVAAPPPVAQLPDAETPSEEDCMFGNGK 487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FYRGKASTDTMGRPCLPWNSATVLQQTYHAHR----SDALQLGLGKHNYCRNPD-NRRRP 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GYRGKKATTVTGTPCQEWAA-----QEPHSHRIFTPETNPRAGLEK-NYCRNPDGDVGGP 541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          46 KSKTCYEGNGHFYRGKASTDIMGRPCLPWNSAIVLQQIYHAHRSDAL-----QLGLGKHN 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----HCEIDKSKTCYEGNGH 56
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Diasmin (EC 3.4.21.7) precursor - dog (fragments)
NyAlternate names: plasminogen
C;Species: Canis lupus familiaris (dog)
C;Date: 28-Oct.1994 #sequence_revision 28-Oct.1994 #text_change 12-May-1995
C;Accession: E61545
R;Schaller, J; Rickli, E.E.
Enzyme 40, 63-69, 1988
A;Title: Structural aspects of the plasminogen of various species.
A;Reference number: A61545; MUID:89005015; PMID:3168975
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19.1%; Score 159.5; DB 2; Length 810; 31.4%; Pred. No. 1e-06; ive 12; Mismatches 66; Indels 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 120;
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Pred. No. 2.2e-07;
8; Mismatches 32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19.0%;
38.9%;
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Best Local Similarity 31.4%
Matches 49; Conservative
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Best Local Similarity
    Accession: B32869
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Gaps

26;

Thu Dec 4 06:31:01 2003

422 NYPNAGL-TMNYCRNPDADKSPWCYT---TDPRVRWEFCNLKKCSETPEGVPAAP 472

QQ

Search completed: December 3, 2003, 14:44:18 Job time : 7.39655 secs homo sapien homo sapien canis famil homo sapien

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SEQUENCE FROM N.A. Holmes W.E., Pennica D., Blaber M., Rey M.W., Guenzler W.A., Steffens G.J., Heyneker H.L.; "Cloning and expression of the gene for pro-urokinase in Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                        Urokinase-type plasminogen activator precursor (EC 3.4.21.73) (uPA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE=65215647; PubMed=2987867;
Riccio A., Grimaldi G., Verde P., Sebastio G., Boast S., Blasi F.;
"The human urokinase-plasminogen activator gene and its promoter.";
Nucleic Acids Res. 13:2759-2771(1985).
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MEDLINE=22388257; PubMed=12477932;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Strausher R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                [4]
SQUENCE FROM N.A.
MEDLINE=85203359; PubMed=3888571;
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
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MEDLINE=86056954; PubMed=2415429;
Magai M., Hiramatsu R., Kaneda T., Hayasuke N., Arimura H.,
Nishida M., Suyama T.;
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SEQUENCE FROM N.A.
Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Poel
Nickerson D.A.;
Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
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P00749; Q15844; Q16618; Q369W6;
21-JUL-1986 (RRL) 01, Created)
20-MAR-1987 (RRL) 04, Last sequel
15-SEP-2003 (Rel, 42, Last annot
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MBDLLNES-20266327; PubMed=10805774;
Sperl S., Jacob U., Arroyo de Frada N., Sturzebecher J., Wilhelm O.G., Bode W., Magdolen V., Huber R., Moroder L.;
"(4-aminomethyl)phenylyguanidine derivatives as nonpeptidic highly selective inhibitors of human urokinase.";
Proc. Natl. Acad. Sci. U.S.A. 97:5113-5118 (2000).
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Oswald R.E., Bogusky M.J., Bamberger M., Smith R.A.G., Dobson C.M.;
"Dynamics of the multidomain fibrinolytic protein urokinase from two-
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Verde P., Stoppelli M. Galeffi P., di Nocera P., Blasi F.;
"Identification and primary sequence of an unspliced human urokinase
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MEDLINE=83055099; PubMed=6754572;
Steffens G.J., Gunzler W.A., Otting F., Frankus E., Flohe L.;
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Hoppe-Seyler's Z. Physiol. Chem. 363:1043-1058(1982).
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MEDLINE-83055084; PubMed-6754569;
Gunzler W.A., Steffens G.J., Otting F., Kim S.-M.A., Frankus E.,
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MEDLINE=83003608; PubMed=6749491;
Schaller J., Nick H., Rickli E.E., Gillessen D., Lergier W.,
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STUCTURE BY NMR OF 67-155.
MEDLINE=93003110, PubMed=1327118;
Li X., Smith R.A.G., Dobson C.M.;
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MEDLINE=97337920; PubMed=9194591;

MEDLINE=97337920; PubMed=9194591;

MULTARIAN B. Schmatth M., Schmatter M., Schmatter M., Schmatter M., Schmatter M., Schmatter M., Schmatter M., Schmatter M., Schmatter M., Schmatter M., Schmatter M., Schmatter M., Schmatter M., Schmatter M., Schmatter M., Schmatter M., Schmatter M., Schmatter M., Schmatter M., Schmatter M., Schmatter M., Schmatter M., Schmatter M., Schmatter M., Schmatter M., Schmatter M., Schmatter M., Schmatter M., Schmatter M., Schmatter M., Schmatter M., Schmatter M., Schmatter M., Schmatter M., Schmatter M., Schmatter M., Schmatter M., Schmatter M., Schmatter M., Schmatter M., Schmatter M., Schmatter M., Schmatter M., Schmatter M., Schmatter M., Schmatter M., Schmatter M., Schmatter M., Schmatter M., Schmatter M., Schmatter M., Schmatter M., Schmatter M., Schmatter M., Schmatter M., Schmatter M., Schmatter M., Schmatter M., Schmatter M., Schmatter M., Schmatter M., Schmatter M., Schmatter M., Schmatter M., Schmatter M., Schmatter M., Schmatter M., Schmatter M., Schmatter M., Schmatter M., Schmatter M., Schmatter M., Schmatter M., Schmatter M., Schmatter M., Schmatter M., Schmatter M., Schmatter M., Schmatter M., Schmatter M., Schmatter M., Schmatter M., Schmatter M., Schmatter M., Schmatter M., Schmatter M., Schmatter M., Schmatter M., Schmatter M., Schmatter M., Schmatter M., Schmatter M., Schmatter M., Schmatter M., Schmatter M., Schmatter M., Schmatter M., Schmatter M., Schmatter M., Schmatter M., Schmatter M., Schmatter M., Schmatter M., Schmatter M., Schmatter M., Schmatter M., Schmatter M., Schmatter M., Schmatter M., Schmatter M., Schmatter M., Schmatter M., Schmatter M., Schmatter M., Schmatter M., Schmatter M., Schmatter M., Schmatter M., Schmatter M., Schmatter M., Schmatter M., Schmatter M., Schmatter M., Schmatter M., Schmatter M., Schmatter M., Schmatter M., Schmatter M., Schmatter M., Schmatter M., Schmatter M., Schmatter M., Schmatter M., Schmatter M., Schmatter M., Schmatter M., Schmatter M., Schmatter M
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"Sequential 1H NMR assignments and secondary structure of the kringle domain from urokinase.";
Biochemistry 31:9562-9571(1992).
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Sawasaki Y., Hanada K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conne B., Berczy M., Belin D.;
"Detection of polymorphisms-in the human urokinase-type plasminogen
                                                                                                                              MEDLINE=94149701; PubMed=8107091;
Li X., Bokman A.M., Llinas M., Smith R.A.G., Dobson C.M.;
"Solution structure of the kringle domain from urokinase-type
plasminogen activator.";
J. Mol. Biol. 235:1548-1559(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                 activator with a novel amino-acid substitution in the kringle
                                                                                                                                                                                                                                                                                                                                                                                                     "Characterization of single chain urokinase-type plasminogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Biochim. Biophys. Acta 1293:83-89(1996).
                                                                                                        STRUCTURE BY NMR OF 67-155.
MEDLINE=94149701; Pubmed=8107091;
                                                                                                                                                                                                                                                                                            VARIANT LEU-141.
MEDLINE=96186279; PubMed=8652631;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=97218551; PubMed=9065988;
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Thromb. Haemost. 78:973-973(1997)
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EMBL, X02760; CAA26535.1,
EMBL, AF377330; AAKS3822.1;
EMBL, BC013575; AAH13575.1;
FMBL; K03226; AAC97138.1;
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EMBL; M15476; AAA61253.1; -.
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EMBL; A18397; CAA01390
PIR; A00931; UKHU;
PDB; 1KDU; 31-OCT-93.
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KASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVGLK 120
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MEDLINE=85087954; PubMed=6096832;
Nagamine Y., Pearson D., Altus M.S., Reich E.;
"CDNA and gene nucleotide sequence of porcine plasminogen activator.";
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R SMART; SM00181; EGF; 1.

R SMART; SM00130; KR; 1.

R PROSITE; SM00130; Tryp SPc; 1.

R PROSITE; PS00022; EGF_1; 1.

R PROSITE; PS000186; EGF_2; FALSE_NEG.

R PROSITE; PS000186; EGF_2; FALSE_NEG.

R PROSITE; PS00019; KRINGLE_2; 1.

R PROSITE; PS00134; TRYPSIN_DOM; 1.

R PROSITE; PS00135; TRYPSIN_SER; 1.

R PROSITE; PS00135; TRYPSIN_SER; 1.

R PROSITE; PS00135; TRYPSIN_SER; 1.

R PROSITE; PS00135; TRYPSIN_SER; 1.

R PROSITE; PS00135; TRYPSIN_SER; 1.

R PROSITE; PS00135; TRYPSIN_SER; 1.

R PLANTINGEN activation; PYOTOlase; Serine protease; Glycoprotein; Kringle; EGF-1ke domain; Zymogen; Signal.
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13-AUG-1987 (Rel. 05, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
Urokinase-type plasminogen activator precursor (EC 3.4.21.73) (uPA)
(U-plasminogen activator).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
NCBI_TaxID=9823;
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CHAIN A (BY SIMILARITY)
SHORT A CHAIN (A1) (BY SIMILARITY)
EGF-LIKE.
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ses 132; Conservative
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TISSUE=Thoracic aorta;
MEDLINE=9029734; PubMed=2113276;
MAY Y.P.T., Wang T.W., Clowes A.W.;
"Nucleotide and deduced amino acid sequences of baboon urokinase-type
                                                                                                                   Gaps
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01-APR-1990 (Rel. 14, Last sequence update)
01-APR-2003 (Rel. 41, Last annotation update)
Urokinase-type plasminogen activator precursor (EC 3.4.21.73) (uPA)
(U-plasminogen activator).
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae;
                                                                                                               .
                                 Query Match
100.0%; Score 837; DB 1; Length 431;
Best Local Similarity 100.0%; Pred. No. 1.2e-73;
Matches 143; Conservative 0; Mismatches 0; Indels
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InterPro; IPR006509; EGF like.
InterPro; IPR006501, EGF.
InterPro; IPR0010154; Sar_protease_Try.
Pfam; PF00081; kringle; I.
Pfam; PF00081; kringle; I.
Pfam; PF00089; trypsin; I.
PRINTS; PR00122; CHYMOTRYPSIN.
PRODOM; PR001395; KRINGLE.
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NCBL_TaxID=9556;
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SEQUENCE FROM N.A
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                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                 Nagamine Y.;
Submitted (DEC-1986) to the PIR data bank.
-!- CATALYTIC ACTIVITY: Specific cleavage of Arg-|-Val bond in plasminogen to form plasmin.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
-!- SIMILARITY: Contains 1 kringle domain.
-!- SIMILARITY: Contains 1 EGF-like domain.
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-> H (IN REF. 1; CAA25511).
-> GS (IN REF. 1; CAA25806)
EE32FCEF501321EE CRC64.
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73.4%; Pred. No. 3.2e-53;
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EMBL, X02724; CAA26511.1; -
FIR, A00932; UKPG.
HSSP, P00749; IKDU.
MEROPS, S01.231; -
INTERPO: IPR001314; Chymotrypsin.
INTERPO: IPR00509; EGF like.
INTERPO: IPR001244; Sar protease_Try.
Fram, PP00051; Kringle; 1.
Fram, PP00051; Kringle; 1.
Nucleic Acids Res. 12:9525-9541(1984)
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Best Local Similarity 73.49
Matches 113; Conservative
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42 AA,
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Gaps

11;

19; Indels

11; Mismatches

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                                                                            RGKASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVG 118
                                                                                                               81 RGKANTNIGGRPCLPWNSATVLLNIYHAHRPDALQLGLGKHNYCRNPDNQRRPWCYVQVG 140
                     SHELHQESGASNCGCLNGGKCVSYXYFSNIQRCSCPKKFQGEHCEIDTSQTCFEGNGHSY 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ravn P., Berglund L., Petersen T.E., "Cloning and characterization of the bovine plasminogen activators uPA and tPA.";
SNELHQV - - PSNCDCLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFY
                                                                                                                                                                                                                                                                                  UNDOK BOVIN STANDARD; PRT; 433 AA.

Q05589; Q28209;
Q15FB1-1994 (Rel. 28, Created)
Q1-FB2-1994 (Rel. 28, Last sequence update)
Z8-FB2-2003 (Rel. 41, Last annotation update)
Urokinase-type plasminogen activator precursor (EC 3.4.21.73) (uPA)
PLAD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
Bovidae, Bovinae, Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Int. Dairy J. 5:605-617(1995).
-!- CATALYTIC ACTIVITY: Specific cleavage of Arg-|-val bond in plasminogen to form plasmin.
-!- INDUCTION: By retinoic acid.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
-!- SIMILARITY: Contains 1 kringle domain.
-!- SIMILARITY: Contains 1 EGF-like domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Bovine urokinase-type plasminogen activator and its receptor: cloning and induction by retinoic acid.";
Gene 125:177-183(1993).
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MEDLINE=9216119; PubMed=8385052;
Kraetzschmar J., Haendler B., Kojima S., Rifkin D.B.,
Schleuning W.-D.;
                                                                                                                                                        LKPLVQECMVHDCA------DGKKPSSPPEE 143
                                                                                                                                                                                           141 LKQLVQECMVPNCSGGESHRPAYDGKNPFSTPEK 174
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EMBL; X85801; CAA59796.1; --
PIR; JN0560; JN0560.
HSSP; P00749; ILMW.
MEROPS; S01.231.
InterPro; IPR001314; Chymotrypsin.
InterPro; IPR0001314; Chymotrypsin.
InterPro; IPR000001; Kringle.
InterPro; IPR0001554; Ser_Irotease_Try.
Pfam; PF00051; Kringle; I.
Pfam; PF00089; Kringle; I.
PRINTS; PR00722; CHYMOTRYPSIN.
PRINTS; PR00128; KRINGLE.
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us-09-880-503-8.rsp

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plasminogen activator gene expression in metastatic tumor cells.";
Cancer Res. 52:2489-2496(1992).
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R Probom, PD000395; Kringle; 1.

R RAART; SMO0130; KR; 1.

R PROSITE; S00022; EGF 1; 1.

R PROSITE; PS01186; EGF 2; FALSE NEG.

R PROSITE; PS000186; EGF 2; FALSE NEG.

R PROSITE; PS000186; EGF 2; FALSE NEG.

R PROSITE; PS0001; KRINGLE 2; 1.

R PROSITE; PS00135; TRYPSIN DOM; 1.

R PROSITE; PS00135; TRYPSIN SER; 1.

R PROSITE; PS00135; TRYPSIN SER; 1.

R PROSITE; PS00135; TRYPSIN SER; 1.

R PROSITE; PS00136; TRYPSIN SER; 1.

R PROSITE; PS00136; TRYPSIN SER; 1.

R SIGNAL 1 20
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
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CONNECTING PEPTIDE.
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WM, 4DE1B8D4DA47027A CRC64;
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01-APR-1993 (Rel. 25, Last sequence update)
01-APR-1993 (Rel. 41, Last annotation update)
Urokinase-type plasminogen activator precursor (EC 3.4.21.73) (uPA)
(U-plasminogen activator).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               UROKINASE-TYPE PLASMINOGEN ACTIVATOR
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SEQUENCE FROM N.A.
STRAIN=Fischer 344;
MEDLINE-92233409; PubMed=1568219;
Henderson B.R., Tansey W.P., Phillips S.M., Ramshaw I.A.,
Kefford R.F.;
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UROKINASE-TYPE PLASMINOGEN ACTIVATOR
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SHORT A CHAIN (A1) (BY SIMILARITY)
CHAIN B (BY SIMILARITY)
BGF-LIKE.
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KRINGLE.
CONNECTING PEPTIDE.
SERINE PROTEASE.
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                                                                                                                                                                                                                                                                                89 RPCLAWNSPAVLQQTYNAHRSDALSLGLGKGHNYCRNPDNQRRPWCYVQIGLKQFVQECMV 148
                                                                                                                                                                                                                                                           RPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVGLKPLVQECMV 128
                                                                                                                                                                                  89
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                                                                                                                                            Gaps
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28-FEB-2003 (Rel. 41, Last annotation update)
Urokinase-type plasminogen activator precursor (EC 3.4.21.73) (uPA)
PLAU.
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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Belin D., Vassalli J.-D., Combepine C., Godeau F., Nagamine Y., Reich E., Kocher H.P., Duvoisin R.M., "Cloning, nucleotide sequencing and expression of cDNAs encoding mouse urokinase-type plasminogen activator.";

Eur. J. Biochem. 148:225-232(1985).
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  N -> H (IN REF. 2).
E -> G (IN REF. 2).
D -> N (IN REF. 2).
7 + ABBIB96C716244C8 CRC64;
                                                                                                70.7%; Score 592; DB 1;
75.6%; Pred. No. 5.4e-50;
tive 10; Mismatches 23;
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MHSSP, R00749; IKDU.
MEROPS; S01.231; -.
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                                                                                                                                        Conservative
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  16
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332
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432 AA;
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Matches 102; Conserv
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P06869;
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69 RPCLPWNSATVLQQTYHAHRSDALQLGLGXHNYCRNPDNRRRPWCYVQVGLKPLVQECMV 128
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THEOFPO; IPR00114; Chymotrypsin.

THEOFPO; IPR001214; Chymotrypsin.

THEOFPO; IPR001219; EGF like.

THEOFPO; IPR000210; EGF.

THEOFPO; IPR000101; Kringle.

THEOFPO; IPR000101; Kringle.

PRONTS; PR000101; Kringle; I.

PRINTS; PR001018; KRINGLE.

PRODOM; PR000101; EGF; I.

SWART; SW00118; EGF; I.

SWART; SW00118; EGF; I.

PROSITE; PS01021; KRINGLE.

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PROSITE; PS01021; KRINGLE I.

PROSITE; PS01031; KRINGLE I.

PROSITE; PS01031; TRYPSIN INS.

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01-APR-1990 (Rel. 14, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-Ivary plasminogen activator alpha 2 precursor (EC 3.4.21.68) (DSPA alpha-2) (BAT-PA) (T-plasminogen activator).
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CHAIN B (BY SIMILARITY)
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-!- DOMAIN: THE FIBRONECTIN TYPE-I DOMAIN MEDIATES BINDING TO FIBRIN,
AND THE KRINGLE DOMAIN APPARENTLY MEDIATES FIBRIN-INDUCED
STIMULATION OF ACTIVITY.
-!- SIMILARITY: ORDIAINS I SEPTIDASE FAMILY SI.
-!- SIMILARITY: COntains I EgF-like domain.
-!- SIMILARITY: Contains I fibronectin type I domain.
-!- SIMILARITY: Contains I fibronectin type I domain.
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"Pleasinogen activators from the saliva of Desmodus rotundus (common "Pleasinogen activators from the saliva of Desmodus rotundus (common wampire bat): unique fibrin specificity.";
Ann. N.Y. Acad. Sci. 667:395-403(1992).
-i- FUNCTION: PROBABLY ESSENTIAL TO SUPPORT THE FEEDING HABITS OF TH:
EXCLUSIVELY HAEMATOPHAGOUS ANIMAL. PROBABLE POTENT THROMBOLYTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            plasminogen to form plasmin.
ENZYME REGULATION: ACTIVITY TOWARD PLASMINOGEN IS STIMULATED IN
THE PRESENCE OF FIBRIN I.
                                                                                                                                         SECUENCE FROM N.A.

TISSUB=Salivary gland;

MEDILINE=92039036; PubMed=1937019;

Kraetzschnar J., Haendler B., Langer G., Boidol W., Bringmann P., Alagon A., Donner P., Schleuning W.D.;

"The plasminogen activator family from the salivary gland of the vampire bat Desmodus rotundus: cloning and expression.";

Gene 105:229-237(1991).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi
Mammalia; Eutheria; Chiroptera; Microchiroptera; Phyllostomidae;
                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
TISSUE=Salivary gland;
MEDLINE=9003.6867; PubMed=2509450;
Gardell S.G., Duong L.T., Diehl R.E., York J.D., Hare T.R.,
Register R.B., Jacobs J.W., Dixon R.A.F., Friedman P.A.;
"Isolation, Characterization, and cDNA cloning of a vampire bat salivary plasminogen activator.";
J. Biol. Chem. 264:17947-17952(1989).
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CHARACTERIZATION.
ABDILINE-93393059; PubMed=1309059;
Schleuning W.-D., Alagon A., Boidol W., Bringmann P., Petri T
Kraetzschmar J., Haendler B., Langer G., Baldus B., Witt W.,
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InterPro; IPR001254; Ser_Drotease_Try.
Pfam; PP00008; EGF; 1.
Pfam; PP00009; Enl; 1.
Pfam; PP00089; Kningle; 1.
Pfam; PP00089; trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
PRINTS; PR00129; KRINGLE.
ProDom; PD000395; Kringle; 1.
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IPR000083; Fibrnctn1.
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EMBL, JOSO82, AAA31596.1, -.
PIR, JSO598, JSO598.
HSSP, P98119, IA51.
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                                                         Desmodontinae, Desmodus.
NCBL_TaxID=9430;
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59 RGKASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVG 118
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R SWART; SM00181; EGF; 1.

SWART; SM000181; EGF; 1.

SWART; SM00130; KR; 1.

R SWART; SM00020; TRYP SPC; 1.

R PROSITE; PS00022; EGF 1; 1.

R PROSITE; PS01023; FIBROWCTIN 1; 1.

R PROSITE; PS01021; KRINGLE 1; 1.

R PROSITE; PS01014; TRYPSIN Dom; 1.

R PROSITE; PS01014; TRYPSIN Dom; 1.

R PROSITE; PS01014; TRYPSIN Dom; 1.

R PROSITE; PS01014; TRYPSIN SER; 1.

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
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28-FEB-2003 (Rel. 41, Last annotation update)
Urokinase-type plasminogen activator precursor (EC 3.4.21.73) (uPA)
(U-plasminogen activator).
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-> H (IN REF. 2).
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| BMBL; J05188; AAA49131.1; -
| BMBL; J05188; AAA49131.1; -
| BMBL; J05188; AAA49131.1; -
| BMBL; J05188; AAA49131.1; -
| BMBL; J05188; ABSO05.
| BRSPP; P00763; 1DP0.
| BR InterPro; IPR0062019; EGF like.
| InterPro; IPR0062019; EGF like.
| InterPro; IPR000101; Kringle; I.
| RR PR00712; CHYMORYPSIN; I.
| PRINTS; PR00102; CHYMORYPSIN; I.
| PRNITS; PR00103; KRINGLE.
| BRNTS; PR00139; KRINGLE.
| BRNSTIE; SM00130; KRINGLE.
| BRNSTIE; PS00102; TRYSIN DOM; I.
| PROSITE; PS01186; EGF 1; I.
| PROSITE; PS01186; EGF 2; I.
| PROSITE; PS01186; EGF 2; I.
| PROSITE; PS01186; EGF 1; I.
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| PROSITE; PS01186; EGF 3; I.
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272
373
228
434 AA;
   Gallus.
NCBI_TaxID=9031;
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DB 1; Length 434;

40.0%; Score 334.5;

Query Match

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                   11 CDCLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFYRGKASTDTMGRP 70
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Ann. N.Y. Acad. Sci. 667:395-403 (1992).
-!- FUNCTION: PROBABLY ESSENTIAL TO SUPPORT THE FEEDING HABITS OF THIS EXCLUSIVELY HAEMATOPHAGOUS ANIMAL. PROBABLE POTENT THROMBOLYTIC
                                                                           CQCLNGGTCITYRFFSQIKRCLCPEGYGGLHCEIDINSICYSGNGEDYRGMAEDP----G
                                                                                                                                                                                                                                                                                               01-FEB-1996 (Rel. 33, Created)
1-FEB-1996 (Rel. 33, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Salivary plasminogen activator beta precursor (EC 3.4.21.68) (DSPA
                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Chiroptera, Microchiroptera, Phyllostomidae,
Desmodontinae, Desmodus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Salivary gland;
MEDLINE=92039036; PubMed=1937019;
MEDLINE=92039036; PubMed=1937019;
MISTAGETSCHMAR J., Haendler B., Langer G., Boidol W., Bringmann P., Alagon A., Donner P., Schleuning W.D.;
"The plasminogen activator family from the salivary gland of the vampire bat Desmodus rotundus: cloning and expression.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=93393059; PubMed=1309059;
Schleuning W.-D., Alagon A., Boidol W., Bringmann P., Petri T.,
Kraetzschmar J., Haendler B., Langer G., Baldus B., Witt W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CATALYTIC ACTIVITY: Specific cleavage of Arg-|-val bond in plasminogen to form plasmin.
SUBDINIT: Monomer.
SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
SIMILARITY: Contains 1 kringle domain.
SIMILARITY: Contains 1 EGF-like domain.
                                                                                                                                                      CLYWDHPSVIRWGDYHADLKNALQLGLGKHNYCRNPNGRSRPWCYTK 142
                                                                                                                              CLPWNSATVLQ-QTYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQ 116
54.2%; Pred. No. 4e-25; ive 14; Mismatches 30; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Desmodus rotundus (Vampire bat).
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HSSP; P98119; 1A51.
                 Conservative
                                                                                                                                                                                                                                                             STANDARD;
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Best Local Similarity
Matches 58; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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CHARACTERIZATION.
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Nucleic Acids Res. 18:1086-1086(1990).
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MEDLINE=90192129, PubMed=2107528,
Siebert P.D., Fong K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       structural domains.
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R PFam; PF00009; trypein; 1.

R PRINTS; PR00722; CHYMCIRYPSIN.

R PRINTS; PR001395; KRINGLE.

R PRODOM; PD000395; KRINGLE.

R SMART; SM00130; KR; 1.

R SMART; SM00130; KR; 1.

R PROSITE; PS0102; EGF 1; 1.

R PROSITE; PS0102; EGF 1; 1.

R PROSITE; PS0103; KRINGLE 2; 1.

R PROSITE; PS0103; TRYPSIN IN; 1.

R PROSITE; PS0136; TRYPSIN IN; 1.

R PROSITE; PS0136; TRYPSIN IN; 1.

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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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190750, Q15120, Q3131
21-JUL-1986 (Rel. 01, Last sequence update)
15-SEP-2003 (Rel. 42, Last annoctation update)
Tissue-type plasminogen activator precursor (EC 3 4.21.68) (tPA) (t-PA) (t-plasminogen activator) (Alteplase) (Reteplase).
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; Pred. No. 1.5e-24;
16; Mismatches 48
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139
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431 AA;
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Best Local Similarity
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SEQUENCE FROM N.A.
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X MEDLINE=22388557; Pubmed=12477932;
X MEDLINE=22388557; Pubmed=12477932;
X Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Strausberg R.L., Feingold E.A., Wagner L., Shenmen C.M., Schuler G.D.,
RA Alechul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Stapleton M., Soaree M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bank S.A., McEwan R.J., McKernan K.J., Mallek J.A., Gunzrathe P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Pinlan D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
R Fahry J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
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Hsiung N.)
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NY T., E194h F., Lund B.;
"The structure of the human tissue-type plasminogen activate correlation of intron and exon structures to functional and
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01-NOV-1991 (Rel. 20, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Tissue-type plasminogen activator precursor (EC 3.4.21.68) (tPA)
(t-PA) (t-plasminogen activator).
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                                                                                                    The Structure of the TATA-less rat tissue-type plasminogen activator of the Structure of the TATA-less rat tissue-type plasminogen activator gene. Species-specific sequence divergences in the promoter predict differences in regulation of gene expression.";

"He structure of the TATA-less rat tissue-type plasminogen activator gene. Specific sequence divergences in the promoter predict differences in regulation of gene expression.";

"He structure of the TATA-less rat tissue-type plasminogen product of gene expression.";

"He structure of the TATA-less rat tissue-type plasminogen activator from Plasminogen expression.";

"He structure of the TATA-less rat tissue-type plasminogen activator from plasminogen activator from plasmin."

"The structure of the TATA-Less rat tissue-type plasminogen to form plasmin."

"The structure of the TATA-Less rat tissue-type plasminogen to form plasmin."
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SUBCELLULAR LOCATION: SECRETED; EXTRACELLULAR.

PUN: THE SINGLE CHAIN, ALMOST FULLY ACTIVE ENZYME, CAN BE FURTHER PROCESSED INTO A TWO-CHAIN FULLY ACTIVE FORM BY A CLEAVAGE AFTER PROCESSED INTO A TWO-CHAIN FULLY ACTIVE FORM BY A CLEAVAGE AFTER ARG-308 CATALYZED BY PLASMIN, TISSUE KALLICKEIN OR FACTOR XA.

MISCELLANDEOUS BINDS TO THE KRINGLE STRUCTURE OF THE FIBRIN A CHAIN. BINDING TO FIBRID SINGL STRUCTURE OF THE FIBRIN A CHAIN. BINDING TO PEPTIDASE FAMILY SI.

SIMILARITY: COLLAIDS I EGF-like domain.

SIMILARITY: Contains I fibronectin type I domain.
                                   Ny I., Leonardsson G., Hsueh A.J.W.; "Cloning and characterization of a cDNA for rat tissue-type
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InterPro; IPR000001; Kringle.
InterPro; IPR001254; Ser_protease_Try.
Pfam; PF00008; EGF; 1.
Pfam; PF00039; fn1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                M31185; AAA4226111; JOINED.
M31186; AAA4226111; JOINED.
M31188; AAA4226111; JOINED.
M31189; AAA4226111; JOINED.
M31189; AAA4226111; JOINED.
M31199; AAA4226111; JOINED.
M31199; AAA4226111; JOINED.
M31199; AAA4226111; JOINED.
M31199; AAA4226111; JOINED.
M31199; AAA4226111; JOINED.
M31199; AAA4226111; JOINED.
M31199; AAA4226111; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IPR001314; Chymotrypsin.
IPR006209; EGF_like.
IPR000083; Fibrnctnl.
SEQUENCE FROM N.A.
MEDLINE=89170114; PubMed=3148445,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00051; Kringle; 2.
Pfam; PF00089; trypsin; 1.
PRINTS; PR00722; CHYWOTRYPSIN.
PRODOM; PD000395; KRINGLE; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; M23697; AAA41812.1; -.
EMBL; M31197; AAA42261.1; -.
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EMBL; M31196; AAA42261.1;
EMBL; A19618; CAA01482.1;
PIR; A35029; A36029.
                                                                        plasminogen activator.";
DNA 7:671-677(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro;
InterPro;
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EMBL;
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59 RGKASTDIMGRPCLPWNSATVLQQIYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVG 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protease; Glycoprotein; Signal.
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TISSUE-TYPE PLASMINOGEN ACTIVATOR A
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Pred. No. 4.2e-24;
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7DBD3809C1D1C921 CRC64;
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EGF-LIKE.
SMART; SM00181; EGF; 1.
SMART; SM00158; FN1; 1.
SMART; SM00130; KR; 1.
SMART; SM00120; TYP, SPC; 1.
PROSITE; PS0022; EGF_1; 1.
PROSITE; PS01186; EGF_2; 1.
PROSITE; PS0021; KRINGLE 1; 2.
PROSITE; PS50021; KRINGLE 1; 2.
PROSITE; PS50014; KRINGLE 2; 2.
PROSITE; PS50014; TRYPSIN 1: 1.
PROSITE; PS50140; TRYPSIN 1: 1.
PROSITE; PS50140; TRYPSIN 1: 1.
PROSITE; PS0141; TRYPSIN 1: 1.
PROSITE; PS0141; TRYPSIN 1: 1.
PROSITE; PS0141; TRYPSIN 1: 1.
PROSITE; PS0141; TRYPSIN 1: 1.
PROSITE; PS0141; TRYPSIN 1: 1.
PROSITE; PS0141; TRYPSIN 1: 1.
PROSITE; PS0141; TRYPSIN 1: 1.
PROSITE; PS0141; TRYPSIN 1: 1.
PROSITE; PS0141; TRYPSIN 1: 1.
PROSITE; PS0141; TRYPSIN 1: 1.
PROSITE; PS0141; TRYPSIN 1: 1.
PROSITE; PS0141; TRYPSIN 1: 1.
PROSITE; PS0141; TRYPSIN 1: 1.
PROSITE; PS0141; TRYPSIN 1: 1.
PROSITE; PS0141; TRYPSIN 1: 1.
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P11214; Q91VP2;
01-JUL-1989 (Rel. 11, Created)
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es 64; Conservative 1
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RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA MIEDLINE-22388257; PubMed=12477932;

RA MIEDLINE F.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,

RA Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Altschenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Raha S.S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.M.,

RA Rahes S.W., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.M.,

RA Rahey J., Halton E., Ketteman M.W., Madan A., Rodrigues S., Sanchez A.,

RA Blakesley R.W., Touchman J.W., Greeten E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schwutz J., Myers R.M.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

RA Schneration and initial analysis of more than 15,000 full-length human mouse CDNA sequences.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and mouse CDNA sequences.";

Proc. Natl. Acad. Sci. U.S.A. 99.16899-16903(2002).

-!- FONCTION: CONVERTS THE ABUNDANT, BUT INACTIVE, ZYMOCEN PLASMINOGEN.
TO PLASMIN BY HYDROLYZING A SINGLE AGGAVAL BOND IN PLASMINOGEN. BY CONTROLLING PLASMIN-MEDIATED PROTECLYSIS, IT PLAYS AN IMPORTANT ROLE IN TISSUE REMODELING AND DEGRADATION, IN CELL MIGRATION AND MANY OTHER PHYSIOPATHOLOGICAL EVENTS.

-!- CATALYTIC ACTIVITY: Specific cleavage of Arg-|-Val bond in plasminogen to form plasmin.

-!- SIBUNIT: HETERODIMER OF CHAIN A AND CHAIN B HELD BY A DISULFIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE-88087303; PubMed=2826484;
Rickles R.J., Darrow A.L., Strickland S.;
"Molecular cloning of complementary DNA to mouse tissue plasminogen activator mRNA and its expression during F9 teratocarcinoma cell
                                                                                                          Eukaryota; Medazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI TaxID=10090;
5-SEP-2003 (Rel. 42, Last sequence update)
5-SEP-2003 (Rel. 42, Last annotation update)
issue-type plasminogen activator precursor (EC 3.4.21.68) (tPA)
                                                                                                                                                                                                                                                                                    differentiation.";
J. Biol. Chem. 263:1563-1569(1988)
                                                         (t-PA) (t-plasminogen activator)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL, JO3520; AAA40470.1; -.
EMBL; BC011256; AAH11256.1; -.
PIR; A29941; A29941.
HSSP; P00750; 1A5H.
                                                                                                Mus musculus (Mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE-TYPE PLASMINOGEN ACTIVATOR.
TISSUE-TYPE PLASMINOGEN ACTIVATOR A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CHAIN.
TISSUE-TYPE PLASMINOGEN ACTIVATOR B
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PROSITE; PS00070; KRINGLE 1; 2.
PROSITE; PS000340; TRYPSIN DOM; 1.
PROSITE; PS000134; TRYPSIN HIS; 1.
PROSITE; PS00135; TRYPSIN SER; 1.
Plasminogen activation; Hydrolase; Serine proteas
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MEROPS, SO1.232; ...
MGD, MGI:97640; Plat.
InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001319; EdF_like.
InterPro; IPR00130; EdF_like.
InterPro; IPR006210; IEGF.
InterPro; IPR006210; IEGF.
InterPro; IPR006210; Kringle.
InterPro; IPR00124; Ser_protease_Try.
Pfam; PF00009; Edf; 1.
Pfam; PF00009; Edf; 1.
Pfam; PF00099; Fal; 1.
Pfam; PF00099; Fal; 1.
PRINTS; PR00109; KRINGLE.
PRINTS; PR00109; KRINGLE.
PRODOM; PM00599; KRINGLE.
SWART; SM0059; KRINGLE.
SWART; SM0050; Tryp_SPC; 1.
SWART; SM0050; Tryp_SPC; 1.
PROSITE; PS01186; EGF_2; 1.
PROSITE; PS01186; EGF_2; 1.
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QCHSVPVRSCSEPRCFNGGTCQQALYFSDF-VCQCPDGFVGKRCDIDTRATCFEEQGITY 132
                   RGKASTDIMGRPCLPWNSAIVLQQIYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVG 118
                                 01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 31, Last sequence update)
48-FEB-2003 (Rel. 41, Last annotation update)
Salivary plasminogen activator alpha 1 precursor (EC 3.4.21.68) (DSPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- SUBDUTT: MORDONE.
-!- SUBDUTT: MORDONE.
-!- DOMAIN: THE FIBRONECTIN TYPE-I DOMAIN MEDIATES BINDING TO FIBRIN,
AND THE KRINGLE DOMAIN APPARENTLY MEDIATES FIBRIN-INDUCED
STIMULATION OF ACTIVITY.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY SI.
-!- SIMILARITY: Contains I EGF-like domain.
-!- SIMILARITY: Contains I fibronectin type I domain.
-!- SIMILARITY: Contains I fibronectin type I domain.
                                                                                                                                                                                                                                                                                                                                                                                                    "Plasminogen activators from the saliva of Desmodus rotundus (common vampire bat): unique fibrin specificity."; Ann: N.Y. Acad. Sci. 667:395-403(1992).
                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
TISSUE=SAlivary gland;
MEDLINE=92039036. PubMed=1937019;
Kraetzschmar J., Haendler B., Langer G., Boidol W., Bringmann P.,
Alagon A., Donner P., Schleuning W.D.;
The plasminogen activator family from the salivary gland of the
vampire bat Desmodus rotundus: cloning and expression.";
Gene 105:229-237(1991).
                                                                                                                                                                                                Desmodus rotundus (Vampire bat).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Chiroptera; Microchiroptera; Phyllostomidae;
Desmodontinae; Desmodus.
                                                                                                                                                                                                                                                                                                                                                                      Schleuning W.-D., Alagon A., Boidol W., Bringmann P., Petri T., Kraetzschmar J., Haendler B., Langer G., Baldus B., Witt W.,
                                                                                                                              477 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                            K-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                                                   CHARACTERIZATION.
MEDLINE=93393059; PubMed=1309059;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Salivary gland;
MEDLINE=98022741; PubMed=9354616;
                                                          119 LKPLVQECMVHDCADGK 135
                                                                             193 GKYTTEFCSTPACPKGK 209
                                                                                                                              STANDARD;
                                                                                                                                                                                                                                        NCBI_TaxID=9430;
                                                                                                                             URT1 DESRO
P98119;
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CC or send an email to licensesish-sib.ch).

BREAL, M6396; AAA119211.

BREAL, M6396; AAA119211.

BREAL, M6396; AAA11921.

BREAL, M6396; AAA11921.

BREAL, M6396; AAA11921.

BREAL, M6396; AAA11921.

BREAL, M6396; AAA11921.

BREAL, M6396; AAA11921.

BREAL, M6396; AAA1192.

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                                                             BOND.

-- SUBGELLULAR LOCATION: SECRETED, EXTRACELLULAR.

-- SUBGELLULAR LOCATION: SECRETED, EXTRACELLULAR.

-- SUBGELLULAR LOCATION: SECRETED, EXTRACELLULAR.

-- STACE-SIGNATE CHAIN FULLY ACTIVE FORM BY A CLEAVAGE AFTER ARC-314 CATALYZED BY PLASMIN, TISSUB KALLIKREIN OR FACTOR XA.

-- MISCELLANEOUS: BINDS TO THE KRINGLES STRUCTURE OF THE FIBRIN A CHAIN BINDING TO FIBRIN SHAHOMES ITS CATALYTIC ACTIVITY.

-- SIMILARITY: BELONGS TO PEPTIDASE FAMILY SI.

-- SIMILARITY: Contains 1 EGF-like domain.

-- SIMILARITY: Contains 2 kringle domains.
TO PLASMIN BY HYDROLYZING A SINGLE ARG-VAL BOND IN PLASMINOGEN. B CONTROLLING PLASMIN-MEDIATED PROPEDLYSIS, IT PLAYS AN IMPORTANT ROLE IN TISSUE REMODELING AND DEGRADATION, IN CELL MIGRATION AND ANY OTHER PHYSIOPATHOLOGICAL EVENTS.
                                                                                                                                                                                                                                                                                                                                                                             CATALYTIC ACTIVITY: Specific cleavage of Arg- -Val bond in plasminogen to form plasmin.
SUBUNIT: HETERODIMER OF CHAIN A AND CHAIN B HELD BY A DISULFIDE
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CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
BY SIMILARITY.
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InterPro; IRRO01314; Chymotrypsin.
InterPro; IRRO006309; EGF like.
InterPro; IRRO006319; Fibrnctnl.
InterPro; IRRO00631; Fibrnctnl.
InterPro; IRRO00631; Fibrnctnl.
InterPro; IRRO00631; Kringle.
InterPro; IRRO00631; Kringle.
Ffam; PF00099; EGF; 1.
Ffam; PF00099; trypsin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KRINGLE 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CHAIN.
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 61 KASIDIMGRPCLPWNSAIVLQQTYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVGLK 120
                                                                                                                                                                                                                                                                                                                                                     9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ravn P., Berglund L., Petersen T.E.; "Cloning and characterization of the bovine plasminogen activators uPA and tPA.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INC. Dairy J. 5:605-617(1995).
-!- FUNCTION: CONVERTS THE ABUNDANT, BUT INACTIVE, ZYMOGEN PLASMINOGEN
                                                                                                                                                                                                                                                                                                                                                                                                  5 HOVPSN-CD---CLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFYRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bos taurus (Bovine).
Eukaryota, Metazoa; Chordata, Craniata, Vertebrata, Euteleostomi,
Bommalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
Bovidae, Bovinae, Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TPA BOVIN STANDARD; PRT; 566 AA.
Q28198;
Q28198;
G1-NOV-1997 (Rel. 35, Last sequence update)
O1-NOV-1997 (Rel. 41, Last annotation update)
Tissue-type plasminogen activator precursor (EC 3.4.21.68) (tPA)
(t-PA) (t-plasminogen activator).
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                                                                                                                                                                                                                                                                                           53616 MW; AA06FD1739C10E5E CRC64;
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                                                                                                                                                                                                                                                                                                                        Best Local Similarity 45.5
Matches 60; Conservative
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[1]
SEQUENCE FROM N.A.
TISSUE=Kidney;
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ALPHA-FACTOR XIIA LIGHT
FIBRONECTIN TYPE-II.
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EGF-LIKE 2.
KRINGLE.
       -!- SIMILARITY: Contains 2 EGF-like domains.
-!- SIMILARITY: Contains 1 kringle domain.
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HSSP, P00763; 1DPO.
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Rambaru T., Okabe H.;
Rambara T., Okabe H.;
Rembaru T., Okabe H.;
Purnimary structure of guinea-pig Hageman factor: sequence around the rightmary structure of guinea-pig Hageman factor: sequence around the primary structure of guinea-pig Hageman factor: sequence around the structure of guinea-pig Hageman factor: sequence around the structure of guinea-pig Hageman factor: sequence around the structure of guinea-pig Hageman factor: sequence around the structure of guinea-pig Hageman factor: sequence around the structure of guinea-pig Hageman factor: sequence around the sequence of sequence around the structure sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequen
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                                                                                                                                                                                                                                                                                                                                                                                                                  5; Gaps
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Hystricognathi, Caviidae, Cavia.
MCBI_TaxID=10141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Coaquiation factor XII precursor (EC 3.4.21.38) (Hageman factor)
(HAF) (Fragment).
                                                                                                                                                                                                                                                                                                  N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
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TISSUE=Liver;
MEDLINE=93003367; PubMed=1390917;
                                                                                                                                                                                                                                                                                                                                                                             DB 1; Length 566;
                                                                                                                                                                                                                                                                                                                                                                         th 35.9%; Score 300.5; DB 1; Length 56
l Similarity 44.0%; Pred. No. 9.9e-22;
59; Conservative 16; Mismatches 54; Indels
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 Query Match
Best Local Similarity
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182 CLNGGRCLE---VEGHHLCDCPMGYTGPFCDLDTTASCYEGRGVSYRGMARTTVSGAKCQ 238
                                                                                                                                                                                                                                                                                                            73 PWNSATVLQQTYHAHRSD-ALQLGLGKHNYCRNPDNRRRPWCYVQVGLKPLVQECMVHDC 131
                                                                                                                                                                                                                                                                                                                             239 RWAS----EATYRNMTAEQALRRGLGHHTFCRNPDNDTRPWCFVWMGNRLSWEYCDLAQC 294
                                                                                                                                                                                                                                                        72
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Miyazawa K., Shimomra T., Kitamura A., Kondo J., Morimoto Y., Kitamura N., Kitamura N., Kitamura N., Morimoto Y., Kitamura N., Molecular cloning and sequence analysis of the CDNA for a human serine protease reponsible for activation of hepatocyte growth factor. Structural similarity of the protease precursor to blood coagulation factor XII.", J. Biol. Chem. 268:10024-10028(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                HGFA HUMAN STANDARD; PRT; 655 AA.

Q04756; Q14726;
01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
activatory growth factor activator precursor (EC 3.4.21.-) (HGF HGFAC.
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                                                                                                                                                                                              32.0%; Score 268; DB 1; Length 603; 38.6%; Pred. No. 1.5e-18; Live 21; Mismatches 52; Indels
                                                                                                                                                                      48DC6B946FB9ED59 CRC64;
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TICHELL FROM N.A., AND PARTIAL SEQUENCE.
TISSUB-Liver, and Serum;
MEDLINE-93252878; PubMed=7683665;
                                                                                                                                                                     66795 MW;
                                                                                                                                                                                                                            51; Conservative
                                                                                                                                                                                                                                                                                                                                                                   132 ADGKKPSSPPEE 143
                                                                                                                                                                                                                                                                                                                                                                                             295 QYPPQPTATPHD 306
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  Similarity
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                     EMBL; AF209117 AAF01499-11 --

BEMBL; AF204124; AAF34712.1; --

BEMBL; AF204124; AAF34712.1; --

BEMBL; AF204124; AAF34712.1; --

BERCHER, FOOTS3; 1DFO.

BERCHER, FOOTS3; 1DFO.

BERCHER, INFOOTS4; EGF_2.

BERCHER, IPRO00142; EGF_2.

BERCHER, IPRO0003; EGF_11Ke.

BERCHER, IPRO0003; EGF_11Ke.

BERCHER, IPRO0003; EGF_11Ke.

BERCHER, IPRO0001; Kringle.

BERCHER, FOOTS4; Kringle, 1.

BERCHER, FOOTS5; Kringle, 1.

BERCHER, FOOTS5; Kringle, 1.

BERCHER, FOOTS5; Kringle, 1.

BERCHER, FOOTS5; Kringle, 1.

BERCHER, FOOTS5; Kringle, 1.

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BERCHER, FOOTS6; FRY, 1.

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BERCHER, FOOTS6; FRY, 1.

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           SIMILARITY: Contains 2 EGF-like domains. SIMILARITY: Contains 1 fibronectin type I domain. SIMILARITY: Contains 1 fibronectin type II domain. SIMILARITY: Contains 1 kringle domain.
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EGF-LIKE 1.
FIBRONECTIN TYPE-I.
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           242 HTACLSSPCLNGGTC-----HLIVATGTTVCACPPGFAGRLCNIEPDERCFLGNGT 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    57 FYRGKASTDIMGRPCLPWNSAIVLQQIYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQ 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            293 GYRGVASTSASGLSCLAWNSDLLYQELHVDSVGAAALLGLGPHAYCRNPDNDERPWCYVV 352
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.

Van Adelsberg J.S., Sehgal S., Kukes A., Brady C., Barasch J.,

Yang J., Huan Y.;

Yang J., Huan Y.;

Mactivation of HGF by endogenous HGF activator is required for
metanephric kidney morphogenesis in vitro.";

Submirted (JAN-2000) to the EMEL/GenBank/DDBJ databases.

IT FROM A SINGLE CHAIN TO A HETERODIMERIC FORM (BY SIMILARITY).

SUBMILT: DIMER OF A SHORT CHAIN AND A LONG CHAIN LINKED BY A
DISULFIDE BOND (BY SIMILARITY).

SUBCELLULAR LOCATION: SECRETED AS AN INACTIVE SINGLE-CHAIN
PRECURSOR AND IS THEN ACTIVATED TO A HETERODIMERIC FORM (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         57; Indels 30; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse).
Skaryota: Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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99R038; Q9JKV4;
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
activator) (HGFA).
                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Score 262; DB 1; Length 655;
; Pred. No. 6e-18;
12; Mismatches 57; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Itch H., Kataoka H., Koono H.; "Mouse hepatocyte growth factor activator."; Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    117 VGLKPLVQECMVHDC------ADGKKPSSP 140
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36.9%;
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WRIANT TENRI CYS-53.

WRELINE=9990785; PubMed=10361128;

MEDLINE=9990785; PubMed=10361128;

Kondo S., Tokunaga F., Kawano S., Ono Y., Kumagai S., Koide T.;

Kondo S., Tokunaga F., Kawano S.,

Tofficiency, occurs through a proteasome-mediated degradation.";

Blood 93:4300-43300-4308 [1999].

The Intra Trons FACTOR XII IS A SERUM GLYCOPROTEIN THAT PARTICIPATES IN THE INITIATION OF BLOOD COAGULATION, FIBRINOLYSIS, AND THE GENERALTON OF BRADYKININ AND ANGIOTENBIN.

CHARLYTIC ACTIVITY: Cleaves selectively Arg-|-1le bonds in factor VII to form factor VIIa and factor XI to form factor XIa.

VII to form factor VIIa and factor XI to form factor XIa.

CHARLYTIC ACTIVITY: Cleaves selectively Arg-|-1le bonds in factor VII to FDM: O AND N-GLYCOSYLATED.

CHARLY STANDARD ON CLOATING SYMPTOMS. THE SOLE EFFECT IS THAT WHOLE-BLOOD CLOTTING TIME IS PROLONGED.

CHARLY STANDARD ON THE STANDARD NOR AND HWW KININGGEN FORM A
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           "Characterization of human blood coagulation factor XII cDNA. Prediction of the primary structure of factor XII and the tertiary structure of beta-factor XIIa.";
J. Biol. Chem. 260:13666-13676(1985).
                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=85182674; PubMed=3886654;
McMullen B.A., Fujikawa K.;
"Amino acid sequence of the heavy chain of human alpha-factor XIIa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Coagulation factor XII (Hageman factor) Washington D.C.: inactive factor XIIa results from Cys-571-->Ser substitution.";
Proc. Natl. Acad. Sci. U.S.A. 86:8319-8322(1989).
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MEDLINE-94325559; PubMed=8049433;
Hovinga J.K., Schaller J., Stricker H., Wuillemin W.A., Furlan M.,
Laemmle B.;
                                                                                                                                                                                                             Que B.G., Davie E.W.; "Characterization of a cDNA coding for human factor XII (Hageman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CARBOHYDRAIE-LINKAGE SITE THR-109.
MEDLINE-92184750; PubMed=1544894;
Harris R.J., Ling V.T., Spellman M.W.;
"O-linked fuccose is present in the first epidermal growth factor domain of factor XII but not protein C.";
J. Biol. Chem. 267:5102-5107(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VARIANT WASHINGTON D.C. SER-590.
MEDLINE=90046788; PubMed=2510163;
Miyata T., Kawabata S.-I., Iwanaga S., Takahashi I., Alving
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=96133302; PubMed=8528215;
Schloesser M., Hofferbert S., Bartz U., Lutze G., Lammle
"The novel acceptor splice site mutation 11396(G-->A) in
XII gene causes a truncated transcript in cross-reacting in
negative patients.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 354-362 AND 373-615.
MEDLINE-83291041; PubMed=6604055;
Fujikawa K., McMullen B.A.;
"Amino acid sequence of human beta-factor XIIa.";
J. Biol. Chem. 258:10924-10933(1983).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (activated Hageman factor).";
J. Biol. Chem. 260:5328-5341(1985)
                                                                                                                                               SEQUENCE OF 146-615 FROM N.A.
MEDLINE=86216049; PubMed=3011063;
Que B.G., Davie E.W.;
                                                                                                                                                                                                                                                                factor).";
Biochemistry 25:1525-1528(1986)
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           239 HTACLSSPCLNGGTC-----HLIVGTGTSVCTCPLGYAGRFCNIVPTEHCFLGNGT 289
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   290 EYRGVASTAASGLSCLAWNSDLLYQELHVDSVAAAVLLGLGPHAYCRNPDKDERPWCYV 348
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Nucleic Acids Res. 14:3146-3146(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             [1] = SEQUENCE FROM N.A. SEQUENCE FROM N.A. MEDLING=88007593; PubMed=2888762; MEDLING=88007593; PubMed=2888762; Cool D.E., McGillivray R.T.A.; "Characterization of the human blood coagulation factor XII gene. Intron/exon gene organization and analysis of the 5'-flanking
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FA12_HUMAN STANDARD; PRT; 615 AA.
P00746, P70339, P70339, 01
21_UUL-1966 (Rel. 01, Created)
01_OCT-1989 (Rel. 12, Last sequence update)
28_FEB-2003 (Rel. 41, Last annotation update)
Coagulation factor XII precursor (EC 3.4.21.38) (Hageman factor)
(HAF).
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MEDLINE=86033830; PubMed=3877053;
Cool D.E., Edgell C.-J.S., Louie G.V., Zoller M.J., Brayer G.D.
McGillivray R.T.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Score 250.5; DB 1; Length 653; Pred. No. 7.7e-17; 11; Mismatches 41; Indels 17;
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SEQUENCE FROM N.A., AND VARIANTS ALA-207; ASP-545 AND HIS-605.
Rieder M.J., Armel T.Z., Carrington D.P., Ozuna M., Kuldanek & Rajkumar N., Toch E.J., Yi Q., Nickerson D.A.; at Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.
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SEQUENCE 96176794; PubMed=3754331;
Tripodi M., Citarella F., Guida S., Galeffi P., Fantoni A.,
Cortese R.;
                                                                                                                                                                          SIMILARITY).
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FA12 HUMAN
AC P00748,
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DT 21-07U-
DT 28-FEB-
DE (HAF).
GN F12.
GN HUMON SK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Plasminogen activators from the saliva of Desmodus rotundus (common vampire bat): unique fibrin specificity.";
Ann. N.Y. Acad. Sci. 667:395-403 (1992).
-!- FUNCTION: PROBABLY ESSENTIAL TO SUPPORT THE FEEDING HABITS OF THIS EXCLUSIVELY HAEMATOPHAGOUS ANIMAL. PROBABLE POTENT THROMBOLYTIC
                                                                            SERINE PROTEASE.

O-LINKED (FUC).

N-LINKED (GUCNAC. . .).

O-LINKED (POTENTIAL).

O-LINKED (POTENTIAL).

O-LINKED (POTENTIAL).

O-LINKED (POTENTIAL).

O-LINKED (POTENTIAL).

O-LINKED (POTENTIAL).

CHANGE RELAY SYSTEM (BY SIMILARITY).

CHANGE RELAY SYSTEM (BY SIMILARITY).
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01-FEB-1996 (Rel. 33, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Salivary plasminogen activator gamma precursor (EC 3.4.21.68) (DSPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Desmodus rotundus (Vampire bat).
Eukaryota: Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Chiroptera; Microchiroptera; Phyllostomidae;
Desmodontinae; Desmodus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.

TISSUB-Salivary gland;

MEDLINE-2019vary gland;

MEDLINE-2019vary gland;

MEDLINE-2019vary gland;

Kraetzschnar J., Haendlar B., Langer G., Boidol W., Bringmann P.,

Alagon A., Donner P., Schleuning W.D.;

The plasminogen activator family from the salivary gland of the

vampire bat Desmodus rotundus: cloning and expression.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=93393059; PubMed=1309059;
Schleuning W.-D., Alagon A., Boidol W., Bringmann P., Petri T.,
Kraetzschmar J., Haendler B., Langer G., Baldus B., Witt W.,
                                                                                                                                                                                                                                                                                   ..
60
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-| Plasminogen to form plasmin.
-| SUBUNIT: Monomer.
-| SIMILARITY: BELONGS TO PEPTIDASE FAMILY SI.
-| SIMILARITY: Contains 1 kringle domain.
                                                                                                                                                                                                                                                     ; Score 233; DB 1; Length 615; 
; Pred. No. 3.6e-15; 
12; Mismatches .40; Indels
                                                                                                                                                                                                                                                                                                                                                                    73 PWNSATVLQQTY-HAHRSDALQLGLGKHNYCRNPDNRRRPWCYV 115
                                                                                                                                                                                                                                                                                                                                                                                     240 PWAS----EATYRNVTAEQARNWGLGGHAFCRNPDNDIRPWCFV 279
FIBRONECTIN TYPE-II.
             EGF-LIKE 1.
FIBRONECTIN TYPE-I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       394 AA
                                         EGF-LIKE 2.
                                                                      PRO-RICH
                                                     KRINGLE
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                                                                                                                                                                                                                                                                      Similarity
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CHARACTERIZATION.
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or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DKSKTCYEGNGHFYRGKASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRN 104
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R InterPro; IPR00114; Chymotrypsin.

R InterPro; IPR001201; Kringle.

R EnterPro; IPR00121; Kringle.

R Pfam; PF00089; trypsin; 1.

R PRINTS; PR00072; CHYMORRYPSIN.

R RINTS; PR00018; KRINGLE.

R RMART; SM00103; KRINGLE.

R RMART; SM00103; KRINGLE.

R ROSITE; PS00021; KRINGLE.

R ROSITE; PS00021; TRYPSIN.

R ROSITE; PS00013; TRYPSIN.HIS; 1.

R ROSITE; PS000135; TRYPSIN.HIS; 1.

R ROSITE; PS00135; TRYPSIN.HIS; 1.

R ROSITE; PS00135; TRYPSIN.HIS; 1.

R ROSITE; PS00135; TRYPSIN.HIS; 1.

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R ROSITE; PS00135; TRYPSIN.HIS; 1.

R ROSITE; PS00135; TRYPSIN.HIS; 1.
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CHARGE RELAY SYSTEM (BY SIMILARITY).
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
                                                                                                                                                                                                                                                                                                                                                                                                                                            SALIVARY PLASMINOGEN ACTIVATOR GAMMA.
KRINGLE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY).
SIMILARITY).
SIMILARITY).
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ID _FR12 BOUIN

AC P01425.

DT 01-FEB-1996 (Rel. 33, Created)

DT 01-FEB-1996 (Rel. 33, Last sequence update)

DT 02-FEB-2003 (Rel. 41, Last annotation update)

DE Coagulation factor XII precursor (EC 3.4.21.38) (Hageman factor)

DE (HAF) (Fragment).

GN F12.

GN F12.

GN F12.

GN F12.

GN F12.

GN F12.

GN F12.

Coagulation (Coardiate)

GN F13.

Coagulation (Coardiate)

GN F13.

Coagulation (Coardiate)

GN F13.

Coagulation (Coardiate)

Coagulation (Coardiate)

Coagulation (Coardiate)

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Coagulation (Coardiate)
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                                                                                                       EMBL, M63990, AAA31595.1; -. \
PIR, J80600, J80600.
HSSP, P98119; 1A51.
MEROPS, S01.239; -.
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394 AA;
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TECTORY...

Biochemistry 16:2270-2278 (1977)

C. I- FUNCTION: FACTOR XII IS A SERUM GLYCOPROTEIN THAT PARTICIPATES IN THE INITIATION OF BLOOD COAGULATION, FIBRINGLYSIS, AND THE GENERATION OF BLADDYRININ AND ANGIOTENSIN.

C. CATALYTIC ACTIVITY: Cleaves selectively Arg-|-I-le bonds in factor VII to form factor VII and factor XI to form factor XII.

C. I- PTM: O. AND N-GLYCOSYLATED (BY SIMILARITY)

C. I- PTM: O. AND N-GLYCOSYLATED (BY SIMILARITY)

C. I- PTM: O. AND N-GLYCOSYLATED (BY SIMILARITY)

C. I- ALPHA-FACTOR XII. PREKALLIKEREN IS CLEAVED BY COMPLEX BOUND TO AN ANIONIC SURPACE. PREKALLIKEREN IS CLEAVED BY COMPLEX BOUND TO AN ANIONIC SURPACE. PREKALLIKEREN IS CLEAVED BY COMPLEX BOUND TO AN ANIONIC SURPACE. PREKALLIKERIN ALPHA-FACTOR XII. A LAPHA-FACTOR XII. A LAPHA-FACTOR XII. A SIMILARITY: DELONGS TO PEPTIDASE FAMILY SI.

C. CLEAVED DOLLY TO ALPHA-FACTOR XIIA AS IT LACKS THE TRYPSIN/

KALLIKERIN CLEAVAGE SITE.

C. SIMILARITY: Contains I fibronectin type I domain.

C. SIMILARITY: Contains I fibronectin type II domain.
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                                                                                                                  TISSUE-Liver;

MEDLINE=9442782; PubMed=8186251;

Shibuya Y., Semba U., Okabe H., Kambara T., Yamamoto T.;

Shibuya Y., Semba U., Okabe H., Kambara T., Yamamoto T.;

"Primary structure of bovine Hageman factor (blood coagulation factor
"Primary structure of bovine Hageman factor (blood coagulation factor
"It comparison with human and guinea pig molecules.";

Biochim. Biophys. Acta 1206:63-70(1994).
                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 10-21, 350-364 AND 525-550.
MEDIANE=712112; PubMed=861210;
FUIKAWA X., Walsh A.K., Davie W.E.;
"Isolation and characterization of bovine factor XII (Hageman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR001314, Chymotrypsin.
InterPro; IPR001209, EGF like.
InterPro; IPR000083, Fibrnctnl.
InterPro; IPR000562; FN Type_II.
InterPro; IPR006510; IEGF.
InterPro; IPR001018, Kringle.
InterPro; IPR001254; Ser_protease_Iry.
Pfam; PF00008; EGF; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PEAM: PF00008; EGF; 2. PF00085-LIFY.

PEAM: PF00008; EGF; 2. PF00005-LIFY.

PEAM: PF00005; FILS; 1. PEAM: PF00005; LIZY.

PRINTS; PR00013; FNTYPEIN: 1. PRINTS; PR00013; FNTYPEIN: PF00009; RRINGLE.

PF000M: PD000995; RNINGLE.

PF000M: PD000395; RNINGLE.

PF000M: PM0013; FNIN; 1. SWART; SW00181; EGF; 2. SWART; SW00059; FNI; 1. SWART; SW00059; FNI; 1. SWART; SW00059; FNI; 1. SWART; SW00059; FNI; 1. SWART; SW00059; Tryp. SPC; 1. PROSITE; PS001020; Tryp. SPC; 1. PROSITE; PS001086; EGF_2; FALSE NEG.

PROSITE; PS01186; EGF_2; FALSE NEG.

PROSITE; PS01186; EGF_2; FALSE NEG.
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HSSP; P00763; 1DPO.
MEROPS; S01.211; -.
                                                                      SEQUENCE FROM N.A.
NCBI_TaxID=9913,
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TILSGAPCQSWAS----EATYWNVTAEQVLNWGLGDHAFCRNPDNDTRPWCFIWKGDRLS 278
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R PROSITE; PS00023; FIBRONECTIN_2; 1.

R PROSITE; PS00021; KRINGLE 1; 1.

R PROSITE; PS50240; TRYPSIN_DOM; 1.

R PROSITE; PS50240; TRYPSIN_DOM; 1.

R PROSITE; PS00134; TRYPSIN_ER; 1.

R PROSITE; PS00134; TRYPSIN_ER; 1.

R PROSITE; PS00134; TRYPSIN_ER; 1.

R PROSITE; PS00134; TRYPSIN_ER; 1.

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R PROSITE; PS00134; TRYPSIN_ER; 1.

R PROSITE; PS00134; TRYPSIN_TRYPE_II.

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28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Tyrosine-protein kinase transmembrane receptor Ror precursor (EC 2-7.112) (dRor).
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OC Norsophila melangester (First 11),

CONTRICTOR WELLORD ARTHOGODA, HARADODA, INSECTA, PRECYDER,

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STDIMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDN-RRRPWCYVQVGLKP 121

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                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PSO0130; KR; 1.
PROSITE; PSS0039; FZ; 1.
PROSITE; PSS0019; FZ; 1.
PROSITE; PSS0010; FRINGLE 1; 1.
PROSITE; PSS0010; PROTEIN_KINASE_DOM; 1.
PROSITE; PSS0010; PROTEIN_KINASE_DOM; 1.
PROSITE; PSS0010; PROTEIN_KINASE_DOM; 1.
PROSITE; PS00109; PROTEIN_KINASE_TOM; 1.
PROSITE; PS00139; RECEPTOM_TYR_KIN_II; 1.
PROSITE; PS00239; RECEPTOM_TYR_KIN_II; 1.
TRANSFEARSE; Kinase; Tyrosine-protein kinase; ATP-binding; Receptor; Iransmembrane; Signal; Glycoprotein; Kringle; Phosphorylation;
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TYROSINE-PROTEÍN KINASE TRANSMEMBRANE
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                                                                                                                                   EMBL; L20297; AAA28860.1; --
EMBL; AE002628; AAF52885.1; --
EMBL; AA002908; CAA05743.1; --
PIR; A48289; A42289.
HSSP; P11362, 1FGK.
FlyBase; FBGn0010407; Ror.
GO, GO:0016621; C:integral to membrane; NAS.
GO; GO:000413; F:protein tyrosine kinase activity; NAS.
GO; GO:000417; P:central nervous system development; IEP.
GO; GO:0006488; P:protein amino acid phosphorylation; NAS.
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    -!- SIMILARITY: Contains 1 kringle domain.

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InterPro; IPR000021; KrIngle.
InterPro; IPR000011; KrIngle.
InterPro; IPR000119; Pro: Kingse.
InterPro; IPR002011; RTKingseII.
InterPro; IPR001245; Tyr_pkingse.
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PROMINS; PRODO19; TYRKINASE.
PRODON; PROD00395; Kringle; 1.
PRODOM; PD000001; Prot_kinase; 1.
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Pfam, PF00069; pkinase;
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MEDLINE=21303595; PubMed=11294842;
Garner B., Merry A.H., Royle L., Harvey D.J., Rudd P.M., Thillet J.;
Structural elucidation of the N- and O-glycans of human
apolipoprotein(a): role of o-glycans in conferring protease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WEDLINE=9502201; PubMed=7918682;
Scann A.M., Pfaffinger D., Lee J.C., Hinman J.;
Scann A.M., Pfaffinger D., Lee J.C., Hinman J.;
A single point mutation (Trp72-->Arg) in human apo(a) kringle 4-37
associated with a lysine binding defect in Lp(a).";
Blochim. Biophys. Acta 122741-4511994).
-: FUNCTION: Apo(a) is the main constituent of lipoprotein(a)
(Lp(a)). It has serine proteinase activity and is able of autoproteolysis. Inhibits tissue-type plasminogen activator 1.
Lp(a) may be a ligand for megalin/Gp 330.
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MINDLINES-86217891, PUDMEd=86462595,

Mikol V., Lograsso P.V., Boettcher B.R.;

"Crystal structures of apolipoprotein(a) kringle IV37 free and complexed with 6-aminohexanoic acid and with p-aminomethylbenzoic acid; existence of novel and expected binding modes.";

J. Mol. Biol. 256:751-761(1996).
                                                                                                                                                                                                                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE=88039109; PubMed=3670400;
MCLean J.W., Tomlison J.E., Kuang W.-J., Eaton D.L., Chen E.Y.,
Fless G.M., Scanu A.W., Lawn R.M.;
"CDNA sequence of human apolipoprotein(a) is homologous to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=90076123; PubMed=2531657; Salonen E.-M., Jauhiainen M., Zardi L., Vaheri A., Ehnholm C., "Lipoprotein(a) binds to fibronectin and has serine proteinase activity capable of cleaving it."; EMBO J. 8:4035-4040(1989).
                                                                                                                                                                                                                             01-AUG-1988 (Rel. 08, Created)
1-AUG-1988 (Rel. 08, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Apolipoprotein(a) precursor (EC 3.4.21.-) (Apo(a)) (Lp(a)).
                                                                                                                                                                                         PRT; 4548 A.A.
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Science 246:904-910(1989).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nature 330:132-137(1987).
                                                       122 LVQECMVHDCAD 133
                                                                                          301 IIELCDIPKCAD 312
                                                                                                                                                                                         STANDARD;
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                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9606;
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Best Loc Matches

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Q92484;
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                                                                                                                                                                                                                                                    DISEASE: Blevated plasma concentrations of apo(a) and its naturally occurring proteolytic fragments are correlated with arthrashly occurring proteolytic fragments are correlated with arthrashlogom kringles IV and V is thought to underlie the atherogenicity of the protein, because the fragments are competing with plasminogen for fibrin(ogen) binding. MISCELLANEOUS: Apo(a) is known to be proteolytically cleaved, leading to the formation of the so called mini-lp(a). Apo(a) fragments accumulate in atherosclerotic lesions, where they may promote thrombogenesis. O-glycosylation may limit the extent of proteolytic fragmentation. Observable SIMILARITY: BELONGS TO PEPTIDASE FAMILY SI. PLASMINOGEN SUBFAMILY. SIMILARITY: Contains 38 kringle domains.
               TYPE. N. and O-glycosylated. The N-glycans are complex biantennary structures present in either a mono- or disialylated state. The O-glycans are mostly (80%) represented by the monosialylated core type I structure, NeuMakcalpha2-3Galbeta1-3GalNAc, with smaller amounts of disialylated and non-sialylated O-glycans also
SUBUNIT: Disulfide-linked to apo-B100. Binds to fibronectin and
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3742 NVRWEYCNLTOCPVTESSVLATSTAVSEQAPTEQSPTVQDCYHGDGQSYRGSFSTTVTGR 3801
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28-FEB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Kremen protein in precursor (Kringle-containing protein marking the eye and the nose) (Dickkopf receptor).
KREMENI OR KREMENI
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Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Receptor for Dickkopf protein. Cooperates with Dickkopf
to block wnt/Deta-catenin signaling (By similarity).
-!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rattus norvegicus (Rat).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
NCBI_TaxID=10116;
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4548 AA; 501313 MW; 96921BE96A465C5F CRC64;
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Best Local Similarity 33.1.,
Thes 41; Conservative
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50 CYEGNGHFYRGKASTDIMGRPCLPWNSATVLQ--QTYHAHRSDALQLGLGKHNYCRNPDN 107
 MEDLINE=89174660; PubMed=2925643;
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EMBL, AB065090; BAB62003.1; -

R GO; GO:0016021; C:integral comembrane; ISS.

InterPro; IPR000869; CUB domain.

R InterPro; IPR002889; WSC.

R Fam; PF00431; CUB; I.

R Pfam; PF00431; CUB; I.

R Pfam; PF00018; KRINGLE; I.

R PRODG; PF0000395; KRINGLE; I.

R RMART; SM00130; KR: I.

R RMART; SM00130; KR: I.

R RMART; SM00130; KR: I.

R RNOSITE; PS00101; KRINGLE 1; I.

R RNOSITE; PS00021; KRINGLE 2; I.

R PROSITE; PS00021; KRINGLE 2; I.

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R PROSITE; PS00021; KRINGLE 1; I.
                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the buropean Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      47 SKTCYEGNGHFYRGKASTDTM--GRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRN 104
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Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae,
Cercopithecinae, Macaca.
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Pred. No. 2.5e-08;
7; Mismatches 28; Indels
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01-JAN-1990 (Rel. 13, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Apolipoprotein(a) (EC 3.4.21.-) (Apo(a)) (Lp(a)) (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EXTRACELLULAR (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
KRINGLE.
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9B510857DF856F08 CRC64;
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-!- SIMILARITY: Contains 1 CUB domain.
-!- SIMILARITY: Contains 1 kringle domain.
-!- SIMILARITY: Contains 1 WSC domain.
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SEQUENCE FROM N.A.
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Synthesis.";

J. Biol. (Chem. 264:5857-5965(1889)

J. Biol. (Chem. 264:5857-5965(1889)

Libiol. Chem. 264:5857-5965(1889)

Libiol. Chem. 264:5857-5965(1889)

Libiol. Chem. 264:5857-5965(1889)

Libiol. Libiol. It has serine proceinase activity and is able of attoproteolysis. Inhibits tissue-type plasminogen activator 1.

Lip(a) may be a liganic for megalin/Gp 330.

Lip(a) may be a liganic for megalin/Gp 330.

Lipiol. Dislates. Elevated plasma concentrations of apo(a) and its and 0-glycosylated (By similarity).

Lipiol. Since and 0-glycosylated (By similarity).

Lipiol. Dislates. Elevated plasma concentrations of apo(a) and its anternacions of the protein, because the thought to underlie the atherogenicity of the protein, because the fragments are competing with plasminogen for fibrin (ogen) binding.

Commonte thrombogenesis. Or placesolarotic legions, where they may promote thrombogenesis. Or placesolarotic legions, where they may promote thrombogenesis. Or placesolarotic legions, where they may promote thrombogenesis. Or placesolarotic legions.

SIMILARITY: Contains at lesst 10 kringle domains.
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Tomlinson J.E., McLean J.W., Lawn R.M.; "Rhesus monkey apolipoprotein(a). Sequence, evolution, and sites
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    953 1031 KRINGLE 9.
1067 1145 KRINGLE 10.
1191 1420 SERINE PROTEASE.
1420 AA; 158367 MW; BE102949E03CSB0E CRC64;
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InterPro; IPR001001; Kringle.
InterPro; IPR001254; Ser_protease_Try.
Pfam; PF00051; Kringle; II.
Pfam; PF00089; trypsin; 1.
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31.4%; Pred. No. 5.8e-08;
tive 12; Mismatches 66
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  CHYMOTRYPSIN
              PR00018; KRINGLE.
PR01505; PROTHROMBIN.
PD000395; Kringle; 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 49; Conservative
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365
810 AA;
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  PR00722;
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1068 CYHGNGQSYRGTFSTTVTGRTCQSWSSMTPHQHKRTPENHPNDDLTM-----NYCRNPDA 1122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PICAGLES.

SECULATION: CONVERTED INTO PLASMIN BY PLASMINOGEN
ACTIVATORS BETH PLASMINOGEN AND ITS ACTIVATOR BEING BOUND TO
FIBRIN. ACTIVATED BUTH CATALYTIC AMOUNTS OF STREPTOKINASE.

MISCELLANEOUS: PLASMIN IS INACTIVATED BY ALPHA-2-ANTIPLASMIN
IMMEDIATELY AFFER DISSOCIATION FROM THE CLOT.

MISCELLANEOUS: IN THE PRESENCE OF THE INHIBITOR, THE ACTIVATION
INVOLVES ONLY CLEAVAGE AFFER ARG-580, RESULTING IN 2 CHAINS HELD
ACTIVATION INVOLVES ALSO REMONS. WITHOUT THE INHIBITOR, THE
ACTIVATION INVOLVES ALSO REMOVAL OF THE ACTIVATION PEPTIDE.
SIMILARITY: CONTAINS 5 Kringle domains.
                                                                                                                                                                                                                                                                                                                                                       synthesis.",
J. Shol. Chem. 264:5957-5965(1989).

J. Biol. Chem. PLASMIN DISSOLVES THE FIBRIN OF BLOOD CLOTS AND ACTS AS

-!- FUNCTION: PLASMIN DISSOLVES THE FIBRIN OF BLOOD CLOTS AND ACTS AS

- BRRYONIC DEVELOPMENT, TISSUE REMODELING, TUMOR INVASION,

AND INFLAMMATION, IN OVULATION IT WEAKENS THE WALLS OF THE

GRAAFIAN FOLLICLE. IT ACTIVATES THE URCKINASE-TYPE PLASMINGEN

ACTIVATOR, COLLAGENASES AND SEVERAL COMPLEMENT ZYMOGENS, SUCH

AS CI AND CS. IT CLEBAVES FIBRIN, FIBRONECTIN, THROMBOSPONDIN,

LAMININ AND VON WILLEBRAND FACTOR.

-!- CATALYTIC ACTIVITY: PREFERENTIAL CHEAVES INTO THE CATALYTIC ACTIVITY: PREFERENT CONVERTS fibrin into soluble
                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE=89174660; PubMed=2925643;
Tomlinson J.E., McLean J.W., Lawn R.M.;
"Rhesus monkey apolipoprotein(a). Sequence, evolution, and sites of
                                                                                                                                                                                                                                        Euteleostomi;
                                                                                                                                                                                                                       Macaca mulatta (Rhesus macaque).

Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Eutele,
mamalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Macaca.
                                                                                                                                                          01-OCT-1989 (Rel. 12, Created)
01-OCT-1989 (Rel. 12, Last sequence update)
01-EBS-2003 (Rel. 14), Last annotation update)
Plasminogen precursor (EC 3.4.21.7)
                                                                                                                                  810 AA
                                                                DIGPWCFT --- MDPSVRREYCNLTRCSD 1147
                                        108 RRRPWCYVQVGLKPLVQE--CMVHDCAD 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR003609; Pan app.
InterPro; IPR003966; ProEhrombin.
InterPro; IPR001254; Ser protease_Try.
Pfan; PP00051; Kringle; 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR001314; Chymotrypsin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IPR000001; Kringle.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; J04697; AAA36901.1; -. PIR; B32869; B30848.
HSSP; P00747; 1PMK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PF00089; trypsin; 1.
                                                                                                                                  STANDARD;
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                                                                                                                                PLMN MACMU
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InterPro;
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                                                                 1123
                                                                                                       RESULT 25
PLMN MACMU
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487
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                                                                                                                                                                                 99
                                                                                                                                                                                                                                428 NPDADKGPWCFTTDPSVRWEYCNLKKCSGTEGSVAAPPPVAQLPDAETPSEEDCMFGNGK
                                                                                                                                                                               10 NCDCLNGGTCVSNKYFSNIHWCNCPKKFGGQ-------HCEIDKSKTCYEGNGH
                                                                                                                                   Gaps
965 O-LINKED (GALNAC. . .) (BY SIMILARITY)
90255 MW, A75ElC51AlA0F24A CRC64;
                                                                                                                                29;
                                                                               DB 1; Length 810;
                                                                                                                                Indels
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KRM1 MOUSE
Q99N43;
  CARBOHYD
SEQUENCE
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488 GYRGKKATTVTGTPCQEWAA-----QEPHSHRIFTPETNPRAGLEK-NYCRNPDGDVGGP 541
                                                                                                                                                              (Kringle-containing protein marking the eye
                                                                                                                                                                                                                                                                              Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
-!-PUNCINON: Receptor for Dickkopf protein. Cooperates with Dickkopf to block Wnt/bera-catenin signaling (By similarity).
-!-SUBCELLULAR LOCATION: Type I membrane protein (Potential).
-!-SIMILARITY: Conteains 1 CVB domain.
-!-SIMILARITY: Conteains 1 Kringle domain.
-!-SIMILARITY: Conteains 1 Kringle domain.
                                                                                                                                                                              Xenopus laevis (African clawed frog).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
Xenopodinae, Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CYTOPLASMIC (POTENTIAL).
                                             542 WCYT-TNPRKLFDYCDVPQCAASSPDCGKPQVBPKK 576
                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL, AB070851, BAB64294.1; -...
InterPro; IRR000869; CUB domain.
InterPro; IRR000869; CUB domain.
InterPro; IRR000801; Kringle.
Fam; PF00411; CUB; 1
Ffam; PF00421; Kringle; 1.
Ffam; PF00051; Kringle; 1.
Ffam; PF00051; Kringle; 1.
FroDom; PF000051; Kringle; 1.
SWART; SW00042; CUB; 1.
SWART; SW00130; KR; 1.
SWART; SW00131; WSC; 1.
SWART; SW00121; WSC; 1.
FROSITE; PS01180; CUB; 1.
FROSITE; PS01180; CUB; 1.
FROSITE; PS00021; KRINGLE 1; 1.
FROSITE; PS00021; KRINGLE 2; 1.
Who signaling pathway; Glycoprotein; Kringle; Iransmembrane; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (GLCNAC.
(GLCNAC.
(GLCNAC.
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(GLCNAC.
                                  112 WCYVQVGLKPLVQECMVHDCA----DGKKPSSPPEE
                                                                                                                              (Rel. 42, Created)
(Rel. 42, Last sequence update)
(Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KREMEN PROTEIN 1
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                                                                                                                                                            Kremen protein 1 precursor (Kring
and the nose) (Dickkopf receptor)
KREMEN1.
                                                                                                          STANDARD;
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390
452
                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. Nakamura T.;
                                                                                                                              15-SEP-2003
15-SEP-2003
15-SEP-2003
                                                                                                         KRM1 XENLA
Q90Y90;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22 CSDSFHSECYTVNGADYRGTQNOTSLDGGKPCLFWNE--TFOHPYNTLKYPNGEGGLGEH 79
                                                                                                                                                                             CEIDKSKTCYEGNGHFYRGKASTDTM--GRPCLPWNSATVLQQTYHAHRSDALQLGLGKH
                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28-FEB-2003 (Rel. 41, Created) .
28-FEB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
15-SEP-2003 (Rel. 42, Last annotation update)
Aremen protein 1 precursor (Kringle-containing protein marking the and the nose) (Dickkopf receptor).
KREMENI OR KREMEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
44 N-LINKED (GLCNAC. . .) (POTENTIAL).
50188 MW; ED24BCD1AF4564E2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A., DEVELOPMENTAL STAGE, AND TISSUE SPECIFICITY. TISSUE=Brain, and Kidney;
MEDLINE=21167372; Pubmed=11267660;
Nakamura T., Aoki S., Kitajima K., Takahashi T., Matsumoto K.,
                                                                                                                              4
                                                                         19.0%; Score 159; DB 1; Length 452; 40.8%; Pred. No. 3.7e-08; ive 9; Mismatches 32; Indels
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GO; GO:0016021; C:integral to membrane; NAS.
InterPro; IPR000899; CUB_domain.
InterPro; IPR000801; Kringle.
InterPro; IPR02889; WSC.
Pfam; PF00431; CUB; 1.
Pfam; PF001822; WSC; 1.
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HSSP; P00747; 1CBA.
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                                               Query Match
Query Match
Best Local Similarity 40.00.
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  344
452 AA;
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CARBOHYDRATE-LINKAGE SITES
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     50 CYEGNGHFYRGKASTDTM--GRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDN 107
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Malinowski D.P., Sadler J.E., Davie E.W.;
"Characterization of a complementary deoxyribonucleic acid coding for human and bovine plasminogen.";
human and bovine plasminogen.";
[4]
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Mammalia, Butheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
Bovidae, Bovinae, Bos.
NCBI_TaxID=9913,
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N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
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MEDLINE=88203906; PubMed=3846532;
Schaller J., Moser P.W., Dannegger-Muller G.A.K., Rosselet S.J.,
Kampfer U., Rickli E.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Berglund L., Andersen M.D., Petersen T.E.; "Cloning and characterization of the bovine plasminogen cDNA."; Int. Dairy J. 5:593-603(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                           19.0%; Score 159; DB 1; Length 473; 45.6%; Pred. No. 3.8e-08; arive 7; Mismatches 26; Indels
                                                                                                                                                            KREMEN PROTEIN 1.
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                               586827788BE3FDD1 CRC64;
                                                                                                                            Transmembrane; Kringle
                                                                                                                                                                                                               CYTOPLASMIC (POTENTIAL) KRINGLE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DE PLMN BOVIN STANDARD; PRT; 812 AA. AC P06868, Q28162; BDT 01-JAN-1988 (Rel. 06, Created) DT 01-NOV-1997 (Rel. 35, Last sequence update) DT 28-FEB-2003 (Rel. 41, Last annotation update) DE Plasminogen precursor (EC 3.4.21.7).
                                                                                                                                                                                                POTENTIAL
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PRINTS; PRO0018; KRINGLE.
PRODOM; PD000395; Kringle; 1.
SWART; SM00042; CUB; 1.
SWART; SM00130; KR; 1.
PROSITE; PS010180; CUB; 1.
PROSITE; PS00021; KRINGLE 1; 1.
PROSITE; PS00070; KRINGLE 2; 1.
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Gaps 11;
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SEQUENCE FROM N.A. (ISOFORM LONG).
MEDLINE=93100347; Pubmed=1334494;
Masiakowski P., Carroll R.D.;
"A novel family of cell surface receptors with tyrosine kinase-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YET
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Q01973; Q92776;

L6-OCT-2001 (Rel. 40, Last sequence update)
15-OCT-2001 (Rel. 40, Last annotation update)
15-SEP-2003 (Rel. 42, Last annotation update)
Tyrosine-protein kinase transmembrane receptor ROR1 precursor
(EC 2.7.1.112) (Neurotrophic tyrosine kinase, receptor-related 1).
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Homo sapiens (Human).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. (ISOFORM SHORT).

MEDLINE-970300043; PubMed=8875995;

Reddy U.R., Phatak S., Pleasure D.;

"Human neural tissues express a truncated Rorl receptor tyrosine kluman neural tissues express a truncated Rorl receptor tyrosine arbanes, lacking both extracellular and transmembrane domains.";

Oncogene 13:1555-1559(1996).

-!- FUNCTION: TYROSINE-PROTEIN KINASE RECEPTOR WHOSE ROLE IS NOT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  19.0%; Score 159; DB 1; Length 812; 28.0%; Pred. No. 6.5e-08;
                                       5.59 KRINGLE 4.
5.64 KRINGLE 5.
5.64 SERINE PROTESSE.
315 N-LINKED (GLCNAC. . . ).
5.65 (GLNAE) (GALNAC. . . ).
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-!- SUBCELLULAR LOCATION: Type I membrane protein.
-!- ALTERNATIVE PRODUCTS:
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IsoId=Q01973-1; Sequence=Displayed;
Name=Short; Synonyms=T-ROR1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Biol. Chem. 267:26181-26190(1992)
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Matches 49; Conservative
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                       DEVELOPMENTAL STAGE: EXPRESSED AT HIGH LEVELS DURING EARLY EMBRYONIC DEVELOPMENT. THE EXPRESSION LEVELS DROP STRONGLY AROUND DAY 16 AND THERE ARE ONLY VERY LOW LEVELS IN ADULT TISSUES. SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. ROR SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GO; GO:0005737; C:cytoplasm; TAS.
GO; GO:0005887; C:integral to plasma membrane; TAS.
GO; GO:0004714; F:transmembrane receptor protein tyrosine kin. .;
GO; GO:0007169; P:transmembrane receptor protein tyrosine kin. .;
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ISOID=001973-2; Sequence=VSP 005008; TISSUE SPECIFICITY: EXPRESSED STRONGLY IN HUMAN HEART, LUNG, KIDNEY, BUT WEAKLY IN THE CNS. THE SHORT ISOFORM IS STRONGLY EXPRESSED IN FETAL AND ADULT CNS AND IN A VARIETY OF HUMAN CANCERS, INCLUDING THOSE ORIGINATING FROM CNS OR PNS NEUROECTODERM.
                                                                                                                                                                                                                                                   SIMILARITY: Contains 1 frizzled (FZ) domain.
SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
SIMILARITY: Contains 1 kringle domain.
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PROTEIN KINASE.
SER/THR-RICH.
PRO-RICH.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; M97675; AAA60275.1; -
EMBL; U38894; AACS0714.1; -
PIR; A45082; A45082.
HSSP; P00747; 1CEA.
MIM: A67032.
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us-09-880-503-8.rsp

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296 CIRIGIPMADPINKNHKCYNSTGVDYRGTVSVTKSGRQCQPWNS-----QYPHTHSFTAL 350
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATP (BY SIMILARITY).
BY SIMILARITY.
PHOSPHORYLATION (AUTO-) (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYROSINE-PROTEIN KINASE TRANSMEMBRANE
                                                                                           MGD, MGI:13475.0; Rowin.

RICEPTO; IPR00024; Fz domain.

RICEPTO; IPR0013598; Ig 2c2.

RICEPTO; IPR0013598; Ig 2c2.

RICEPTO; IPR00101; KTING1 g 1 g 2c2.

RICEPTO; IPR00101; KTING1 g 2c2.

RICEPTO; IPR00101; KTING1 g 2c2.

RICEPTO; IPR00118; Fz; I.

REAM; PP010132; Fz; I.

REAM; PP0103192; Fz; I.

REAM; PP00018; KRING1 g 1.

REAM; PP00018; KRING1 g 1.

REAM; PR00019; TYRKINASE.

REAM; PR00019; TYRKINASE.

REAM; PR00019; TYRKINASE.

REAM; SMART; SM00109; TYRK; I.

REAM; SMART; SM00119; FX; I.

REAM; SMO0109; TYRK; I.

REAM; SMO0119; FX; I.

REAM; SMO0110; FX; I.

REAM; SMO0110; FX; I.

REAM; SMO0110; FX; I.

REAM; RESSON REAM; KRING1E. 2; I.

REAM; PROSITE; PS00101; RRING1E. 2; I.

REAM; PROSITE; PS00101; PROTEIN KINASE.

REAM; PROSITE; PS00101; PROTEIN KINASE.

REAM; PROSITE; PS00101; PROTEIN KINASE.

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47 N-LINKED (GLCNAC. .) (POTENTIAL)

66 N-LINKED (GLCNAC. .) (POTENTIAL)

184 N-LINKED (GLCNAC. .) (POTENTIAL)

315 N-LINKED (GLCNAC. .) (POTENTIAL)

104156 MW; D728733E67D1782C CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                51; Indels
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EXTRACELLULAR (POTENTIAL)
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ATP (BY SIMILARITY)
ATP (BY SIMILARITY)
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SER/THR-RICH.
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                                          EMBL; AB010383; BAA75480.1;
HSSP; P00747; 1CEA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               296 CIRIGIPMADPINKNHKCYNSTGVDYRGTVSVTKSGRQCQPWNS-----QYPHTHTFTAL 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                236 DÉTSSVPKPRDLCRDECEILENVLCQTEYIFARSNPMILMRLKLPNCEDLPQPESPEAAN 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 NELHOVP------BNCDCLNGGTCVSNKYFS-----NIHWCNC-----PKKFGGQH 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C-----EIDKSKTCYEGNGHFYRGKASTDTMGRPCLPWNSATVLQQTYHAHRSDAL 92
SER/THR-RICH.

ATP (BY SIMILARITY).

ATP (BY SIMILARITY).

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

Missing (in isoform Short).

FTIG=VSP_005008.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=99248426; PubMed=10231392; MEDLINE=99248426; PubMed=10231392; Oishi I., Takeuchi S., Hashimoto R., Nagabukuro A., Ueda T., Liu Z.J., Hatta T., Akira S., Mareuda Y., Yammaura H., Otani H., Minani Y.; Spatio-temporally regulated expression of receptor tyrosine kinases, mRorl, mRorl, during mouse development: implications in development and function of the nervous system."; Genes Cells 4:41-56(1999).

-!- FUNCTION TYROSINE-PROTEIN KINASE RECEPTOR WHOSE ROLE IS NOT YET CLEAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              51; Indels 37; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein tyrosine phosphate.
-!- SUBCELLULAR LOCATION: Type I membrane protein.
-!- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. ROR SUBFAMILY.
-!- SIMILARITY: Contains I frizzled (F2) domain.
-!- SIMILARITY: Contains I immunoglobulin-like C2-type domain.
-!- SIMILARITY: Contains I kringle domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
17-SEP-2003 (Rel. 42, Last annotation update)
17-SEP-2003 (Rel. 42, Last annotation update)
18-SEP-2003 (Rel. 42, Last annotation update)
18-SEP-2003 (Rel. 42, Last annotation update)
18-SEP-2003 (Rel. 42, Last annotation update)
18-SEP-2001 (Rel. 42, Last annotation update)
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; Pred. No. 8.4e-08;
14; Mismatches 51; Indels 37;
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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AAR05117
AAR06244
AAR10057
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ALIGNMENTS

Human; urokinase-type plasminogen activator; uPA; therapy; hypertension; stroke; hypotension; atherosclerosis; heart attack; thrombotic disorder; microvascular occlusion; angiogenic disorder; pulmonary fibrosis; asthma; tumour cell metastasis; glaucoma; diabetic retinopathy; wound healing; clotting disorder; uterine contraction disorder; respiratory distress syndrome; amino terminal fragment; ATF; male impotence. Human uPA amino terminal fragment (ATF) and connecting peptide. AAE16549 standard; Protein; 143 AA (first entry) 09-APR-2002 AAE16549; RESULT 1

WO200197752-A2. Homo sapiens.

27-DEC-2001.

13-JUN-2001; 2001WO-US18976. 20-JUN-2000; 2000US-212874P. (UYPE-) UNIV PENNSYLVANIA.

Higazi AA; Cines DB, a

Thu D

N-PSDB; AAH34897.

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Human colon cancer antigen protein SEQ ID NO:6256.
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                                                                                                                                                                                                                                                                                AAG75492 standard; Protein; 337 AA
                                         Claim 24; Fig 1H; 117pp; English
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Matches 143; Conservative
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2002-122240/16
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     N-PSDB; AAD27082
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03-NOV-1999;
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143 AA;

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Birse CE,

99US-0157137.

(first entry)

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AAH32943 to AAH37195 and AAG73514 to AAG7778B represent human colon cancer-associated nucleic acid molecules (N) and proteins (P), where the proteins are collectively known as colon cancer antigens. The colon cancer antigens have cytostatic activity and can be used in gene therapy and vaccine production. N and P may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate P categorists. For example, N and P may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of P by expressing in a patient's genome that affect the activity of P by expressing in a patient's genome that affect the activity of P by expressing the rucleins or to supplement the patients own production of P. Additionally, N may be used to produce the colon cancer-associated Ps, by inserting the nucleic acids into a host cell and culturing the cell to teatment of colorectal carcinomas and cancers. AAH37196 to AAH37204 and AAB7789 represent sequences used in the exemplification of the present invention.

N. B. Pages 666 to 682 and page 7053 of the sequence listing were missing at time of publication, meaning no sequences are present for SEQ ID NO:1027 to 1052, 7921 and 7922.
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                                                 Nucleic acids encoding 4277 human colon cancer-associated polypeptides, useful for preventing, diagnosing and/or treating colorectal cancers
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100.0%; Pred. No. 3.8e-54;
ive 0; Mismatches 0;
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                                                                                                                                           Claim 11; Page 7707-7708; 9803pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 SNELHQVPSNCDCLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFYRG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Gaps
                                                                                Composition for modulating muscle cell and tissue contractility for treating atherosclerosis, asthma, hypertension, glaucoma, impotence, comprising domains from urokinase-type plasminogen activator -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; colon cancer; colon cancer antigen; diagnosis; detection; colorectal carcinoma; chromosome 10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 837; DB 23; Length 143; 100.0%; Pred. No. 1.9e-54; ive 0; Mismatches 0; Indels 0;
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Urokinase zymogen is cleaved into the two-chain form composed of characteristic urokinase H (molecular wt.of 30,000) and L (molecular wt.of 20,000) and L (molecular wt.of 20,000) and L (molecular rhe patentors claim a new urokinase zymogen which has mol. wt. ca. 50,000, a single chain molecular structure, and selective affinity for fibrin. It is a thrombolytic agent which manifests its plasminogen activator activity on cleavage by proteolytic enzymes (e.g. plasmin) and has higher affinity for fibrin than known forms
                                                                                                                        Thrombolytic agent; plasminogen activator activity; fibrin affinity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Zymogen AAP50871 is the inactive precursor form of human urokinase.
                                                                                                                                                                                                                                                                                             /note= "potential cleavage site which generates the two-chain form from the zymogen"
                                                   Sequence encoded by cDNA sequence for human urokinase zymogen (Japanese Patent Application No.37119/84).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New urokinase zymogen - useful as thrombolytic agent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nishhida M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PLVQECMVHDCADGKKPSSPPEE 143
                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 12; 30pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mori K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              83JP-0170354.
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Matches 143; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1985-106530/18.
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                                                                                                                                                                                                                                                                     Cleavage-site
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                                                                                                                                                                                                   Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EP139447-A
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                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to 2175 novel human ovarian antigens (ABP41054-ABP41228) and to cDNAs encoding them (ABD54131-ABD56305), and also encompasses polypeptides 90% identical and polynucleotides 95% identical control of the encompasses polypeptides 90% identical and polynucleotides 95% identical control of the sequences of the invention. The invention additionally relates to recombinant vectors and host cells comprising human ovarian antigen and the use of ovarian antigen polynucleotides and polypeptides in diagnosing, treating, prognosing or preventing various ovary and/or breast cancer, and disorders. Such conditions include ovarian cancer and breast cancer, and disorders (e.g., infertility, disorders of pregnancy, anovulation, activated covary syndrome, ovarian cysts, and dysmenorrhoea), endocrine disorders, inflammatory conditions (e.g., mastitis, cophoritis and toxic shock syndrome, juflammatory conditions (e.g., mastitis, cophoritis and vapinitis), immune disorders (e.g., anathorance), inflammatory conditions (e.g., mastitis, cophoritis and vapinitis), immune disorders (e.g., anathorance), inflammatory conditions (e.g., mastitis, and toxic shock syndrome), inflammatory conditions (e.g., congenital and acquired covarian antigen be used in screening for compounds which modulate ovarian antigen expression or activity. The polynucleotides may also be used in screening for compounds which modulate ovarian antigen expression or activity. The polynucleotides may be used as food additives or to prepare antibodies consecution in disease diagenosis, drug targeting and aphenotyping. The printed sequence represents a human avarian antigen of the invention.

Note: The sequence data for this patent did not form part of the printed sequence. The sequence data for this patent did not formet directly from MIPO. In Funboning the order of sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KASTDIMGRPCLPWNSAIVLQQIYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVGLK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNRRPWCYVQVGLK 146
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                                                                                                                                                                                                                                                                Isolated nucleic acid molecules encoding novel ovarian polypeptides, useful in the prevention, treatment and diagnosis of cancer (e.g. ovarian cancer), immune disorders, cardiovascular disorders and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .,
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                                                                                                                                                                                                                                                                                                                                                                               Claim 11; SEQ ID No 2927; 2922pp; English.
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                                                                                            (HUMA-) HUMAN GENOME SCI INC
07-JUN-2001; 2001WO-US18569.
                                                07-JUN-2000; 2000US-209467P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100.0
Matches 143; Conservative
                                                                                                                                                                                                                                                                                                                                        neurological diseases
                                                                                                                                             Birse CE, Rosen CA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       337 AA;
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KASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVGLK 120
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100.0%; Score 837; DB 6; Length 411; 100.0%; Pred. No. 4.4e-54; ive 0; Mismatches 0; Indels
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AAP50871

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KASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVGLK 120
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(first entry)
                                                                                                                                                                                                       UK-S3 as encoded by pUKS3.
                                                                                                                                                                                                                            Urokinase; glycosylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sasaki K, Nishi T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1990-165029/22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                411 AA;
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                                                                                                                                                                                                                                                                                  misc_difference
                                                                                                                                                                                                                                                                                                                   misc_difference
                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                             28-SEP-1989;
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                                                                                                                                                                     25-MAR-2003
04-OCT-1990
                                                                                                                                                                                                                                                                                                                                                                                      30-MAY-1990
                                                                                                                                                                                                                                                                                                                                                                EP370205-A
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                                                                                                  RESULT 6
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                                                               셤
                                                                                                                                    New variants of human prourokinase (hPUK) comprise a hPUK deficient in (i) at least part of the first loop region of the epidermal growth factor (EGF) domain, (ii) at least part of the first loop and at least part of the second loop; or (iii) at least part of the third loop. The hPUK variants show an increased blood half-life comparable to that of the whole EGF domain-deficient hPUK variant and urokinase while retaining the same properties as those of hPUK. They have potent thrombolytic activity and very little tendency to cause hPUK protein, including the EGF domain.
                                                                                                Human; prourokinase; hPUK; variant; half-life; increase; EGF;
epidermal growth factor domain; deletion; thrombolysis; fibrinolysis.
                                                                                                                                                               10..42
/label= EGF_domain
/note= "in Claimed variants, at least part of the
/note= "in Claimed variants, at least part of the
EGF_domain is deleted (see comments)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
100.0%; Score 837; DB 11; Length 411;
Best Local Similarity 100.0%; Pred. No. 4.4e-54;
Matches 143; Conservative 0; Mismatches 0; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human pro-urokinase variants - deficient in loop regions of epidermal growth factor, showing long blood half-life, as fibrinolytic agent
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Amatsuji Y, Hirose M, Kasai S, Kawabe H;
Tanabe T;
                                                                                                                                                                                                                                     20..31
/label= second_loop
                                                                                                                                                        location/Qualifiers
                                                                                                                                                                                                              10..19
/label= first_loop
         AAW13634 standard; Protein; 411 AA
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/label= third_loop
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure, Fig 1, 22pp; English.
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89JP-0126433.
86JP-0156936.
87JP-0036495.
89JP-0126434.
                                                                                                                                                                                                                                                                                                                                       90EP-0109472
                                                     (first entry)
                                                                          Human native prourokinase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1990-350146/47.
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18-MAY-1989;
03-JUL-1986;
18-FEB-1987;
18-MAY-1989;
                                                                                                                                  Homo sapiens
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                                                    04-JUN-1997
                                                                                                                                                                                                                                                                                                                  22-NOV-1990
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                              AAW13634;
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Domain
                                                                                                                                                                                                                Region
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KASTDTWGRPCLPWNSATVLQQTYHAHRSDALQLGLGKGKHNYCRNPDNRRPWCYVQVGLK 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The polypeptide is a deriv. of mature urokinase, designated (Nr.S3 which has 2 amino acid substins. which result in an N-linked glycosylation site giving the new protein improved stability and activity.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Polypeptide(s) with added carbohydrate chains - formed by modification of amino acid sequence, used to improve physiochemical properties and/or activities.
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100.0%; Pred. No. 4.4e-54;
ive 0; Mismatches 0;
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field.)
field.)
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(Updated on 25-MAR-2003 to correct PR
(Updated on 25-MAR-2003 to correct PA
(Updated on 25-MAR-2003 to correct PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /label=synthetic_mutat
/note="old_seg_(Pro)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'note="old seg (Leu)"
                                                                        PLVQECMVHDCADGKKPSSPPEE 143
                                                                                                                    121 PLVQECMVHDCADGKKPSSPPEE 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                AAR05117 standard; protein; 411 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 100.0
Matches 143; Conservative
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(KYOW ) KYOWA HAKKO KOGYO KK
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                Yasamura S, Nishi T,
                                                                                                                                                                                                                                  WPI; 1991-008678/02.
N-PSDB; AAQ10169.
                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                     411 AA
                            18-MAR-1991
                                                                                                                                                       .8-JUN-1990;
                                                                                               Homo sapiens
                                                                                                                                                                           19-JUN-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18-MAR-1991
                                                                                                                                    02-JAN-1991.
                                                                                                                 EP405285-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 143;
                                                                                                                                                                                                                                                                                            infarction
          AAR10057;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121
                                                                                                                                                                                                                                                                                                                                                                                                     Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61
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                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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ID AAR1
XX AAR1
XX AAR1
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XX Y B-M
XX BC-
XX XX CCF
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          KASTDIMGRPCLPWNSATVLQQIYHAHRSDALQLGLGKGKHNYCRNPDNRRRPWCYVQVGLK 120
KASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVGLK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVGLK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 SNELHQVPSNCDCLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFYRG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SNEIHQVPSNCDCLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFYRG
                                                                                                                                                                                Urokinase precursor, fibrinolysis, thrombolytic, cerebral thrombosis, myocardial infarction,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                             Urokinase precursor-lipid composite - used as thrombolytic agent, having prolonged half-life in the blood, enhanced bio:availability and improved activity
                                                                                                                                                                                                                                                                                                                                                                                                                                   By forming a precursor-lipid composite, the half-life of this thrombolytic agent in the blood may be increaced, exhibiting improved activity without abnormal acceleration of fibrinolytic activity. Compound is useful as a thrombolytic agent in treatment of cerebral thrombosis, myocardial infarction etc.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 837; DB 11; Length 411; 100.0%; Pred. No. 4.4e-54;
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0
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                                                      PLVQECMVHDCADGKKPSSPPEE 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PLVQECMVHDCADGKKPSSPPEE 143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAR10057 standard; Protein; 411 AA.
                                     PLVQECMVHDCADGKKPSSPPEE
                                                                                                       AAR06244 standard; protein; 411
                                                                                                                                                                                                                                                                                                                                        Tamanouchi
                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 3; Fig 1; 11pp; English
                                                                                                                                                               Urokinase precursor protein.
                                                                                                                                                                                                                                                                                         89JP-0121405.
89JP-0016406.
                                                                                                                                                                                                                                                                      90EP-0300772
                                                                                                                                            07-DEC-1990 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100.
Matches 143; Conservative
                                                                                                                                                                                                                                                                                                                     (GREC ) GREEN CROSS CORP.
                                                                                                                                                                                                                                                                                                                                        Ueda Y,
                                                                                                                                                                                                                                                                                                                                                            WPI; 1990-233117/31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                411 AA;
                                                                                                                                                                                                                                                                      25-JAN-1990;
                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                        17-MAY-1989;
27-JAN-1989;
                                                                                                                                                                                                                                                   01-AUG-1990.
                                                                                                                                                                                                                                                                                                                                        Matsuda H,
                                                                                                                          AAR06244;
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AAR10057
ID AAR10
                                                                                    RESULT 7
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61 KASTDIMGRPCLPWNSATVLQQIYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVGLK 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 SNELHQVPSNCDCLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFYRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SNELHQVPSNCDCLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFYRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       UK-T4 is one example of a plasminogen activator which differs from natural human pro-urokinase at positions 153 and 155 (Leu substituted by Ser; Pro substituted by Thr, respectively). The derivative has decreased susceptibility to thrombin compared to natural type pro-UK and higher specific activity.
                                                                            pro-urokinase, UK-T4; plasminogen activator; myocardial infarction; cerebral thrombosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pro-urokinase, UK-S3; plasminogen activator; myocardial infarction; erebral thrombosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New plasminogen activator almost identical to natural pro:urokinase - is thrombin resistant and used for prophylaxis, treatment of cerebral thrombosis or myocardial
Pro-urokinase derivative UK-T4 with Ser(153) and Thr(155).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pro-urokinase derivative UK-S3 with Asn(153) and Thr(155).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PLVQECMVHDCADGKKPSSPPEE 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 8; 84pp; English.
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61 KASTDIMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVGLK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 KASTDIMGRPCLPWNSATVLQQIYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVGLK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 SNELHQVPSNCDCLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFYRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 SNELHQVPSNCDCLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFYRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human pre-urokinase can be modified by replacing: Ser, Asn, Pro, Gly, or Tyr in the region ranging from residue 10 to 60 in the N-terminal of the human PUK by Thr, Pro or Ala. These mutants have a longer half-life in the blood and a higher thrombolytic ability. For examples see (AAR47956-R47960).
                                                                                                                                                                                                                                                                                                                                                         Mutant human pre:urokinase - by replacing specified aminoacid(s) in N-terminal for providing longer half-life in blood and higher thrombolytic ability
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 100.0%; Score 837; DB 14; Length 411; Best Local Similarity 100.0%; Pred. No. 4.4e-54; Matches 143; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pro-urokinase; thrombolysis; fibrin clot lysis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
297..313
/note= "flexible loop"
11..19
13..31
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                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Page 14-16; 26pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAR62991 standard; protein; 411 AA
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                               10..19
/label= Loop_1
20..31
/label= Loop_2
33..42
/label= Loop_3
                                                                                                                                                                                                               92JP-0030178
                                                                                                                                                                                                                                            92JP-0030178
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(first entry)
                                                                                                                                                                                                                                                                           (GREC ) GREEN CROSS CORP.
 10..49
/label= 1
                                                                                                                                                                                                                                                                                                        WPI; 1993-277461/35.
N-PSDB; AAQ48228.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          411 AA;
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Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pro-urokinase
                                                                                                                                             JP05192142-A
                                                                                                                                                                                                             20-JAN-1992;
                                                                                                                                                                                                                                              20-JAN-1992;
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                                                                                                                                                                            03-AUG-1993,
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21-SEP-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
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                                Region
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Domain
   Domain
                                                                 Region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGRGHNYCRNPDNRRRPWCYVQVGLK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SNELHQVPSNCDCLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFYRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 SNELHQVPSNCDCLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFYRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                   UK-S3 is one example of a plasminogen activator which differs from natural human pro-urokinase at positions 153 and 155. (Leu substituted by Asn; Pro substituted by Thr, respectively). The derivative has decreased susceptibility to thrombin compared to natural type pro-UK and higher specific activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "Ser, Asn, Pro, Gly, or Tyr in the region 10 to 60 in the N-terminal of the human PUK can be replaced by Thr, Pro or Ala"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ·
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 411;
                                                                                                                                                                                                                                                                    New plasminogen activator almost identical to natural pro:urokinase - is thrombin resistant and used for prophylaxis, treatment of cerebral thrombosis or myocardial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 837; DB 12;
100.0%; Pred. No. 4.4e-54;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "Thr encoded by TAC (sic)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pre-urokinase; thrombolytic; blood; plasmid; PUK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'note= "Thr encoded by AGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PLVQECMVHDCADGKKPSSPPEE 143
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                                                                                                                                                         (KYOW ) KYOWA HAKKO KOGYO KK
                                                                                             90EP-0111471
                                                                                                                            89JP-0156302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 100.
Matches 143; Conservative
                                                                                                                                                                                          Yasamura S, Nishi T,
                                                                                                                                                                                                                       WPI; 1991-008678/02.
N-PSDB; AAQ10170.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Misc-difference 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      411 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Misc-difference 64
                                                                                             18-JUN-1990;
Homo sapiens
                                                                                                                            19-JUN-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10-FEB-1994
                                                            02-JAN-1991
                           EP405285-A
                                                                                                                                                                                                                                                                                                                      infarction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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Key Region

RESULT 10 AAR40225

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KASTDIMGRPCLPWNSAIVLQQIYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVGLK 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 SNBLHQVPSNCDCLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFYRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVGLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        described in AAR62992-863006 were derived. These mutants retain the thrombolytic activity of the wild type protein, useful for the reactment of thromboembolism, but have a reduced fibrinogenolysis activity and non-specific plasminogen activation. The mutants can therefore be used for the lysis of fibrin clots without inducing systemic bleeding, as can be the case with the wild type protein. (Updated on 25-WAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAR62991 is the wild type pro-urokinase, from which the new mutants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pro-urokinase mutants - have thrombolytic activity but reduced fibrinogenolysis activity and non-specific plasminogen activation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 837; DB 16; Length 411; larity 100.0%; Pred. No. 4.4e-54; Conservative 0; Mismatches 0; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   (NEWE-) NEW ENGLAND DEACONESS HOSPITAL
                                                    297..313
/note= "flexible loop"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PLVQECMVHDCADGKKPSSPPEE 143
                                  Socation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PLVQECMVHDCADGKKPSSPPEE
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                                                                                                                                                                                                                                                                                                                                                                                 94WO-US07278
                                                                                                                                                                                                                                                                                                                                                                                                                93US-0087163
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(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1995-060991/08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gurewich V, Liu J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
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Disulfide-bond
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21-SEP-1995
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Pred. No. 4.4e-54;
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ID AAR62992 standard, protein, 411 AA.
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              AAR62994 standard; protein; 411 AA.
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                                            Pro-urokinase, thrombolysis, fibrin clot lysis, mutant His300, reduced fibrinogenolysis, non-specific plasminogen activation;
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100.0%; Pred. No. 4.4e-54;
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/note= "flexible loop"
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                                                                                                                                            Location/Qualifiers
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            Pro-urokinase mutant His300
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1es 143; Conservative
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SNELHQVPSNCDCLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFYRG
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100.0%; Pred. No. 4.4e-54;
iive 0; Mismatches 0;
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/note= "flexible loop"
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            PLVQECMVHDCADGKKPSSPPEE 143
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Query Match

Length 411; Indels

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KASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVGLK 120
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described in AAR62992-R63008 were derived. These mutants retain the thromboblytic activity of the wild type protein, useful for the remaint of thromboembolism, but have a reduced fibrinogenolysis activity and non-specific plasminogen activation. The mutants can therefore be used for the lysis of fibrin clots without inducing systemic bleeding, as can be the case with the wild type protein. (Updated on 25-MAR-2003 to correct PN field.)
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                                                                                                                    100.0%; Score 837; DB 16; Length 411; 100.0%; Pred. No. 4.4e-54; ive 0; Mismatches 0; Indels 0
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                                                                               SNELHQVPSNCDCLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFYRG 60
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                                     Length 411;
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                                  100.0%; Score 837; DB 16;
100.0%; Pred. No. 4.4e-54;
ive 0; Mismatches 0;
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Best Local Similarity 100.
Matches 143; Conservative
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            411 AA;
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                                                                                                                                                                                                AAR62991 is the wild type pro-urokinase, from which the new mutants described in AAR62992-R63008 were derived. These mutants retain the thrombolytic activity of the wild type protein, useful for the treatment of thromboembolism, but have a reduced fibrinogenolysis activity and non-specific plasminogen activation. The mutants can therefore be used for the lysis of fibrin oldts without inducing systemic bleeding, as can be the case with the wild type protein. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                         Pro-urokinase mutants - have thrombolytic activity but reduced fibrinogenolysis activity and non-specific plasminogen activation
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                                                                                                                                                                     Claim 11; Fig 1; 46pp; English
93US-0087163
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(first entry)
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                                                            Gurewich V, Liu J;
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              Pro-urokinase mutants - have thrombolytic activity but reduced fibrinogenolysis activity and non-specific plasminogen activation
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100.0%; Pred. No. 4.4e-54;
tive 0; Mismatches 0;
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/note= "flexible loop'
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                                                           Claim 11; Fig 1; 46pp; English.
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AAR62991 is the wild type pro-urokinase, from which the new mutants described in AAR62992-R63008 were derived. These mutants recain the thrombolytic activity of the wild type protein, useful for the treatment of thromboembolism, but have a reduced fibrinogenolysis activity and non-specific plasminogen activation. The mutants can therefore be used for the lysis of fibrin clots without inducing systemic bleeding, as can be the case with the wild type protein. (Updated on 25-MAR-2003 to correct PN field.)
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reduced fibrinogenolysis; non-specific plasminogen activation;
systemic bleeding; mutant Serl75 His187 Ala313.
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/note= "flexible loop"
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                                                                                                              (NEWE-) NEW ENGLAND DEACONESS HOSPITAL
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Best Local Similarity 100.
Matches 143; Conservative
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   Length 411;
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100.0%; Score 837; DB 16; 100.0%; Pred. No. 4.4e-54;
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Pro-urokinase; thrombolysis; fibrin clot lysis; reduced fibrinogenolysis; non-specific plasminogen activation; systemic bleeding; mutant Serl75 His187 His1313.
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/note= "flexible loop"
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Matches 143; Conserv
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100.0%; Pred. No. 4.4e-54;
ive 0; Mismatches 0;
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/note= "flexible loop"
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100.0%; Pred. No. 4.4e-54;
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297..313 /note= "flexible loop"

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Location/Qualifiers

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(NEWE-) NEW ENGLAND DEACONESS HOSPITAL.
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Matches 143; Conservative
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PLVQECMVHDCADGKKPSSPPEE 143
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                                                         AAR63005 standard; protein, 411
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KASTDIMGRPCLPWNSAIVLQQIYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVGLK 120
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These mutants retain the thrombolytic activity of the wild type protein, useful for the treatment of thromboembolism, but have a reduced fibrinogenolysis activity and non-specific plasminogen activation. The mutants can therefore be used for the lysis of fibrin clots without inducing systemic bleeding, as can be the case with the wild type protein. (Updated on 25-MAR-2003 to correct PN field.)
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           Best Local Simi
Matches 143;
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21-SEP-1995
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Domain
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/label= Linker_region
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/label= A-chain
                   Claim 16; Fig 1; 46pp; English.
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/note= "p
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                                                                                                                                Gaps
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actvity and non-specific plasminogen activation. The mutants can therefore be used for the lysis of fibrin clots without inducing systemic bleeding, as can be the case with the wild type protein. (Updated on 25-MAR-2003 to correct PN field.)
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                                                                                                    Length 411;
                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pro-urokinase mutant Ser175 His187 His300 Ala301 His313
                                                                                                  DB 16;
                                                                                                 Query Match 100.0%; Score 837; DB 16
Best Local Similarity 100.0%; Pred. No. 4.4e-54
Matches 143; Conservative 0; Mismatches 0
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AAR62991 is the wild type pro-urokinase, from which the new mutants described in AAR62992-R63008 were derived. These mutants retain the thrombolytic activity of the wild type protein, useful for the treatment of thromboembolism, but have a reduced fibrinogenolysis actvity and non-specific plasminogen activation. The mutants can therefore be used for the lysis of fibrin clots without inducing systemic bleeding, as can be the case with the wild type protein. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pro-urokinase; plasminogen activator; fusion drug; drug delivery; platelet; cardiovascular disease; thrombolytic.
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                                                                                                                                                                                               DB 16;
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/label= Growth_factor_domain
46..132
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location/Qualifiers
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les 143; Conservative
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                             thrombolytic
                                                  sapiens
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                                                                                                                                                                                                                                                                                                                         A portion of the A-chain (pref. amino acids 1-132) of pro-urokinase (AAR92926) can be linked to a drug, e.g. hirudin, somatostatin or their amalogues (see also AAR92925 and AAR92927-33) and used in the prodn. of new fusion drugs. The constructs can be obtd. by expression of the appropriate nucleotide sequences in transformed host cells. When administered to a patient, the A-chain binds the fusion drug to the platelet outer membrane, i.e. to the site of thrombosis or vascular injury. Cleavage sites for thrombin and/or plasmin with the fusion drug allow the release of the drug at the target site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SNELHQVPSNCDCLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFYRG
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                                                                                                                                                                                                                                                                            Fusion product of plasminogen activator A chain and drug – targeted to platelets, useful for treatment of cardiovascular disease
        "disulfide bond between Cys148 and Cys279"
                                                                                       Cys341"
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Pred. No. 4.4e-54;
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Best Local Similarity 100.
Matches 143; Conservative
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N-PSDB; AAT18237.
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The present sequence shows the wild-type uroxinase plasmangen activator (URA). Cyclic peptides based on the amino acids residues 20-30 (the receptor-binding region) of upA are claimed. These cyclic peptides target the ubA receptor (uPAP), allowing therapeutic or diagnostic agents to be delivered to uPAR-expressing cells. The cyclic peptides are used, optionally when linked to a therapeutic agent, to inhibit migration, invasion and proliferation of cells, or angiogenesis, or to induce to treat diseases characterized by these processes, e.g. solid tumors, therapends or lymphoma (or their metastasses), benign hyperplasts; atheracian activations of their metastasses), benign hyperplasts; atheracian diaberic retinopathy; arthritis; fibrosis; bone fracture etc., most particularly growth, invasion and metastasis of tumors. When labeled, the cyclic peptides can be used for diagnostic detection of upAR and mobilized they are used to isolate upAR or cells that express them. The cyclic peptides are stable, soluble in water, bind strongly to upAR, are relatively inexpensive to produce and may be derivatized by affecting their binding. Since they target upAR, they should have relatively low systemic toxicity and only low doses are required.
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anti-cancer, anti-metastatic, anti-proliferative, anti-atherosclerotic,
anti-thrombotic, anti-angiogenic, anti-inflammatory, anti-arthritic,
anti-fibrotic, apoptotic, vasotropic, anti-diabetic, ophthalmological;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New cyclic peptide, useful for treatment or diagnosis of e.g. tumors and other diseases involving cell proliferation or migration, targets the urokinase plasminogen activator recent
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; Pred. No. 4.4e-54;
0; Mismatches 0;
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Search completed: December 3, 2003, 14:39:15 Job time : 23.5259 secs

us-09-880-503-9.rai

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Sequence 43, Appl
Sequence 50, Appl
Sequence 50, Appl
Patent No. 5186259
Patent No. 5200340
Patent No. 5344773
Sequence 9, Appl
Sequence 51, Appl
Sequence 57, Appl
Sequence 10, Appl
Sequence 10, Appl
Sequence 10, Appl
Sequence 10, Appl
Sequence 10, Appl
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Sequence 10, Appl
Sequence 10, Appl
Sequence 10, Appl
Sequence 10, Appl
Sequence 11, Appli
Sequence 11, Appli
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ch 100.0%; Score 554; DB 4; Length 200;
l Similarity 100.0%; Pred. No. 2e-58;
96; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                      Sequence 73. Application US/09101272G
Patent No. 6509445
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: CANCEROUS METASTASIS INHIBITOR
FILE REPRENCE: 165099
CURRENT APPLICATION NUMBER: US/09/101,272G
CURRENT PILING DATE: 1998-07-08
PRIOR APPLICATION NUMBER: US/09/101,272G
PRIOR FILING DATE: 1996-01-08
NUMBER OF SEQ ID NOS: 107
SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 98, Application US/09101272G
Patent No. 6509445
GENERAL INFORMATION:
APPLICANT: Missin Food Products Co., Ltd.
ITLE OF INVENTION: CANCEROUS METASTASIS INHIBITOR
FILE REFERENCE: Q5099
CURRENT APPLICATION NUMBER: US/09/101,272G
CURRENT FILING DATE: 1998-07-08
PRIOR APPLICATION NUMBER: JP 1059/1996
PRIOR FILING DATE: 1996-01-08
PRIOR FILING DATE: 1905-01-08
NUMBER OF SEQ ID NOS: 107
SOFTWARE: Patentin version 3:1
5520913-1

5200340-6

US-08-560-098A-53

US-08-883-795A-38

5185259-3

5200340-2

5344773-2

US-08-811-949-51

US-08-811-949-55

US-08-811-949-57

US-08-811-949-57

US-08-811-949-57

US-09-611-949-67

US-09-611-949-67

US-09-611-949-67

US-09-611-949-67

US-09-611-949-67
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                                                                                                                                                                                                                       ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc feature
; OTHER INFORMATION: ATF domain of uPA
US-09-101-272G-73
  ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 96; Conserv
  RESULT 1
US-09-101-272G-73
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US-09-101-272G-98
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LENGTH: 200
TYPE: PRT
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Sequence 84, Appl
Sequence 24, Appl
Sequence 25, Appl
Sequence 18, Appl
Sequence 18, Appl
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Sequence 1, Appl
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Sequence 1, Appl
Sequence 2, Appl
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                                                                         ; Search time 4.96552 Seconds (without alignments) 818.010 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 73,
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Sequence 12,
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1 KTCYEGNGHFYRGKASTDTM......QECMVHDCADGKKPSSPPEE 96
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(/gnz_6/ptodata1/liaa/6B_COMB.pep:*

(/gnz_6/ptodata1/liaa/PCTUS_COMB.pep:*

(/gnz_6/ptodata1/liaa/PCTUS_COMB.pep:*
          GenCore version 5.1.6
(c) 1993 - 2003 Compugen Ltd.
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                                                                         December 3, 2003, 14:35:43
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Maximum Match 100%
Listing first 45 summaries
                                                      OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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length: 2000000000
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Match Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: STEFFENS, GEND J.
APPLICANT: WIENDT, STEPHAN
APPLICANT: WIENDIDER, ODFANNES
APPLICANT: BINZEL-WIELAND, REGINA
APPLICANT: BINZEL-WIELAND, REGINA
APPLICANT: SAUNDERS, DEREK J.
TITLE OF INVENTION: BIFUNCTIONAL UROKINASE VARIANTS WITH
TITLE OF INVENTION: INHIBITING EFFECT
NUMBER OF SEQUENCES: 83
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPOTER: IBM PC compatible
COMPOTER: IBM PC compatible
COMPOTER: IBM PC compatible
COMPOTER: IBM PC compatible
CORRENT APELICATION DATA:
APPLICATION NUMBER: US/08/093,741
FILING DATE: 20-JUL-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P43 23 754.1
FILING DATE: 15-JUL-1993
ATTONERY/AGENT INFORMATION:
ANDER CONTREY/AGENT INFORMATION:
ANDER CONTREY/AGENT INFORMATION:
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1200 G Street, N. W. Suite 700
Washington, D.C.
Y: U.S.
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100.0%; Pred. No. 2.1e-58;
ive 0; Mismatches 0;
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                                                                        TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
1 OTHER INFORMATION: ATFHI-ML chimeric protein
US-09-101-272G-98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 83, Application US/08093741
Patent No. 5681721
GENERAL INFORMATION:
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REGISTRATION NUMBER: 26,269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 12
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)628-8800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (202) 628-8800
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amino acid
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 100.
Matches 96; Conservative
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Best Local Similarity
Matches 96; Conserv
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US-08-093-741-83
SEQ ID NO 98
LENGTH: 208
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APPLICANT: WINNING, STEPHAN
APPLICANT: WINNING, STEPHAN
APPLICANT: HEINZEL-WIELAND, REGINA
APPLICANT: SCHNDERS, DERREK J.
ITILE OF INVENTION: BIFUNCTIONAL UROKINASE VARIANTS WITH
TITLE OF INVENTION: IMPROVED FIBRINOLYTIC CHARACTERISTICS AND THROMBIN
TITLE OF INVENTION: INHIBITING EFFECT
CORRESPONDENCE: 83
CORRESPONDENCE ADDRESS:
KTCYEGNGHFYRGKASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDN
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100.0%; Score 554; DB 1;
Best Local Similarity 100.0%; Pred. No. 4.2e-58;
Matches 96; Conservative 0; Mismatches 0;
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                                              61 RRRPWCYVQVGLKPLVQECMVHDCADGKKPSSPPEE
                                                                                            RRRPWCYVQVGLKPLVQECMVHDCADGKKPSSPPEE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Evenson, McKeown, Edwards & STREET: 1200 G Street, N. W. Suite 700 CITY: Washington, D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PAPLICATION DATA:
PELING DATE: 20-JUL-1993
APPLICATION NUMBER: DE P43 23 754.1
FILING DATE: 15-JUL-1993
ATTONNEY, AGENT INFORMATION:
NAME: EVANS, JOSEPH D.
REGISTRATION NUMBER: 26,269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/720,012
FILING DATE: 27-SEP-1996
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US-08-560-098A-44
Sequence 44, Application US/08560098A
Patent No. 5976841
GENERAL INFORMATION:
                                                                                                                                                                                                                ; Sequence 83, Application US/08720012; Patent No. 5747291; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 14
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)628-8800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 83: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acids
TOPOLOGY: 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Washington, D.C.
COUNTRY: U.S.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
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1 KTCYEGNGHFYRGKASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDN 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Felese #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/967,024C
CLASSIFICATION: 435
FILING DATE: 30-NOV-1994
ATTORNEY AGENT: INFORMATION:
NAME: EVANS, JOSEPH D.
REGISTRATION NUMBER: 148/4244
TELECOMMUNICATION INFORMATION:
NAME: EVANS, JOSEPH D.
REPERENCE/DOCKET NUMBER: 148/42444
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: (202) 628-8840
TELEFAX: (202) 628-8844
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 393 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/WS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/967,024C
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1200 G Street, N.W., Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
100.0%; Score 554; DB 3;
Best Local Similarity 100.0%; Pred. No. 4.6e-58;
Matches 96; Conservative 0; Mismatches 0;
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PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION UNDRER:
FLING DATE: 30-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: BVANS, JOSEPD D.
REGISTRATION NUMBER: 26,269
REFERENCE/DOCKET NUMBER: 148/42444
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 7
US-08-967-024C-25
; Sequence 25, Application US/08967024C
; Patent No. 6133011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 1200 G Street,
CITY: Mashington
STATE: DC
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 KTCYEGNGHFYRGKASIDIMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDN 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 393;
                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOSTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/560,098A
FILING DATE: 17-NOV-1995
PRIOR APPLICATION DATA: P 44 40 892.7
FILING DATE: 17-NOV-1994
ATTORICATION NUMBER: P 44 40 892.7
FILING DATE: 17-NOV-1994
ATTORICATION NUMBER: 26,269
ATTORICATION NUMBER: 26,269
REFERENCE/DOCKET NUMBER: 148/42448
TELEPHONE: (202) 628-8840
TELEPHONE: (202) 628-8840
TELEPHONE: (202) 628-884
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
LENGTH: 393 amino acids
TUNDER: AMINO ACIDS
TELEPHONE: AMINO ACIDS
TELEPHONE: AMINO ACIDS
TELEPHONE: AMINO ACIDS
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TELEPHONE: AMINO ACIDS
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APPLICANT: WNENDT, Stephan, Regina
APPLICANT: HEINZEL-WIELAND, Regina
APPLICANT: STEFFENS, Gerd Josef
TITLE OF INVENTION: Proteins having Fibrinolytic and
TITLE OF INVENTION: Coagulation-inhibiting Properties
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Evenson, McKeown, Edwards & Lenahan
                                                                                                                                                ADDRESSEE: Evenson, McKeown, Edwards & Lenahan
STREET: 1200 G Street, N.W., Suite 700
CITY: Washington
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Obert Match
Obert Local Smilarity 100.0%; Pred. No. 4.6e-58,
Matches 96; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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MOLECULE TYPE: protein
US-08-560-098A-44
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                                                                                                                                                                                        CITY: Was
STATE: DO
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Gaps

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48 KTCYEGNGHFYRGKASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDN 107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CONTAIN AFFLICATION NUMBER: US/08/286,748B
FILING DATE: August 5, 1994
CLASSIFICATION: 424
PRIOR APPLICATION: 424
PRIOR APPLICATION NUMBER:
APPLICATION NUMBER:
FILING DATE:
ATORNEY/AGENT INFORMATION:
NAME: J. Peter Fasse
REGISTRATION NUMBER: 32,983
REGISTRATION NUMBER: 32,983
REGISTRATION NUMBER: 04547/013001
TELEPHONE: (617) 542-5070
TELEPHONE: (617) 542-5906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 18, Application US/08153799; Patent No. 5766883; GENERAL INFORMATION:
APPLICANT: Ballance, David J APPLICANT: Goodey, Andrew R ITLE OF INVENTION: Polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.0
Matches 96, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (617) 542-890
TELEX: 200154
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Boston
STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Di
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ZIP: 02110-2804
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US-08-286-748B-18
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US-08-153-799-18
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                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                              Length 393;
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100.0%; Score 554; DB 1; Length 411;
Best Local Similarity 100.0%; Pred. No. 4.8e-58;
Matches 96; Conservative 0; Mismatches 0; Indels (
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100.0%; Score 554; DB 3;
Best Local Similarity 100.0%; Pred. No. 4.6e-58;
Matches 96; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                     63 RRRPWCYVQVGLKPLVQECMVHDCADGKKPSSPPEE 98
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MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 1.5" Diskette, 1.44 Mb
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM SYSTEM: MS-DOS (VERSION 5.0)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/087,163
FILING DATE: 07/02/93
CLASSIFFCRATION: 5.14
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Liu, Jian-Ning
APPLICANT: Liu, Jian-Ning
APPLICANT: Gurewich, Victor
TITLE OF INVENTION: PRO-URCKINASE MUTANTS
NUMBER OF SQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    04353/003001
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US-08-087-163-1
; Sequence 1, Application US/08087163
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Fasse, J. Peter
REGISTRATION NUMBER: 32,983
REPRENCE/DOCKET NUMBER: 0435
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-8906
TELEFAX: (617) 542-8906
  TELEFAX: (202) 628-8844
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: ATTORNEY/AGENT INFORMATION:
                                                                       : 393 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEX: 200154
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                               ; TOPOLOGY: __inear
; MOLECULE TYPE: protein
US-08-967-024C-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
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CITY: Boston
                                                                                                               STRANDEDNESS:
                                                                       LENGTH:
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                                                                                                                                                                      Sequence 18, Application US/08286748B
Patent No. 5759542
GENERAL INFORMATION:
APPLICANT: Victor Gurewich
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DELIVERY
TITLE OF INVENTION: CARDIOVASCULAR AND OTHER DISEASES
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS: ADDRESS: ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
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                                               108 RRRPWCYVQVGLKPLVQECMVHDCADGKKPSSPPEE 143
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100.0%; Pred. No. 4.8e-58;
ative 0; Mismatches 0;
96
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/note= "WAP signal"
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MOLECULE TYPE: protein
HYPOTHETICAL: NO
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: Peptide
LOCATION: 1..19
OTHER INFORMATION: /
CTHER INFORMATION: /
FBATURE:
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ORGANISM: Homo sapiens
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LOCATION: (21)..()
OTHER INFORMATION:
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Best Local Similarity
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US-09-101-272G-1
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100.0%; Score 554; DB 1; Length 41:
Best Local Similarity 100.0%; Pred. No. 4.8e-58;
Matches 96; Conservative 0; Mismatches 0; Indels
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Patent No. 5648253
GENERAL INFORMATION:
TITLE OF INVENTION: Inhibitor-Resistant Urokinase
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kilpatrick & Cody
STREET: 1100 Peachtree Street Suite 2800
                                                                                                                                                                                                                                                               COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/153,799
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                             CORRESPONDENCE ADDRESS:
ADDRESSEE: R Hain Swope, BOC Health Care Inc STREET: 100 Mountain Avenue CITY: Murray Hill STATE: New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/847975
FILING DATE: 06-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 6909916.2
FILING DATE: 29-APR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB90/00650
FILING DATE: 26-APR-1990
PRIOR APPLICATION NUMBER: US 07/775952
FILING DATE: 29-OCT-1991
ATTONNEY/AGENT DATA:
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REGISTRATION NUMBER: 24864
REFERENCE/DOCKET NUMBER: 92H
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 655 2400
TELEFAX: (908) 771 6159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEX: 219484
INFORMATION FOR SEQ ID NO: 18:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     : 411 amino acids
amino acid
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NUMBER OF SEQUENCES:
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STATE: Georgia
COUNTRY: USA
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US-07-942-157A-3
                                                                                                                                                                                                       COUNTRY:
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67 KTCYEGNGHFYRGKASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDN 126
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| NAME/KEY: Modified-site
| LOCATION: 198.203
| OTHER INFORMATION: /label= modified
| OTHER INFORMATION: /note= "six amino acids deleted in mutant" US-07-942-157A-3
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COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/942,157A
FILING DATE: 1992008
CLASSIFICATION 1435
PRIOR APPLICATION TOWER: US 07/631673
FILING DATE: 20-DEC-1990
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFRENCE/DOCKET NUMBER: 31,284
REFRENCE/DOCKET NUMBER: TS1108Cont.
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION SEQ ID NO: 3:
SEQUENCE CHRARACTERISTICS:
LENGTH: 430 amino acids
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Sequence 1, Application US/09101272G

BAPPLOANT: Nissin Food Products Co., Ltd.

TILLE OF INVENTION:
CURRENT APPLICATION NUMBER: US/09/101,272G

CURRENT FILING DATE: 1998-07-08

PRIOR APPLICATION NUMBER: US/09/101,272G

WHICH APPLICATION NUMBER: US/09/1096

PRIOR FILING DATE: 1996-01-08

NUMBER OF SEQ ID NOS: 107

SEQ ID NO 1

LENGTH 431
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100.0%; Pred. No. 5.1e-58;
tive 0; Mismatches 0;
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US-09-181-816-1
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                                                                                                                                                                           1 KTCYEGNGHFYRGKASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDN 60
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                                                                                             Length 431;
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APPLICANT: KOBAVASHI, YO-ICHI,OMORI, MUNEKI,YAMADA, CHIKAKO
TITLE OF INVENTION: RAPIDLY ACTING PROUROKINASE
NUMBER OF SEQUENCES: 23
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/340,007
FILING DATE: 18-AUG-1988
                     ; LOCATION: (20)...()
; OTHER INFORMATION: Urokinase-type plasminogen activator (uPA)
US-09-101.-272G-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 47, Application US/08560098A
Fatent No. 5976841
Fatent No. 5976841
FAMERAL INFORMATION:
APPLICANT: HEINZEL-WIELAND, Regina
APPLICANT: HEINZEL-WIELAND, Regina
APPLICANT: STEFFENS, Gerd Josef
TITLE OF INVENTION: Coagulation-inhibiting Properties
UNMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSED: ROBERSON, MCKGOWN, Edwards & Lenahan
STREET: 1200 G Street, N.W., Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                    Indels
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APPLICATION NUMBER: US/08/560,098A FILING DATE: 17.NOV-1995
PRIOR APPLICATION DATA: P 44 40 892.7 FILING DATE: 17.NOV-1994
                                                                                                                                                                                                                                                                                    128 RRRPWCYVQVGLKPLVQECMVHDCADGKKPSSPPEE 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             128 RRRPWCYVQVGLKPLVQECMVHDCADGKKPSSPPEE 163
                                                                                           ch 100.0%; Score 554; DB 4; Similarity 100.0%; Pred. No. 5.1e-58; 96; Conservative 0; Mismatches 0;
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100.0%; Pred. No. 5.1e-58;
tive 0; Mismatches 0;
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.0
Matches 96; Conservative
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NAME/KEY: misc_feature
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                                                                                               Query Match
                                                                                                                     Best Local
Matches 9
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5188829-1
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48 KTCYEGNGHFYRGKASTDIMGRPCLP#NSATVLQQIYHAHRSDALQLGLGKHNYCRNPDN 107
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APPLICANT: JONES, Terence R.
TITLE OF INVENTION: CYCLIC PEPTIDE LIGANDS THAT TARGET UROKINASE
TITLE OF INVENTION: PLASMINOSEN ACTIVATOR RECEPTOR
FILE REFERENCE: 329042000300 SIDN 1-7
CURRENT APPLICATION NUMBER: US/09/181,816
CURRENT FILLIG DATE: 1998-10-29
NUMBER OF SEG ID NOS: 7
SOFTWARE: PATCHIN Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 432;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98.2%; Score 544; DB 3; Length 411; 99.0%; Pred. No. 7.5e-57; tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
100.0%; Score 554; DB 2; Length 43
Best Local Similarity 100.0%; Pred. No. 5.1e-58;
Matches 96; Conservative 0; Mismatches 0; Indels
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APPLICANT: WNENDT, Stephan
APPLICANT: HEINZEL-WIELAND, Regina
APPLICANT: STEFFENS, Gerd Josef
TITLE OF INVENTION: Proteins having Fibrinolytic and
TITLE OF INVENTION: Coagulation-inhibiting Properties
NUMBER OF SEQUENCES: 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       108 RRRPWCYVQVGLKLLVQECMVHDCADGKKPSSPPEE 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 RRRPWCYVQVGLKPLVQECMVHDCADGKKPSSPPEE 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 RRRPWCYVQVGLKPLVQECMVHDCADGKKPSSPPEE 96
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ATTORNEY/AGENT INFORMATION:
NAME: EVANS, Joseph D.
REGISTRATION NUMBER: 26,269
REFERENCE/DOCKET NUMBER: 148/4
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-8840
INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
LENGTH: 432 aming acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1, Application US/09181816
Patent No. 6277818
                                                                                                                                                                                                                                                  : 432 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 99.0 Matches 95; Conservative
                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
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GOETINCK,

CORRESPONDENCE ADDRESS:

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48 KTCYEGNGHFYRGKASTDIMGRPCLPWNSAYVLQQIYHARRQALQLGLGGGHNYCRNPQN 107
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APPLICANT: Guitton, Jean-Dominique
APPLICANT: Guitton, Jean-Dominique
APPLICANT: Jung, Gerard
APPLICANT: Yeh, Patrice
TITLE OF INVENTION: NOVEL BIOLOGICALLY ACTIVE POLYPEPTIDES,
TITLE OF INVENTION: PREPARATION THEREOF AND PHARMACEUTICAL COMPOSITION
NUMBER OF SEQUENCES: 36
                                                                                                   RESULT 18
US-08-142-2508-25
US-08-142-2508-25
Squence 25, Application US/08142590B
Patent No. 6120765
GENERAL INFORMATION:
APPLICANT: HIBINO, Tashihiko; TAKAHASHI, Tadahito; HORII, Izumi; and ITILE OF INVENTION: URCKINASE PLASMINOGEN ACTIVATOR FRAGMENTS
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
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128 RRRPWCYVQVGLKPLVQECMVHDCADG-KPSSPPEE 162
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Pred. No. 1.1e
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                             STREET: 28 STATES STREET
STREET: Boston
STATE: Massachusetts
COUNTRY: USA
ZIF: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/142,590B
FILING DATE: 25-OCT-1993
ATTORNEY/AGENT INPORMATION:
NAME: MYSTEM POSMATION:
NAME: MYSTEM POSMATION:
NAME: MYSTEM POSMATION:
NAME: MYSTEM POSMATION:
NAME: MYSTEM POSMATION:
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NAME: MYSTEM POSMATION:
NAME: MYSTEM POSMATION:
NAME: MYSTEM POSMATION:
TELEPHONE: (617) 227-7400
                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: LAHIVE & COCKFIELD, LLP STREET: 28 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 12, Application US/08797689
Patent No. 5876569
GENERAL INFORMATION
APPLICANT: Fleer, Reinhard
APPLICANT: Fournier, Alain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  95.78;
95.88;
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INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 157 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 95.8
Matches 92, Conservative
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FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
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US-08-797-689-12
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Pred. No. 3.6e-56;
0; Mismatches 0; Indels 1;
                                                                                                                                                          COMPUTER READABLE FORM:

MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CUBRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/560,098A
FILING DATE: 17-NOV-1995
PRIOR APPLICATION NUMBER: P 44 40 892.7
FILING DATE: 17-NOV-1994
ATYONEY/AGENT INFORMATION:
NAME: EVANS, USGEPD D.
REGISTRATION NUMBER: 26,269
REFERENCE/DOCKET NUMBER: 26,269
REFERENCE/DOCKET NUMBER: 26,269
REJERPAN: (202) 628-8840
TELEPHONE: (202) 628-8840
TELEPHONE: (202) 628-8844
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
FWATH: 411 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 98.0%; Score 543; DB 2; Length 411; Best Local Similarity 99.0%; Pred. No. 9.9e-57; Matches 95; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;Patent No. 5219569
; APPLICANT: BLABER, MICHAEL;HEYNEKER, HERBERT L.;VEHAR,
                      ADDRESSEE: Evenson, McKeown, Edwards & Lenahan
STREET: 1200 G Street, N.W., Suite 700
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      108 RRRPWCYVQVGLKPLVQECMVHDWADGKKPSSPPEE 143
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TITLE OF INVENTION: PROTEASE RESISTANT UROKINASE
NUMBER OF SEQUENCES: 6
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/766,858
FILING DATE: 16-AUG-1985
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 725,468
FILING DATE: 22-APR-1985
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Best Local Similarity 99.01
Matches 95; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS:
                                                                                  CITY: Washi:
STATE: DC
COUNTRY: US.
ZIP: 20005
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5219569-2
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US-09-101-272G-80
Squence 80, Application US/09101272G
Squence 80, Application US/09101272G
Patent No. 6509445
GENERAL INFORMATION:
APPLICANT: Nissin Food Products Co., Ltd.
TITLE OF INVENTION: CANCEROUS METASTARIS INHIBITOR
FILE REFERENCE: Q50979
CURRENT APPLICATION NUMBER: US/09/101,272G
CURRENT APPLICATION NUMBER: JP 1059/1996
PRIOR APPLICATION NUMBER: JP 1059/1996
PRIOR FILING DATE: 1996-01-08
PRIOR FILING DATE: 1996-01-08
NUMBER OF SEQ ID NOS: 107
SOFTWARE: PatentIn Version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Pred. ...
100.0%; Mismatches
                                                                                                                                                                           COUNTIL USA

ZIP: 19426
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Macintosh
OPERATING SYSTEM: System 7.1
SOFFWARE: Word 5.1 (Patentin)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/797,689
FILING DATE: 31-JAN-1997
CLASSIFICATION DATA:
APPLICATION WHRER: US 08/256,927
FILING DATE: 28-UUL-1994
APPLICATION NUMBER: FR 92/01064
FILING DATE: 28-UN-1993
APPLICATION NUMBER: PCT/FR93/00085
FILING DATE: 28-JAN-1993
ATTORNEY AGENT INFORMATION:
NAME: Smith Ph.D. Julie K.
REGISTRATION NUMBER: P38,619
REGISTRATION NUMBER: P38,619
REGISTRATION NUMBER: P38,619
REGISTRATION NUMBER: P38,619
REGISTRATION NUMBER: P38,619
REGISTRATION NUMBER: P38,619
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REGISTRATION NUMBER: P38,619
REGISTRATION NUMBER: P38,619
RELECOMMUNICATION INPORMATION:
TELEPONMUNICATION INPORMATION:
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O'OTHER INFORMATION: AIFHI chimeric protein
5:09-101-27125-80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 RRRPWCYVQVGLKPLVQECMVHDCADGK 88
                            ADDRESSEE: Rhone-Poulenc Rorer Inc. STREET: 500 Arcola Road, 3C43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 194
TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 1, SEQUENCE CHARACTERISTICS:
LENGTH: 138 ami--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  88; Conservative
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CORRESPONDENCE ADDRESS:
                                                                                            Collegeville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
Matches 88; Conserva
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                                                                                                                                                         COUNTRY:
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49 KTCYEGNGHFYRGKASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDN 108
                                                                                                                     49 KTCYEGNGHFYRGKASTDIMGRPCLPWNSATVLQQTYHAHRSDALQLGLGGKHNYCRNPDN 108
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                                                                                            1 KTCYEGNGHFYRGKASTDIMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDN 60
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                                                   0; Gaps
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Query Match 91.2%; Score 505; DB 4; Length 194; Best Local Similarity 100.0%; Pred. No. 1.4e-52; Matches 87; Conservative 0; Mismatches 0; Indels
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; OTHER INFORMATION: residues 43-131 of the AIF domain of uFA
US-09-101-272G-62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  88.3%; Score 489; DB 4; Length 89;
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Patent No. 650945

GENERAL INFORMATION:

APPLICANT NISSIN FOOD PrODUCES CO., Ltd.

TITLE OF INVENTION: CANCEROUS METASTASIS INHIBITOR

FILE REFRENCES (500979

CURRENT APPLICATION NUMBER: US/09/101,2726

CURRENT FILING DATE: 1998-07-08

PRIOR PULING DATE: 1998-07-08

NUMBER OF SEQ ID NOS: 107

SOFTWARE: PATENTING DATE: 1996-01-08

NUMBER OF SEQ ID NOS: 107

SEQ ID NO 62

LENGTH: 89
                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION CANCEROUS METASTASIS INHIBITOR FILLE REFERENCE: Q50979 CURRENT APPLICATION NUMBER: US/09/101,272G CURRENT FILLING DATE: 1998-07-08 PRIOR FILLING DATE: 1996-01-08 NUMBER OF SEQ ID NOS: 107 SOFTWARE: Patentin version 3.1 SEQ ID NO 96 LENGTH: 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: ATFHI-CL chimeric protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    109 RRRPWCYVQVGLKPLVQECMVHDCADG 135
                                                                                                                                                                                                                         109 RRRPWCYVQVGLKPLVQECMVHDCADG 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 RRRPWCYVQVGLKPLVQECMVHDCADG 87
                                                                                                                                                                                               61 RRRPWCYVQVGLKPLVQECMVHDCADG 87
                                                                                                                                                                                                                                                                                                                                                              ; Sequence 96, Application US/09101272G; Patent No. 6509445; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                   RESULT 21
US-09-101-272G-96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-101-272G-62
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                                                                                                                                                              KTCYEGNGHFYRGKASTDIMGRPCLPWNSAIVLQQIYHAHRSDALQLGLGGGHNYCRNPDN 65
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                                           0; Gaps
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COUNTRY:
USA
ZIP:
2005

ZOMPUTER READABLE FORM:
MEDIUNT TYPE:
COMPUTER: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM:
OPERATING SYSTEM:
PC-DOS/MS-DOS
SOFTWARE:
PREDICATION DATA:
APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION UMBER: 144 40 892.7
FILING DATE: 17-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: EVANS, JOSSEPh D.
REGISTRATION NUMBER: 26,269
REBERENCE/POCKET NUMBER: 148/42448
TELECOMMUNICATION INFORMATION:
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                                       Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 51, Application US/08560098A

Patent No. 5976841

GENERAL INFORMATION:
APPLICANT: WNENDY.
APPLICANT: HEINZEL-WIELAND, Regina
APPLICANT: STEFFENS, Gerd Josef
TITLE OF INVENTION: Proteins having Fibrinolytic and
TITLE OF INVENTION: Coagulation-inhibiting Properties
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: Everyon, McKeown, Edwards & Lenahan STREET: 1200 G Street, N.W., Suite 700 STATE: DC CONTRESS DC CONTRESS DC CONTRESS DC
Best Local Similarity 100.0%; Pred. No. 4.4e-51; Matches 84; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          43.5%; Score 241; DB 2;
50.0%; Pred. No. 1.3e-20;
tive 12; Mismatches 30
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187 SKPWCYVIKASKFILEFCSVPVCS 210
                                                                                                                                                                                                                                                              RRRPWCYVQVGLKPLVQECMVHDC 84
                                                                                                                                                                                                                                                                                                                                 66 RRRPWCYVQVGLKPLVQECMVHDC 89
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US-07-609-510B-16
; Sequence 16, Application US/07609510B
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INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
LENGTH: 477 amino acids
TYPE: amino acid
STRANDEDNESS: single
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Best Local Similarity 50.0%
Matches 42; Conservative
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US-08-560-098A-51
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US-08-560-098A-51
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APPLICANT: Berg et al.
TITLE OF INVENTION: Method for Altering Post-Translational Processing of Tissue i
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Eli Lilly and Company
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           91 TCYEDQGISYRGTWSTAESGAECTNWNSSALAQKPYSGRRPDAIRLGLGNHNYCRNPDRD 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 TCYEGNGHFYRGKASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNR 61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           36; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: P.C. STREET: P.C. STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400 STATE: VA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CUBRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/811,949
FILING DATE: 05-MAR-1997
CLASSIFICATION: 435
                                                                                                                                                                                                                            ZIP: 46285
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.0 Mb storage
COMPUTER: Macintosh
OPERATING SYSTEM: Macintosh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: SAITO, YOSHIMASA
APPLICANT: SAAITO, YOSHIMASA
APPLICANT: SAASHI, HITOSHI
APPLICANT: HAYASHI, HITOSHI
APPLICANT: HOTANI, JOUJI
APPLICANT: KOBAYASHI, MASAKAZU
TITLE OF INVENTION: TISSUE PLASMINOGEN ACTIVATOR
NUMBER OF SEQUENCES: 67
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 226; DB 1;
Pred. No. 8.8e-19;
9; Mismatches 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 :||||| ::|
151 SKPWCYVFKAGKYSSEFCSTPACSEG 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62 RRPWCYVQVGLKPLVQECMVHDCADG 87
                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Microsoft Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/609,510B
FILING DATE: 19901106
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 39, Application US/08811949
Patent No. 5840533
GENERAL INFORMATION:
                                                                                                                         E: Eli Lilly and Compa
Lilly Corporate Center
                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 16: SEQUENCE CHARACTERISTICS: LENGTH: 527 amino acids TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 40.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 47.7'
Matches 41; Conservative
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ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                             STREET: Lilly Corp. CITY: Indianapolis STATE: IN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
                                                                                                                                                                                                         USA.
GENERAL INFORMATION:
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                                                                                                                                                                                                           COUNTRY:
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2 TCYEGNGHFYRGKASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNR 61
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Fatent No. 5520913

Fatent No. 5520913

APPLICANT: ANDERSON, STEPHEN; BENNETT, WILLIAM F.; BOUSTEIN.

DAVID; HIGGINS, DEBORAH L.; PAONI, NICHOLAS F.; ZOLLER, MARK J.

TITLE OF INVENTION: TISSUE PLASMINOGEN ACTIVATOR HAVING

XYMOGENIC PROPERTIES

NUMBER OF SEQUENCES: 35

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/89,451

FILING DATE: 04-011-1993

PRIOR APPLICATION NUMBER: 770,510

FILING DATE: 24-101-1991

APPLICATION NUMBER: 384,608

FILING DATE: 24-011-1989

APPLICATION NUMBER: 240,856

FILING DATE: 02-SEP-1988
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CANT: GOEDDEL, DAVID V.;KOHR, WILLIAM J.;PENNICA, DIANE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               40.8%; Score 226; DB 6; Length 527;
47.7%; Pred. No. 8.8e-19;
iive 9; Mismatches 36; Indels
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TITLE OF INVENTION: TRUNCATED HUMAN TISSUE PLASMINOGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            40.8%; Score 226; DB 6; L
47.7%; Pred. No. 8.8e-19;
Live 9; Mismatches 36;
                                                                                                                                                                                                                                                                                                                          ; ACTIVATOR
; ACTIVATOR
; NUMBER OF SEQUENCES: 15
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/489,855
; FILING DATE: 02-MAR-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 12,694
; FILING DATE: 09-FEB-1987
; APPLICATION NUMBER: 483,052
; FILING DATE: 07-APR-1983
; FILING DATE: 14-JUL-1982
; FILING DATE: 14-JUL-1982
; FILING DATE: 05-MAY-1982
; FILING DATE: 05-MAY-1982
                                                                                                                                                    151 SKPWCYVFKAGKYSSEFCSTPACSEG 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           151 SKPWCYVFKAGKYSSEFCSTPACSEG 176
                                                                                                           62 RRPWCYVQVGLKPLVQECMVHDCADG 87
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Best Local Similarity 47.7
Matches 41; Conservative
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Best Local Similarity
Matches 41; Conserv
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;Patent No.
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APPLICANT: Genericch, Inc.
TITLE OF INVENTION: Specific Properties
TITLE OF SEQUENCES: 2
CORRESPONDENCE ADDRESS: ADDRESSE: Genericch, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STREET: California
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8.8e-19;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/01025A
FILING DATE:
FLING DATE: 135
                                                                                                                                                                                                                                                                                                                                     Pred. No. 8.8e
9; Mismatches
                                                                                                                                                                                                                                                                                                               Query Match 40.8%; Score 226; Best Local Similarity 47.7%; Pred. No. 8 Matches 41; Conservative 9; Mismatch
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                                                              18-966-0
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APPLICATION NAMBER: 07/486,657
FILING DATE: 1 March 1990
ATTORNEY/AGENT INFORMATION:
NAME: Hasak, Janet E.
REGISTRATION NAMBER: 28,616
REFERENCE/DOCKET NUMBER: 454P2
TELECOMMUNICATION: INFORMATION:
                                                     REFERENCE/DOCKET NUMBER: 18-9
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEPAX: 703-413-220
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 527 amino acids
                                          24,618
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TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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TOPOLOGY:
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,
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amino acid
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Best Local Similarity
Matches 41; Conserva
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TCYEGNGHFYRGKASIDIMGRPCLPWNSAIVLQQIYHAHRSDALQLGLGKHNYCRNPDNR 61
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Best Local Similarity 47.7%; Pred. No. 9.2e-19;
Matches 41; Conservative 9; Mismatches 36; Indels
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APPLICANT: SAITO, YOSHIMASA
APPLICANT: SASATI, HITOSHI
APPLICANT: HAYSHI, MASAKO
APPLICANT: HAYSHI, MASAKO
APPLICANT: HOTANI, JOUJI
APPLICANT: KOBAYASHI, MASAKZU
APPLICANT: KOBAYASHI, MASAKZU
APPLICANT: KOBAYASHI, MASAKZZU
APPLICANT: KOBAYASHI, MASAKZZU
APPLICANT: KOBAYASHI, MASAKZZU
APPLICANT: KOBAYASHI, MASAKZZU
ADBESSEE: P.C.
ADDRESSEE: P.C.
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5200340-6
5200340-6
5PAGANI: FOSTER, DONALD C.;MULVIHILL, EILEEN R.;O'HARA,
FAPPLICANT: FOSTER, DONALD C.;MULVIHILL, EILEEN R.;O'HARA,
FATRICK J.;PINGEL, KURT;YOSHITAKE, SHINJI
TITLE OF INVENTION: THROMBIN-ACTIVATED TISSUE PLASMINOGEN
ACTIVATORS
NUMBER OF SEQUENCES: 34
CURRENT APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 22-MAY-1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               F: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400 ARLINGTON
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COMPUTER READBLE FORM:.
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/811,949
FILING DATE: 05-MR-1997
CLASSIFICATION: 435
                                                                                                                              151 SKPWCYVFKAGKYSSEFCSTPACSEG 176
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; Sequence 43, Application US/08811949
Patent No. 5840533
; GENERAL INFORMATION:
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NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 18-
TELECOMMUNICATION:
TELEPHONE: 703-413-3000
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plasmin (EC 3.4.21
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1 KTCYEGNGHFYRGKASTDTM.....QECMVHDCADGKKPSSPPEE
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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Match Length DB
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C; Keywords: fibrinolysis; glycoprotein; heterodimer; hydrolase; nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimber, nimbe
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C;Species: Papio cynocephalus, Papio hamadryas cynocephalus (yellow baboon)
C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 18-Jun-1999
C;Accession: 314687; S08651
R;Au, Y.P.T.; Wang, T.W.; Clowes, A.W.
Nucleic Acids Res. 18, 311, 1990
A;Ittle: Nucleotide and deduced amino acid sequences of baboon urokinase-type pla.
A;Ittle: Nucleotide and deduced amino acid sequences of baboon urokinase-type pla.
A;Acference number: $14687, MUID:90287734; PMID:2113276
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N,Alternate names: uPA
C,Species: Sus scrofa domestica (domestic pig)
C,Date: 04-Dec-1986 #sequence_revision 17-Mar-1997 #text_change 07-Aug-1998
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Pred. No. 7.4e-48;
1; Mismatches 4; Indels
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A; Molecule type: protein

A; Molecule type: protein

A; Molecule type: protein

A; Mesidues: 189-410. 6.3TE>

B; Mentrer. E.J.; Buko, A; Menon, G.; Sarin, V.K.

B; Mesidues: 189-410. 6.3TE>

A; Reference number: A35689; MUID: 90365737; PMID: 2393398

A; Molecule type: protein

A; Mesidues: 21-30. V.; 32. V.; 34-38. V.; 40-43. < KEN>

A; Molecule type: protein

A; Mesidues: 21-30. V.; 32. V.; 34-38. V.; 40-43. < KEN>

A; Molecule type: protein

A; Mesidues: 21-30. V.; 32. V.; 34-38. V.; 40-43. < KEN>

A; Molecule type: protein

A; Mesidues: 10-80; MuiD: 91097529; PMID: 2125213

A; Molecule type: protein

A; Mesidues: A3687; MuiD: 91097529; PMID: 2125213

A; Molecule type: protein

A; Mesidues: 21-34. < RAB>

R; Li, X.; Bokman, A.M.; Llinas, M.; Smith, R.A.G.; Dobson, C.M.

A; Mesidues: 21-34. < RAB>

R; Li, X.; Smith, R.A.G.; Dobson, C.M.

B; Mohemistry 31, 956-9571, 1992

A; Molecule to the Brookhaven Protein and disulfide bond assignments by (1) H-NMR, residue

A; Contents: annotation; conformation and disulfide bond assignments by (1) H-NMR, residue

R; Hansen, A.P.; Petros, A.M.; Meadows, R.P.; Nettesheim, D.G.; Mazar, A.P.; Olejniczak, A; Reference number: A44375; MUID: 9109164 bond assignments by (1) H-NMR, residue

A; Contents: annotation; conformation and disulfide bond assignments by (1) H-NMR, submitted to the Brookhaven Protein Date Bank, January 1994

A; Reference number: A46822; PBB: 1URX

A; Reference number: A66822; PBB: 1URX

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A; Reference number: A66822; PBB: 1URX

A; Contents: annotation; Conformation and disulfide bond assignments by (1) H-NMR, residue

B; Reference number: A66822; PBB: 1URX

A; Contents: annotation; Conformation and disulfide bond assignments by (1) H-NMR, residue
R;Yoshimoto, M.; Ushiyama, Y.; Sakai, M.; Tamaki, S.; Hara, H.; Takahashi, K.; Sawasaki, Biochim. Biophys. Acta 1293, 63:89, 1996
A;Title: Characterization of Single chain
A;Reference number: 865783; MUID:96186279; PMID:8652631
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A, Pathway: fibrinolysis
C, Superfamily: urokinase-type plasminogen activator, EGF homology, kringle homology,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Map position: 10g24-10g24
A;Introns: 19/3; 29/1; 65/1; 123/2; 154/1; 227/2; 277/1; 324/1; 373/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Description: proteolytically activates plasminogen Pathway: fibrinolysis
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predicted

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C.Superfamily: urokinase-type plasminogen activator; EGF homology; kringle homology; tr. C.Keywords: glycoprotein; heterodimer; hydrolase; kringle; serine proteinase proteinase products is glycoprotein; heterodimer; hydrolase; kringle; serine proteinase proteinase products of Signal sequence #status predicted <Signal-24)Domain: BGP homology eGFPs plasminogen activator chain A #status predicted <ACH>F;31-62,Domain: BGP homology eRGPs plasminogen activator chain B #status predicted <BCH: P;109-432/Product: urokinase-type plasminogen activator chain B #status predicted <BCH: P;179-420,Domain: trypsin homology eRTX' P;179-420,Domain: trypsin homology eRTX' P;168-300,210-226,218-289,314-383,346-362,373-401/Disulfide bonds: #status predicted P;225,276,377/Active site: His, Asp, Ser #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gene 125, 177-183, 1993
A;Title: Bovine urokinase-type plasminogen activator and its receptor: cloning and indu A;Reference number: JN0560; MUID:93216119; PMID:8385052
A;Accession: JN0560
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Fi181-421/Domain: trypsin homology <TRY>
Fi770-301,211-227,219-290,315-384,347-363,374-402/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KTCYHGNGQSYRGKANTDTKGRPCLAMNSPAVLQQTYNAHRSDALSLGLGKHNYCRNPDN 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N.Alternate names: upA
C.Species: Bos primágenius taurus (cattle)
C.Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 16-Jul-1999
C.Accession: JND560
R.Kraetzschmar, J.; Haendler, B.; Kojima, S.; Rifkin, D.B.; Schleuning, W.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           70 KTCYQGNGHSYRGKANRDLSGRPCLAWDSPTVLLKMYHAHRSDAIQLGLGKHNYCRNPDN
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A;Cross-references: EMBL:X66907; NID:g396200; PIDN:CAA47356.1; PID:g938279
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Pred. No. 5.1e-38;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         u-plasminogen activator (EC 3.4.21.73) precursor - bovine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        128 ORRPWCYVÓIGLKOFVÓECMVODCSLSKKPSSTVDO 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 RRRPWCYVQVGLKPLVQECMVHDCADGKKPSSPPEE 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  130 QRRPWCYVQIGLKQFVQFCMVQDCSVGKSPSSPREK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7; Mismatches
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77.18;
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Best Local Similarity 77.14%

Best Local 54 Conservative

TA1 Conservative
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Matches 72; Conservative
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C; Superfamily: urokinase-type plasminogen activator; EGF homology; kringle homology; try
C; Superfamily: urokinase-type plasminogen activator; EGF homology; kringle homology; try
C; Superfamily: signal sequence #status predicted selfs.
F; 1-20/Domain: signal sequence #status predicted cation activator chain A #status predicted cACH>
F; 21-188/Product: urokinase-type plasminogen activator chain B #status predicted cACH>
F; 21-153/Domain: kringle homology cRRS>
F; 190-442/Product: urokinase-type plasminogen activator chain B #status predicted cBCH>
F; 190-400/Domain: trypsin homology cRRS>
F; 190-400/Domain: trypsin homology cRRS>
F; 152/Binding site: carbohydrate (Asn) (covalent) #status predicted
F; 152/Binding site: Asp, Ser #status predicted
F; 135, 286, 387/Active site: His, Asp, Ser #status predicted
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C; Species: Rattus norvegicus (Norway rat.)
C; Date: 18-Oct-1989 #sequence revision 10-Feb-1995 #text_change 18-Jun-1999
C; Accession: S24604; 160186; Ī53472; S18932
R; Rabbani, S.A.
submitted to the EMBL Data Library, April 1992
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Cancer Res. 52, 2489-2496, 1992
AjTitle: Transcriptional and posttranscriptional activation of urokinase plasminogen act
A;Reference number: I60186; WUID:92233409; PMID:1568219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Title: The receptor for the plasminogen activator of urokinase type is up-regulated in Reference number: 153472; MUID:92339549; PMID:1321734
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 70 OTCFEGNGHSYRGKANINIGGRPCLPWNSAIVLLNIYHAHRPDALQLGLGKHNYCRNPDN 129
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                      .Nagamine, Y.; Pearson, D.; Altus, M.S.; Reich, E.
Ordeic Acids Res. 12, 9525-9541, 1984
Title: cDNA and gene nuclectide sequence of porcine plasminogen activator.
Reference number: A00932; MUID:85087954; PMID:6096832
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A;Residues: 1.1-15, H'.17-23,'G',25-331,'N',333-432 <RAB>
A;Cross_references: EMBL:X65651; NID:g57456; PIDN:CAA46601.1; PID:g57457
A;Experimental source: tissue kidney
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Reference number: A37566
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Pred. No. 3.9e-39;
8; Mismatches 10
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N;Molecule type: mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                      Contents: annotation; correction to residue 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             u-plasminogen activator (EC 3.4.21.73) precursor
                                                                                                                                                                                                       A;Molecule type: DNA
A;Residues: 1-240,'H',242-442 <NAG1>
A;Experimental source: kidney cell line LLC-PK1
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74.3%; Pred
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A;Accession: S24604
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EBS Lett. 306, 193-198,
;Title: The receptor for
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Matches 78; Conserv
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                                                                                                                                                                         Accession: A00932
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Cidcossion: A34369
Rigardell, S.J.; Duong, L.T.; Diehl, R.E.; York, J.D.; Hare, T.R.; Register, R.B.; Jack J. Biol. Chem. 264, 11947-17952, 1989
A;Title: Isolation, characterization, and cDNA cloning of a vampire bat salivary plasm: A;Reference number: A34369; MUID:90036867; PMID:2509450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             F)128-209/Domain: kringie homology «KRG»
F)226-471/Domain: trypsin homology «TRY»
F;42-72,70-79,87-98,92-109,111-120,128-209,149-191,180-204,214-345,257-273,265-334,359-
F;272,321,428/Active site: His, Asp, Ser #status predicted
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A; Residues: 1-477 < kRA>
A; Residues: 1-477 < kRA>
A; Residues: 1-477 < kRA>
C; Superfamily: tissue plasminogen activator; EGF homology; fibronectin type I repeat I
C; Reywords: fibrinolysis; glycoprotein; hydrolase; kringle; serine proteinase
F; 1-21/Domain: signal sequence #status predicted < SIG>
F; 2-36/Domain: propeptide #status predicted < PRO>
F; 3-477/Product: plasminogen activator alpha-2 #status predicted < PLA>
F; 2-79/Domain: fibronectin type I repeat homology < 1FA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      t-plasminogen activator (EC 3.4.21.68) precursor - false vampire bat (Megaderma lyra)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Kraetzschmar, J.; Haendler, B.; Langer, G.; Boidol, W.; Bringmann, P.; Alagon, A.;
Gene 105, 232-237, 1991
Affitle: The plasminogen activator family from the salivary gland of the vampire bat
A;Reference number: JS0597; MUID:92039036; PMID:1937019
                                                                                                                                                               81 TCYKDQGVTYRGTWSTSESGAQCINWNSNLLTRRTYNGRRSDAITLGLGNHNYCRNPDNN 140
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A/Status: preliminary
A/Molecule type: mRNA
A/Molecule type: mRNA
A/Molecule type: mRNA
A/Molecule type: mRNA
A/Cross-references: 1-477 cGAR>
A/Cross-references: GB.J05082; NID:g166080; PIDN:AAA31596.1; PID:g166081
C/Superfamily: tissue plasminogen activator; EGF homology; fibronectin type I
C/Keywords: fibrinolysis; glycoprotein, hydrolase; Kringle; serine proteinase
F/1-21/Pomain: signal sequence #status predicted <BIG>
F/2-2-A56 Domain: propeptide #status predicted <PRO>
F/3-477/Product: plasminogen activator #status predicted <PLA>
F/87-19/Domain: EGF homology <EGF>
F/87-120/Domain: EGF homology <EGF>
F/87-120/Domain: EGF homology <EGF>
F/87-120/Domain: FGF homology <EGF>
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C;Species: Desmodus rotundus (common vampire bat)
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 16-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Megaderma lyra
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
                                                                                                  TCYEGNGHFYRGKASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNR
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              30; Indels
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50.0%; Pred. No. 4.5e-18;
iive 12; Mismatches 30;
         12; Mismatches
                                                                                                                                                                                                                                                                                                                                                               164
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                                                                                                                                                                                                                                                                           62 RRPWCYVQVGLKPLVQECMVHDCA
                                                                                                                                                                                                                                                                                                                                                     141 SKPWCYVIKASKFILEFCSVPVCS
              42; Conservative
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Best Local Similarity
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                                                                                                                                                                                                                  A Molecule type: DNA
A Residues: 1-433 «DEG>
A Kesidues: 1-433 «DEG>
A Cross-references: GB: M17922; NID:g202296; PIDN:AAA40539.1; PID:g202297
B R Belin, D.; Vassalli, J.D.; Combepine, C.; Godeau, F.; Nagamine, Y.; Reich, E.; Kocher, Enci. J. Biochem. 148, 225-223, 1985
A Title: Cloning, nucleotide sequencing and expression of CDNAs encoding mouse urokinase A. Reference number: A24615; MUID:85179474; PMID:2985383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Introns: 19/3; 30/1; 66/1; 124/2; 155/1; 229/2; 279/1; 326/1; 375/3; Superfamily: urokinase-type plasminogen activator; EGF homology; kringle homology; try; Keywords: glycoprotein; heterodimer; hydrolase; kringle; serine proteinase; 1-20/Domain: signal sequence #status predicted <SIG; 21-178/Product: urokinase-type plasminogen activator chain A #status predicted <ACH> 32-63/Domain: EGF homology <EGF> 32-63/Domain: EGF homology <EGF> 31-152/Domain: kringle homology <KRG>
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Cross-references: GB:M63989; NID:g166076; PIDN:AAA31594.1; PID:g166077

Superfamily: tissue plasminogen activator; BGF homology; fibronectin type I repeat hom activators: fibrinolysis; glycoprotein; hydrolase; kringle; serine proteinase; 1.21/Domain: signal sequence #status predicted «SIG»

22-36/Domain: propeptide #status predicted «PRO»

37-431/Product: plasminogen activator beta #status predicted «PLA»
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;180-425/Domain: trypsin homology <TRY>
;41-52,46-63,65-74,82-163,103-145,134-158,168-299,211-227,219-288,313-388/Disulfide bon ;419-352/Bindhing site: carbohydrate (Asn) (covalent) #status predicted ;179-180/Cleavage site: His-Ser (plasmin) #status predicted ;226,275,382/Active site: His-Asp, Ser #status predicted ;326,275,382/Active site: His-Asp, Ser #status predicted ;345-361,378-406/Disulfide bonds: #status predicted
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A;Title: The plasminogen activator family from the salivary gland of the vampire A;Reference number: JSOS97; MUID:92039036; PMID:1937019
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Species: Desmodus rotundus (common vampire bat)
Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 16-Jul-1999
Accession: JS0599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 KTCYEGNGHFYRGKASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDN
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5.5e-36;
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;Degen, S.J.F.; Heckel, J.L.; Reich, E.; Degen, J.L.
lochemistry 26, 8270-8279, 1987
;Title: The muxine urckinase-type plasminogen activator gene.;
Reference number: A29420, MUID:88163489; PMID:2831940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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Pred. No. 4.1e-18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    73.6%; Score 408; DB 70.8%; Pred. No. 5.5e cive 12; Mismatches
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82-163/Domain: kringle homology <KRG>
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50.0%;
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Residues: 1-433 <BEL>
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Matches 68; Conserv
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Best Local Similarity
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                                                                                                                                                                                      Accession: A29420
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A Map position: 8p12-8p12

A introns: 24/3; 39/1; 85/1; 122/1; 180/2; 211/1; 268/2

A introns: 24/3; 39/1; 85/1; 122/1; 180/2; 211/1; 268/2

C Superfamily: tissue plasminogen activator; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 21/9; 
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A;Title: The human tissue plasminogen activator gene.
A;Title: The humber: A23529; MUID:86196143; PMID:3009482
                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Status: translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
A; Redudes: 1-291 <818-74
A; Redidues: 1-291 <818-74
A; CFOSS-teferences: EMBL: X13097; NID: 935282; FIDN: CAA31489.1; FID: 935283
C; Comment: For the main splice form, see PIR: UKHUT. This form probably does not have 1
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A;Residues: 1-562 <DEG>
A;Cross-references: GB:K03021; NID:g339817; PIDN:AA98809.1; PID:g339818
A;Cross-references: GB:K03021; NID:g339817; PIDN:AA98809.1; PID:g339818
B;Itagaki, Y.; Yasuda, H.; Morinaga, T.; Mitsuda, S.; Higashio, K.
Agric. Biol. Chem. 55, 1225-1232, 1991
A;Title: Purification and characterization of tissue plasminogen activator secreted
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                                                                            inactive endothelial splice form - human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A,Gene: GDB:PLAT
A,Cross-references: GDB:119496; OMIM:173370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RRPWCYVOVGLKPLVQECMVHDCADG 87
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A,Residues: 1-562 <NYT>
A,Cross-references: GB:L00141
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C;Species: Rattus norvegicus (Norway rat)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession. A35029; A31597
B;Feng, P.; Ohlsson, M.; Ny, T.
J. Biol. Chem. 265, 2022-2027, 1990
A;Title: The structure of the TATA-less rat tissue-type plasminogen activator gene. Spec
A;Reference number: A35029; MUID:90130448; PMID:2105315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Cross-references: GB:M31197; NID:g207429; PIDN:AAA42261.1; PID:g207431; GB:J05226
B;Ny, T.; Leonardsson, G.; Hsueh, A.J.W.
B)NA, 7, 671-677, 1988
A;Title: Cloning and characterization of a cDNA for rat tissue-type plasminogen activate
A;Reference number: A31597; MUID:89170114; PMID:3148445
F;128-209/Domain: kringle homology <KRG>
F;226-471/Domain: trypsin homology <TRY>
F;42-72,70-79,87-98,92-109,111-120,128-209,149-191,180-204,214-345,257-273,265-334,359-
F;48-72,70-79,87-98,52-109,111-120,128-209,149-191,180-204,214-345,257-273,265-334,359-
F;185,398/Binding site: carbohydrate (Amalia (covalent) #status predicted
F;225-226/Cleavage site: His-Ser (plasmin) #status predicted
F;272,321,428/Active site: His, Asp, Ser #status predicted
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                                                                                                                                                                                                                                                                          Length 477;
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                                                                                                                                                                                                                                                                                                                                                       30; Indels
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                                                                                                                                                                                                                                                                          43.5%; Score 241; DB 2;
50.0%; Pred. No. 4.5e-18;
ative 12; Mismatches 30;
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Best Local Similarity
Matches 42; Conserv
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Matches 43; Conserv
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A)Cross-references: GDB:119496; OMIM:173370

A)Map position: 6012-8012

A)Map position: 8012-8012

A)Map position: 8012-8012

A)Map position: 1951; 120/1; 180/2; 211/1; 268/2; 297/1; 362/2; 408/1; 455/3; 5

A)Introns: 24/3; 39/1; 85/1; 122/1; 180/2; 211/1; 268/2; 297/1; 362/2; 408/1; 455/3; 5

A)Map position: 24/3; 39/1; 85/1; 122/1; 180/2; 211/1; 268/2; 297/1; 362/2; 408/1; 455/3; 5

A)Map position: 24/3; 39/1; 85/1; 122/1; 180/2; 211/1; 268/2; 297/1; 362/2; 408/1; 455/3; 5

A)Map position: 24/3; 39/1; 85/1; 122/1; 180/2; 211/1; 268/2; 297/1; 362/2; 408/1; 455/3; 5

C)Superfamily: Lissue plasminogen activator fattus experimental company companies in propertide fattus predicted companies in propertide fattus activator fattus experimental companies in the propertide fattus companies companies in the propertide fattus companies companies in the propertide fattus companies companies companies companies companies companies companies companies companies companies companies companies companies companies companies companies companies companies companies companies companies companies companies companies companies companies companies companies companies companies companies companies companies companies companies companies companies companies companies companies companies companies companies companies companies companies companies companies companies companies companies companies companies companies companies companies companies companies companies companies companies companies companies companies companies com
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R;Fisher, R.; Waller, E.K.; Grossi, G.; Thompson, D.; Tizard, R.; Schleuning, W.D.
J. Biol. Chem. 260, 11223-11310, 1985
A;Tille: Isolation and characterization of the human tissue-type plasminogen activator
A;Reference number: I55232; MUID:85289338; PMID:3161893
                                                                                                                                                                                                                                                                                                                                                                                                                      A;Title: Expression of human uterine tissue-type plasminogen activator in mouse cells A;Reference number: I60110; MUID:88054470; PMID:2824147 A;Accession: I60110
A;Title: Cloning of cDNA coding for human tissue-type plasminogen activator and its A;Reference number: A54645; MUID:86284200; PMID:3090401
A;Accession: A54645
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 TCYEGNGHFYRGKASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNR 61
                                                                                                                                                                                                                                                                A;Cross-references: GB:MI5518; NID:g190031; PIDN:AAA60111.1; PID:g190032
A;Note: parts of this sequence were confirmed by peptide sequencing
R;Reddy, VB.; Garramone, A.J.; Sasak, H.; Wei, C.
DNA 6, 461-472, 1987
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47.7%; Pred. No. 2.1e-16;
live 9; Mismatches 36;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62 RRPWCYVQVGLKPLVQECMVHDCADG 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status: translated from GB/EMBL/DDBJ
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-562 <RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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es 41; Conserv
                                                                                                                                                                       A;Molecule type: mRNA
A;Residues: 1-562 <HAR>
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                                            A Reference number: J1552; MULD:91291340; PRID:BAB008811; PID:9441174
A Reference number: J1552 (TTA)
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A Reference number: J155
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A.Title: Involvement of finger domain and kringle 2 domain of tissue-type plasminogen ad A; Reference number: A37568; MUID:87161761; PMID:3030730

A; Contents: annotation; fibrin binding site
R; Dodd, I.; Numn, B.; Robinson, J.H.
R; Dodd, I.; Numn, B.; Robinson, J.H.
A; Reference number: A60902; MUID:89044681; PMID:3142086
A; Tile: Isolation, identification and pharmacokinetic properties of human tissue-type p A; Reference number: A60902; MUID:89044681; PMID:3142086
B; Harris, T.J.R.; Patel, T.; Marston, F.A.O.; Little, S.; Emtage, J.S.; Opdenakker, G.; Mol. Biol. Med. 3, 279-292, 1986
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A; Contents: annotation; melanoma cells, partial sequence of residues 36-562, active and A; Contents: annotation; melanoma cells, partial sequence of residues 36-562, active and A; Pontents: annotation; melanoma. M.; Wallen, P.; Jornvall, H.
FEBS Lett. 168, 29-12, 1984
A; Title: Differences between uterine and melanoma forms of tissue plasminogen activator.
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A) Residues: 33-45;311-320 < POH>
A) Experimental Source: uterus cleavage of the activation peptide may also occur after 38-Gln
A) Note: in the uterus, cleavage of the activation peptide may also occur after 38-Gln
R, van Zonneveld, A.J.; Veerman, H.; Pannekoek, H.
J, Biol. Chem. 261, 14214-14218, 1986
A) Reference number: A77567; MUID: 973361
A) Contents: annotation; fibrin binding site
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A;Accession: A91322
                      A; Reference number: JT0562; MUID: 91291340; PMID: 1368681
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Length 559

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123 TCFEEQGITYRGTWSTAESGAECINWNSSVLSLKPYNARRPNAIKLGLGNHNYCRNPDRD 182
                                                                                                                                                                                                                                                                                         2 TCYEGNGHFYRGKASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNR
F;149,481/Binding site: carbohydrate (Asn) (covalent) #status predicted F;308-309/Cleavage site: Arg-Ile (plasmin, trypsin) #status predicted F;355,404,510/Active site: His, Asp, Ser #status predicted
                                                                                                                                       ; Score 219; DB 1; 
; Pred. No. 1.2e-15; 
11; Mismatches 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    183 LKPWCYVFKAGKYTTEFCSTPACPKGK 209
                                                                                                                                                                                                                                                                                                                                                                                                                                    62 RRPWCYVQVGLKPLVQECMVHDCADGK 88
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                                                                                                                                           39.5%;
                                                                                                                                       Query Match
Best Local Similarity 46.0°
Matches 40; Conservative
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JC5878
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A.Resteute: 11394 cKRA-
A.Cross-references: GB-M63990; NID:g166078, PIDN:AAA31595.1; PID:g166079
A.Cross-references: GB-M63990; NID:g166078, PIDN:AAA31595.1; PID:g166079
A.Note: the authors translated the codon AIC EGF homelogy; fibronectin type I repeat hom C.Superfamily: tissue plasminogen activator; EGF homelogy; fibronectin type I repeat hom C.Keywords: fibrinolysis: glycoprotein, hydrolase; kringle; serine proteinase
C.Keywords: fibrinolysis: glycoprotein, hydrolase; kringle; serine proteinase
F.1-21/Domain: signal sequence #status predicted <PGO-
F.32-336/Domain: propeptide #status predicted <PGO-
F.37-334/Product: plasminogen activator gamma #status predicted <PLA>
F.45-126/Domain: kringle homelogy ckRG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               t-plasminogen activator (EC 3.4.21.68) precursor - mouse
C.Species: Mus musculus (house mouse)
C.Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 10-Sep-1999
C.Accession: A22941; S48205; S48207; S48206
R.Rickles, R.J.: Darrow, A.L.: Strickland, S.
Biol. Chem. 263, 11563-15569, 1988 ~
A.Title: Molecular cloning of complemntary DNA to mouse tissue plasminogen activator mR
A.Reference number: A29941; MUID:88087303; PMID:2826484
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A,Molecule type: protein
C,Mesidues: 33-37, /X, 39-40 <LLW.
C,Superfamily: tissue plasminogen activator; EGF homology; fibronectin type I repeat hom C;Superfamily: tissue plasminogen activator; bydrolase; kringle; serine proteinase
C,Keywords: fibrinolysis; glycoprotein; hydrolase; kringle; serine proteinase
C,Keywords: fibrinolysis; glycoprotein; hydrolase; kringle; serine proteinase
F;13-130/Domain: propeptide #status predicted <RRO.
F;18-29/Domain: propeptide #status predicted <RAT.
F;30-559/Product: t-plasminogen activator fatus predicted <ACH.
F;38-75/Domain: EGF homology <EGF.
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F;38-68,66-75,83-94,88-105,107-116,124-205,145-187,176-200,213-294,234-276,265-289,297-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         F.143-388/Domain: trypsin homology <TRY>
F.45-126,66-108,97-121,131-262,174-190,182-251,276-351,308-324,341-369/Disulfide bonds:
F.142-143/Cleavage site: His-Ser (plasmin) #status predicted
F.189,238,345/Active site: His, Asp, Ser #status predicted
                                 A,Title: The plasminogen activator family from the salivary gland of the vampire bat A,Reference number: JS0597; MUID:92039036; PMID:1937019
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6.6e-16;
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A;Residues: 1-559 <RIC>
A;Cross-references: GB:J03520; NID:g202109; PIDN:AAA.
R;Lijne, H.R.; van Hoef, B.; Beelen, V.; Collen, D.
Eur. J. Biochem. 224, 863-871, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            39.7%; Score 220; DB 45.2%; Pred. No. 6.6e-tive 13; Mismatches
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A;Residues: 33-37,'X',39-40 <LIJ>A;Accession: S48207
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Best Local Similarity 45.2%
Matches 38; Conservative
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A;Residues: 309-316 <LI2>
A;Accession: S48206
   , 229-237, 1991
                                                                                                                                                  A; Molecule type: mRNA
                                                                                                             A;Accession: JS0600
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plasma hyaluronan-binding protein precursor - mouse cispecies: Mus musculus (house mouse) cispecies: Mus musculus (house mouse) cispecies: Mus musculus (house mouse) cispecies: Mus musculus (house mouse) cispecies: Musculus (house mouse) cispecies: Musculus (house mouse) cispecies: Musculus (house) cispecies: Musculus (house) cispecies: Musculus (house) cispecies: Musculus (house) cispecies: Musculus (house) cispecies: Musculus (house) cispecies: Musculus (house) cispecies: Musculus (house) cispecies: Musculus (house) cispecies: Musculus (house) cispecies: Musculus (house) cispecies: Musculus (house) cispecies: Musculus (house) cispecies: Musculus (house) cispecies: Musculus (house) cispecies: Musculus (house) cispecies: Musculus (house) cispecies: Musculus (house) cispecies: Musculus (house) cispecies: Musculus (house) cispecies: Musculus (house) cispecies: Musculus (house) cispecies: Musculus (house) cispecies: Musculus (house) cispecies: Musculus (house) cispecies: Musculus (house) cispecies: Musculus (house) cispecies: Musculus (house) cispecies: Musculus (house) cispecies: Musculus (house) cispecies: Musculus (house) cispecies: Musculus (house) cispecies: Musculus (house) cispecies: Musculus (house) cispecies: Musculus (house) cispecies: Musculus (house) cispecies: Musculus (house) cispecies: Musculus (house) cispecies: Musculus (house) cispecies: Musculus (house) cispecies: Musculus (house) cispecies: Musculus (house) cispecies: Musculus (house) cispecies: Musculus (house) cispecies: Musculus (house) cispecies: Musculus (house) cispecies: Musculus (house) cispecies: Musculus (house) cispecies: Musculus (house) cispecies: Musculus (house) cispecies: Musculus (house) cispecies: Musculus (house) cispecies: Musculus (house) cispecies: Musculus (house) cispecies: Musculus (house) cispecies: Musculus (house) cispecies: Musculus (house) cispecies: Musculus (house) cispecies: Musculus (house) cispecies: Musculus (house) cispecies: Musculus (house) cispecies: Musculus (house) cispecies: Musculus (house) cispecies:
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A,Residues: 1-477 < kRNA
A,Fesidues: 1-477 < kRNA
A,Cross-references: GB: M63987; NID:g166070; PIDN:AAA31591.1; PID:g166071
C,Superfamily: tissue plasminogen activator; EGF homology; fibronectin type I repeat hc
C,Superfamily: tissue plasminogen activator; RGF homology; fibronectin type I repeat hc
C,Superfamily: signal sequence #status predicted <SIG>
F,12-10/Domain: signal sequence #status predicted <PRO>
F;22-36/Domain: propeptide #status predicted <PRO>
F;22-36/Domain: EGF homology <EGF>
F;21-39/Domain: EGF homology <EGF>
F;22-47/Domain: kringle homology <RRO>
F;22-47/Domain: kringle homology <RRO>
F;26-47/Domain: trypsin homology <RRO>
F;26-47/Domain: kringle homology <RRO>
F;26-47/Domain: kringle homology <RRO>
F;26-47/Domain: kringle homology <RRO>
F;26-47/Domain: kringle homology <RRO>
F;26-47/Domain: kringle homology <RRO>
F;26-47/Domain: kringle homology <RRO>
F;26-77/DOMAIN: kringle homology <RRO>
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F;26-77/DOMAIN: kringle homology <RRO>
F;26-77/DOMAIN: kringle homology <RRO>
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F;26-77/DOMAIN: kringle homology <RRO>
F;26-77/DOMAIN: kringle homology <RRO>
F;26-77/DOMAIN: kringle homology <RO> RO</br/>F;26-72/J,207,273/265-334,359-
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t-plasminogen activator (EC 3.4.21.68) alpha-1 precursor - common vampire bat NyAlternate names: tissue plasminogen activator C;Species: Desmodus rotundus (common vampire bat) C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 16-Jul-1999 C;Accession: JSO597 #sequence_revision 31-Mar-1992 #text_change 16-Jul-1999 Gene 105, 229-237, 1991 A;Ithe: The plasminogen activator family from the salivary gland of the vampire bat IA;Reference number: JSO597; MUID:92039036; PMID:1937019
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C,Comment: This protein acts as serine protease.
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A; Accession: A46688
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                           RESULT 18
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A Generic GDB:HABP2; HABP; HGFAL
A, Cross_references: GDB:H573962
Complexed: a disulfide-bonded heterodimer of chains produced from the same precursor; the C, Superfamily: plasma hyaluronan-binding protein; EGF homology; kringle homology; trypsil C, Keywords: chondroitin sulfate proteoglycan; glycoprotein; hyaluronic acid; hydrolase; F, 1-23/Domain: agnal sequence #status predicted <SIG>
F, 1-31/Product: plasma hyaluronan-binding protein, SOK chain #status predicted <SOK>
F, 1-15-147/Domain: EGF homology <EG2>
F, 154-247/Domain: EGF homology <EG3>
F, 154-247/Domain: kringle homology <EG3>
F, 115-147/Domain: kringle homology <EG3>
F, 114-150/Domain: kringle homology <ER3>
F, 114-150/Domain: kringle homology <ER3>
F, 114-150/Domain: kringle homology <ER3>
F, 114-150/Domain: kringle homology <ER3>
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F, 114-150/Domain: kringle homology <ER3>
F, 114-150/Domain: kringle homology <ER3>
F, 114-150/Domain: kringle homo
C;Superfamily: plasma hyaluronan-binding protein; EGF homology; kringle homology; trypsi F;1-23/Domain: signal sequence #status predicted <SIG> F;24-311/Product: plasma hyaluronan-binding protein large chain #status predicted <MATL> F;75-106/Domain: EGF homology <EG1> F;113-145/Domain: EGF homology <EG2> F;113-145/Domain: EGF homology <EG3> F;113-145/Domain: EGF homology <EG3> F;122-185/Domain: kringle homology <EG3> F;312-558/Product: plasma hyaluronan-binding protein small chain #status predicted <MATS F;312-558/Domain: trypsin homology <TRY>
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A;Note: parts of this sequence, including the amino ends of the mature chains, were dete
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Species: Homo sapiens (man)
C;Date: 15-Oct-1995 #sequence_revision 16-Aug-1996 #text_change 19-Jul-2002
C;Accession: JC6795
R;Choi-Miura, N.H.; Tobe, T.; Sumiya, J.; Nakano, Y.; Sano, Y.; Mazda, T.; Tomita, M. Bicchem. 119, 1157-1165, 1996
A;Title: Purification and characterization of a novel hyaluronan-binding protein (PHBP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4; Gaps 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         192 CYVGDGYSYRGKVSKTVNQNPCLYWNSHLLLQETYNMFMEDAETHGIAEHNFCRNPDGDH 251
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A; Accession: JC4795
A; Molecule type: mRNA
A; Residues: 1.560 < CRIO>
A; Cr.ss.references: GB:S83182; NID:g1836158; PIDN:AAB46909.1; PID:g1836159
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N;Alternate names: hepatocyte growth factor activator-like protein; PHBP
N;Contains: serine proteinase (EC 3.4.21.-)
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Matches 39, Conservative
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A Map position: 4pi6-4pi6

C.Function:
Apachagos: activates hepatocyte growth factor by specific proteolytic cleavage
A.Description: activates hepatocyte growth factor by specific proteolytic cleavage
A.Description: activates hepatocyte growth factor by specific proteolytic cleavage
A.Pachway: tissue repair and regeneration
C.Superfamily: coagulation factor XII; EGF homology, fibronectin type I repeat homology
C.Superfamily: coagulation factor XII; EGF homology in plasma, serine proteinase
C.Superfamily: activates a serine proteinase
F.108-148/Domain: EGF homology xEGI>
F.108-148/Domain: EGF homology xEGI>
F.202-23/Domain: EGF homology xEGI>
F.202-23/Domain: EGF homology xEG2>
F.208-367/Domain: kringle homology xKRG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A, Necastruces, 1.31 (2018). NID: 9212858; PIDN: AAA49131.1; PID: 9212859
C, Superfamily: urokinase-type plasminogen activator; EGF homology; Kringle homology; C; Superfamily: urokinase-type plasminogen activator; EGF homology; Kringle homology; C; Superfamily: at yooprotenin, heterodimer; hydrolase; kringle; serine proteinase
F; 12.17 (Domain: signal sequence #status praddicted <SIG>F; 22.17 (Product: urokinase-type plasminogen activator chain A #status predicted <ACH>F; 9.17 (Product: urokinase-type plasminogen activator chain B #status predicted <BCH F; 173-428 (Product: urokinase-type plasminogen activator chain B #status predicted <BCH F; 173-428 (Product: urokinase-type plasminogen activator chain B #status predicted F; 173-428 (Product: urokinase-type plasminogen activator chain B #status predicted F; 173-428 (Product: urokinase-type plasminogen activator chain B #status predicted F; 173-428 (Product: urokinase-type plasminogen activator chain B #status predicted F; 177, 272, 373 (Active site: His, Asp. Ser #status predicted
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A; Residues: 1-655 «MTV:
A; Cross-references: DDBJ:D14012; NID:g219680; PIDN:BAA03113.1; PID:g219681
A; Experimental source: liver (mRNA); serum (protein)
A; Experimental source: liver (mRNA); serum (protein)
A; Note: sequence extracted from NCBI backbone (NCBIN:131227, NCBIP:131228)
A; Note: parts of the sequence, including the amino ends of the heavy and light chains,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N.Alternate names uPA
N.Alternate names uPA
Cispecies: Gallus gallus (chicken)
Cispecies: Gallus gallus (chicken)
Cibate: 20-Jul.1990 #sequence_revision 20-Jul-1990 #text_change 16-Jul-1999
Cibate: 20-Jul.1990 #sequence_revision 20-Jul-1990 #text_change 16-Jul-1999
Rileslie, N.D.; Kessler, C.A.; Bell, S.M.; Degen, J.L.
J. Biol. Chem. 265, 1339-1344, 1990
A;Fitle: The chicken urokinase-type plasminogen activator gene.
A, Reference number: A35005; MUID:90110185; PMID:2295632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 CYEGNGHFYRGKASTDTMGRPCLPWNSATVLQ-QTYHAHRSDALQLGLGKHNYCRNPDNR
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S5.8%; Score 198.5; DB 1; Length 434;

Best Local Similarity 54.4%; Pred. No. 1.4e-13;

Matches 37; Conservative 7; Mismatches 19; Indels 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Gene: GDB:HGFAC; HGFA; HGFAP
A;Cross-references: GDB:9954514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                135 SRPWCYTK 142
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A;Molecule type: mRNA
A;Residues: 1-434 <LES>
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A/Pathway: blood coagulation; fibrinolysis
C;Superfamily: coagulation; fibrinolysis
C;Superfamily: coagulation; fibrinolysis
C;Superfamily: coagulation; fibrinolysis;
C;Superfamily: coagulation; fibrinolysis;
C;Superfamily: coagulation; fibrinolysis;
F;119/Domain: signal sequence #status predicted <SIG>
F;119/Domain: signal sequence #status predicted <SIG>
F;20-372,373-615/Product: coagulation factor XIIa, alpha form #status experimental <AIZ
F;47-88/Domain: fibronectin type II repeat homology <FB2>
F;18-130/Domain: Eff homology <EG3>
F;18-130/Domain: Eff homology <EG3>
F;18-130/Domain: Eibronectin type I repeat homology <IFI>
F;28-356/Region: proline-rich
F;28-356/Region: proline-rich
F;28-356/Region: proline-rich
F;37-609/Domain: trypsin homology <IRX>
F;38-356/Region: proline-rich
F;38-36.173-515/Product: coagulation factor XIIa, beta form #status experimental <B12
F;38-10,104-119,121-130,135-163,161-170,178-189,183-198,200-209,217-295,238-277,266-25
F;109/Binding site: carbohydrate (Thr) (covalent) #status experimental
F;289,305,328,329,337/Binding site: carbohydrate (Thr) (covalent) #status predicted
F;380/Binding site: carbohydrate (Ser) (covalent) #status predicted
F;380/Binding site: carbohydrate (Ser) (covalent) #status predicted
F;380/Binding site: carbohydrate (Ser) (covalent) #status predicted
F;380/Binding site: carbohydrate (Ser) (covalent) #status predicted
Nucleic Acids Res. 14, 3146, 1986

A;Title: cDNA sequence coding for human coagulation factor XII (Hageman).

A;Reference number: A26814; MUID:86176794; PMID:3754331

A;Accession: A26814

A;Molecule type: mRNA

A;Molecule type: mRNA

A;Molecule type: mRNA

A;Molecule type: mRNA

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Molecule type: mRNA
A;Residues: 146-378, 07,380-615 <QUE>
A;Cross-references: GB:Mil47; NID:g180360; PIDN:AAA70224.1; PID:g180361
A;Cross-references: GB:Mil47; NID:g180360; PIDN:AAA70224.1; PID:g180361
B;McMullen, B.A.; Fujikawa, K.
J. Biol. Chem. 260, 528-5341, 1985
A;Title: Amino acid sequence of the heavy chain of human alpha-factor XIIa (activated
A;Reference number: A22248; MUID:85182674; PMID:3886654
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A/Molecule type: protein
A/Redeus: 354-36233-615 <FUJ>
A/Restria, R.J.; Ling, V.T.; Spellman, M.W.
J. Biol. Chem. 267, 5102-5107, 1992
A/Filte: O'linked fucose is present in the first epidermal growth factor domain of A/Reference number: A46066, MUID: 92184750; PMID:1544894
A/Contents: annotation; carbohydrate binding site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: mRNA
A; Residues: 14-312, S',334-615 <CO2>
A; Cross-references: 18-312, S',334-615 <CO2>
A; Cross-references: 18-312, S',134-615 <CO2>
B; Que, B.G.; Davie, E.W.
B; Que, B.G.; Davie, E.W.
B; Colemistry 25, 1555-1528, 1986
A; Title: Characterization of a cDNA coding for human factor XII (Hageman factor), A; Reference number: A25191, MUD: 86216049; PMID: 3011063
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A,Introns: 19/3; 39/1; 72/2; 96/1; 133/1; 177/1; 212/1; 267/2; 340/1; 417/2;
C;Complex: factor XII, prekallikrein, and HMW kininogen form a complex bound
C;Punction:
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A,Residues: 20-379 <MCM>
R,Fulikawa, K.; McMullen, B.A.
1510. Chem. 258, 1095-10933, 1983
A,Title: Amino acid sequence of human beta-factor XIIa.
A,Reference number: A21037; MUID:83291041; PMID:6604055
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Pred. No. 2e-10;
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A;Cross-references: GDB:119892; OMIM:234000
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48.5%;
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Best Local Similarity
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     F;373-407/Product: hepatocyte growth factor activator light chain #status experimental < F;408-655/Product: hepatocyte growth factor activator heavy chain #status experimental < F;408-641/Domain: trypsin homology <pre>
F;40,48,209,468,492,546,Bluding site: carbohydrate (Asn) (covalent) #status predicted F;40,48,290,468,188-197,202-230,228-237,245-226,250-267,269-278,286-367,307-349,338-36 F;447,497,598/Active site: His, Asp, Ser #status predicted
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R;Semba, U.; Yamamoto, T.; Kunisada, T.; Shibuya, Y.; Tanase, S.; Kambara, T.; Okabe, H.
R;Semba, U.; Yamamoto, T.; Kunisada, T.; Shibuya, Y.; Tanase, S.; Kambara, T.; Okabe, H.
B;Cchim. B;cphys. Acta 1159, 113-121, 1992
A;Title: Primary structure of guinea-pig Hageman factor: sequence around the cleavage si
A;Reference number: S28941; MUID:93003367; PMID:1390917
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A; Status: preliminary
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 1 - 603 < SEMP.
A; Cross references: EMBL: X68615; NID: 949578; PIDN: CAA48600.1; PID: 949579
C; Superfamily: coagulation factor XII; EGF homology, fibronectin type I repeat homology of F2>
C; Keywords: hydrolase; serine proteinase
F; 46-87/Domain: fibronectin type II repeat homology of F5>
F; 134-169/Domain: EGF homology of F6>
F; 177-208/Domain: EGF homology of KG>
F; 177-208/Domain: kringle homology of KRS>
F; 259-597/Domain: trypsin homology of KRS>
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NyAlterrate names: Hageman factor (activated)
NyAlterrate names: Hageman factor (activated)
CyBecies: Homo sapiens (man)
CyBecies: Homo sapiens (man)
CyBecies: Apparat; A26814; A2080; A25191; A22248; A21037
CyBeciession: A29411; A26814; A2080; A25191; A22248; A21037
Marchiavray, R.T.A.
J. Biol. Chem. 262, 13662-13673, 1987
A/Title: Characterization of the human blood coagulation factor XII gene. Intron/exon
A;Reference number: A29411; MUID:88007593; PMID:2888762
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A,Cross-references: GB:M17466; GB:J02807; NID:g180355; PIDN:AAB59490.1; PID:g180357
R,Tripodi, M.; Citarella, F.; Guida, S.; Galeffi, P.; Fantoni, A.; Cortese, R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N;Alternate names: Hageman factor
C;Species: Cavia porcellus (guinea pig)
C;Date: 25-Feb-1994 #sequence_revision 03-Aug-1995 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                        Query Match 35.1%; Score 194.5; DB 1; Length Best Local Similarity 40.4%; Pred. No. 5.7e-13; Matches 42; Conservative 8; Mismatches 41; Indels
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39.6%; Pred. No. 1.1e-12;
tive 15; Mismatches 38;
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Best Local Similarity 39.6*
Matches 38; Conservative
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а;

fact

463/1; 511 to anionic

Length 615;

us-09-880-503-9.rpr

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20-21,'P',23-34;177-179,'N',181-186,'T',188-196,'DKG',200;292-314,'W',316-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        rs of kringle repeats
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Accession: 160906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ?;1054-1131/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A, Gene: GDB: LPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             apoprotein(a) (EC 3.4.21.-) precursor [validated] - human
NAlternate names: apolipoprotein(a); lipoprotein(a) chain apo(a)
C;Species: Homo sapians (man)
C;Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 08-Dec-2000
C;Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 08-Dec-2000
R;McLean, Juw.; Tomlinson, J.E.; Kuang, W.J.; Eaton, D.L.; Chen, E.Y.; Fless, G.M.; Scan Nature 330, 132-137; Fless, G.M.; Scan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: mRNA
A; Residues: 1-4548 cMCL>
A; Crossuces: 1-4548 cMCL>
A; Crossuces: CBCL>
A; Crossuces: CBCL>
A; Crossuces: CBCCSSO; EMBL:X06696; NID:g28619; PIDN:CAA29618.1; PID:g28620
R; Earon, D.L.; Fless, G.M.; Kohr, W.J.; McLean, J.W.; Xu, Q.T.; Miller, C.G.; Lawn, R.M.
Proc. Natl. Acad. Sci. U.S.A. 84, 3224-3228, 1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'Title: Partial amino acid sequence of apolipoprotein(a) shows that it is homologous to 'Reference number: A28017, MUID:87204109; PMID:3472206 A28017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Accession: A32869; A30848

R;Tomlinson, J.B.; McLean, J.W.; Lawn, R.M.
J. Biol. Chem. 264, 5957-5965, 1989

A;Tttle: Rhesus monkey apolipoprotein(a). Sequence, evolution, and sites of synthesis. A;Reference number: A32869; MUID:89174660; PMID:2925643
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'n
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A;Reference number: S00657; MUID:88039109; PMID:3670400
A;Accession: S00657
                                                                                                                        216 SCYDGRGLSYRGLARTILSGAPCQPWAS----EATYRNVTAEQARNWGLGGHAFCRNPDN 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Molecule type: manA
Residues: 1-1420 <TOM>
;Cross-references: GB:J04635; NID:g342072; PIDN:AAA36833.1; PID:g342073
;Cross-references: GB:J04635; NID:g342072; PIDN:AAA36833.1; PID:g342073
;Superfamily: apolipoprotein(a); Kringle homology; trypsin homology
;Keywords: hydrolase; Kringle, lipid binding; lipoprotein; serine proteinase
;50-127/Domain: Kringle homology (KR).
                                                             2 TCYEGNGHFYRGKASTDTMGRPCLPWNSATVLQQTY-HAHRSDALQLGLGKHNYCRNPDN 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 CYEGNGHFYRGKASTDTMGRPCLPWNSATVLQ--QTYHAHRSDALQLGLGKHNYCRNPDN 60
                                                                                                                                                                                                                                                                                                                                                                                                                 oolipoprotein(a) (EC 3.4.21.-) - rhesus macaque (fragment)
Species: Macaca mulatta (rhesus macaque)
Date: 22-Nov-1899 #sequence_revision 22-Nov-1989 #text_change 22-Jun-1999
   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12; Gaps
   5;
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Pred. No. 4.6e-09;
9; Mismatches 31; Indels 13
24;
Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               F;954-1031/Domain: kringle homology <KR9>F;1068-1145/Domain: kringle homology <KR10>F;1191-1413/Domain: trypsin homology <TRY>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                164-241/Domain: Kringle homology «RR2>
278-355/Domain: Kringle homology «RR3>
278-469/Domain: Kringle homology «RR4>
506-583/Domain: Kringle homology «RR5>
620-697/Domain: Kringle homology «RR5>
840-917/Domain: Kringle homology «RR5>
840-917/Domain: Kringle homology «RR6>
9
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Best Local Similarity 40.9
Matches 36; Conservative
Conservative
                                                                                                                                                                                                                                                       DIRPWCFV 279
                                                                                                                                                                                         61 RRRPWCYV 68
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33;
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A;Cross-references: GB:L07899; NID:g967973; PID:g967974
R;Malgaretti, N.; Acquati, F.; Magnaghi, P.; Bruno, L.; Pontoglio, M.; Rocchi, M.; Sacc
Proc. Natl. Acad. Sci. US.A. 89, 11584-11588, 1992
A;Title: Characterization by yeast artificial chromosome cloning of the linked apolipop. A;Reference number: A47233; MUID:93087573; PMID:1454851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bicchemistry 31, 3113-3118, 1992
Afritle: Multiple members of the plasminogen-apolipoprotein(a) gene family associated w
A.Reference number: IS2415, MUID:92207924, PMID:1554698
A.Rocession: IS2415
                                                                                                       related pl
R;Wade, D.P.; Clarke, J.G.; Lindahl, G.E.; Liu, A.C.; Zysow, B.R.; Meer, K.; Schwartz, Proc. Natl. Acad. Sci. U.S.A. 90, 1369-1373, 1993.
A;Title: S' control regions of the apolipoprocein(a) gene and members of the related pl A;Reference number: A47277; MUID:93165698; PMID:7679504
A;Accession: A47277
A;Molecule preliminary; translation not shown; translated from GB/EMBL/DDBJ
A;Residues: 1-16 <RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  first coding
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C;Keywords: hydrolase; kringle; lipid binding; lipoprotein; serine proteinase
F;1-19/Domain: signal sequence #status predicted <SIGs
F;20-4548/Product: apolipoprotein(a) #status experimental <MAT>
F;20-105/Domain: kringle homology <KRl>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A:Status: preliminary; translation not shown; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-16 <RE5>
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A;Map position: 6q26-6q27
A;Note: several genes closely linked on chromosome 6 are identical in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-16 - KRE2-
A;Cross-references: GB:M90078; NID:g178786; PIDN:AAA35547.1; PID:g553188
A;Note: apo(a) gene 1 (nomenclature of reference 152415)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A)Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-16 <RE3>
A;Cross-references: GB:M86877; NID:g178780; PIDN:AAB49909.1; PID:g553185
A;Note: apo(a) gene 1 (nomenclature of reference I52415)
A;Accession: I65286
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/Cross_references: GB:M86878; NID:g178782; PIDN:AAA51749.1; PID:g553186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: GB:M90079; NID:g178784; PIDN:AAA35546.1; PID:g553187
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A,Molecule type: DNA
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kringle homology <KR11>
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F)556-33/Domain: kringle homology «KR2»
F)370-447/Domain: kringle homology «KR3»
F)584-561/Domain: kringle homology «KR5»
F)586-67/Domain: kringle homology «KR5»
F)712-789/Domain: kringle homology «KR6»
F)712-789/Domain: kringle homology «KR8»
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A. NOCEULE LYPE: MRNA
A. Residues: 1-593 cSHI>
A. A. Cross-references: GBS-70164
A. A. Cross-references: GBS-70164
A. Note: the authors translated the codon GAG for residue 23 as Val, GAG for residue 70
B. Pro, CTC for residue 203 as Phe, GTG for residue 247 as Leu, CCG for residue 286 as C
B. Pro, CTC for residue 505 as Leu
R. Fujikawa, K.; Walsh, K.A.; Davie, E.W.
Biochemistry 16, 2270-2278, 1977
B. A. Title: Isolation and characterization of bovine factor XII (Hageman factor).
A. Reference number: A61329; WUID: 77182112; PMID: 861210
A. Accession: A61329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: protein

A; Molecule type: protein

A; Residues: 10-16,7x',18-19;525-550 <PUJ>

C; Superfamily: coagulation factor XII; EGF homology; fibronectin type I repeat homology

C; Keywords: blood coagulation; fibrinolysis; glycoprotein; hydrolase; monomer; plasma;

C; Keywords: blood coagulation; fibrinolysis; glycoprotein; hydrolase; monomer; plasma;

F; 37-78 Domain: fibronectin type II repeat homology <FEL>

F; 125-16()Domain: EGF homology <EGF>

F; 125-16()Domain: kringle homology <FRCS

F; 3500-287 Domain: kringle homology <FRCS

F; 5501-87 Domain: trypsin homology <FRCS

F; 541/Active site: Ser #status predicted
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A, Molecule type: protein
A, Molecule type: protein
A, Residues: 1-89 < GYE>
C, Superfamily: plasmin, kringle homology, plasminogen-related protein precursor homology
C, Keywords: fibrinolysis; glycoprotein; hydrolase; kringle; plasma; serine proteinase
F, 6-83/Domain: kringle homology < KRG.
F, 6-83/Domain: kringle homology < KRG.
F, 6-83, 27-66, 55-78/Disulfide bonds: #status predicted
F; 6-93, 27-66, sis-78/Disulfide bonds: #status (covalent) #status experimental
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
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NiAlternate names: plasminogen
C:Species: Gallus gallus (chicken)
C:Species: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 16-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 TCYE - GNGHFYRGKASTDTMGRPCLPWNSATVLQQTY - HAHRSDALQLGLGKHNYCRNP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  37; Indels
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R, Gyenes, M.; Patthy, L.
Biochim. Biophys. Acta 832, 326-330, 1985
A;Title: The kringle 4 domain of chicken plasminogen.
A, Reference number: A60140; MUID:86077796; PMID:4074753
             A, Reference number: S45281; MUID: 94242782; PMID: 8186251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 155.5; DB 2;
Pred. No. 7.7e-09;
9; Mismatches 37;
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plasmin (BC 3.4.21.7) precursor - sheep (fragments)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          86
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNDTRPWCFIWKGDRLSWNYCRLAPC 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             59 DNRRRPWCYVQVGLKPLVQECMVHDC 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RRRPWCYVQVGLKPLV - QECMVHDCAD
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Best Local Similarity 38.67
Matches 34, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
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Nylternate names: plasminogen

NyAlternate names: plasminogen

C;Species: Canis lupus familiaris (dog)

C;Date: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change 12-May-1995

C;Accession: EG145

Enzyme 40, 63-69, 1988

A;Title: Structural aspects of the plasminogen of various species.

A;Attle: Structural aspects

A;Accession: EG145

A;Accession: EG145

A;Accession: EG145

A;Accession: EG145

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A;Accession: Kelyer

A;Accession: Kelyer

A;Accession: Kelyer

A;Accession: Kelyer

A;Accession: Karingle homology; plasminogen-related protein precursor homology

C;Keywords: hydrolase; serine proteinase

F;37-114/Domain: kringle homology <a href="Market-Related-Related-Related-Related-Related-Related-Related-Related-Related-Related-Related-Related-Related-Related-Related-Related-Related-Related-Related-Related-Related-Related-Related-Related-Related-Related-Related-Related-Related-Related-Related-Related-Related-Related-Related-Related-Related-Related-Related-Related-Related-Related-Related-Related-Related-Related-Related-Related-Related-Related-Related-Related-Related-Related-Related-Related-Related-Related-Related-Related-Related-Related-Related-Related-Related-Related-Related-Related-Related-Related-Related-Related-Related-Related-Related-Related-Related-Related-Related-Related-Related-Related-Related-Related-Related-Related-Related-Related-Related-Related-Related-Related-Related-Related-Related-Related-Related-Related-Related-Related-Related-Related-Related-Related-Related-Related-Related-Related-Related-Related-Related-Related-Related-Related-Related-Related-Related-Related-Related-Related-Related-Related-Related-Related-Related-Related-Related-Related-Related-Related-Related-Related-Related-Related-Related-Related-Related-Related-Related-Related-Related-Related-Related-Related-Related-Related-Related-Related-Related-Related-Related-Related-Related-Related-Related-Related-Related-Related-Related-Related-Related-Related-Related-Related-Rela
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N'Alternate names: Hageman factor (activated)
C'Species Bos primigenius taurus (cattle)
C'Date: 10-Apr-1995 #sequence_revision 22-Apr-1995 #text_change 21-Jan-2000
C'Accession: 845281; A61329
C'Accession: 845281; A61329
C'Accession: 0. Okabe, H.; Kambara, T.; Yamamoto, T.
Biochim. Biophys: Acta 1206, 63-70, 1994
A;Title: Primary structure of bovine Hageman factor (blood coagulation factor XII): comp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CYEGNGHFYRGKASTDIMGRPCLPWNSATVLQQTYHAHRSDAL-----QLGLGKHNYCRN 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  37 CYHGNGQSYRGTSSTTITGRKCQSWSSMT-----PHRHEKTPEHFPEAGL-TMNYCRN 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3950 ABIRPWCYT----MDPSVRWEYCNLTRCPVTESSVLTTPTVAPVPSTEAPSEQAPPEK 4003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  60 NRRRPWCYVQVGLKPLV--QECMVHDC-------ADGKKPSSPPEE 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            36; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 157; DB 1;
Pred. No. 3.7e-08;
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F;2536-2613/Domain: kringle homology «KR23»
F;2650-2737/Domain: kringle homology «KR24»
F;2878-2955/Domain: kringle homology «KR25»
F;2878-2955/Domain: kringle homology «KR25»
F;3106-3183/Domain: kringle homology «KR27»
F;3106-3183/Domain: kringle homology «KR28»
F;334-3411/Domain: kringle homology «KR28»
F;334-3411/Domain: kringle homology «KR28»
F;348-355/Domain: kringle homology «KR31»
F;366-359/Domain: kringle homology «KR31»
F;385-3859/Domain: kringle homology «KR31»
F;386-3973/Domain: kringle homology «KR31»
F;310-4201/Domain: kringle homology «KR35»
F;4104-4201/Domain: kringle homology «KR35»
F;4124-4201/Domain: kringle homology «KR35»
F;4124-4201/Domain: kringle homology «KR37»
F;428-4307/Domain: kringle homology «KR37»
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Best Local Similarity 34.2
Matches 40, Conservative
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AyMolecule type: mRNA
A,Residues; Tofo-743, W. 745-812 cwMLA
A,Residues; Tofo-743, W. 745-812 cwMLA
A,Residues; Tofo-743, W. 745-812 cwMLA
A,Residues; Tofo-743, W. 745-812 cwMLA
A,Residues; Tofo-743, W. 745-812 cwMLa
A,Foresidues; Tofo-743, W. 745-812 cwmlan
B,Formisholz, R.A.; Lerch, P.G.; Schaller, J.; Rickli, B.E.; Lergier, W.; Manneberg, M.
Bur. J. Blochem. 114, 465-470, 1981
A,Fitle: Comparison of the primary structure of the N-terminal CNBr fragments of human
A,Reference number: S03735, MUID: 81212097; PMID: 7238497
A,Molecule type: protein
A,Rolecule type: protein
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C; Keywords: hydrolase; serine proteinase
F;41-118/Domain: kringle homology <KR4>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 CYEGNGHFYRGKASTDTMGRPCLPWNSATVLQQTYHAH----RSDALQLGLGKHNYCRNPD 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           plasmin (EC 3.4.21.7) precursor - goat (fragments)
N;Alternate names: plasminogen
C;Species: Capra aegagrus hircus (domestic goat)
C;Species: Capra Aegagrus hircus (domestic goat)
C;Date: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change 12-May-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 CYEGNGHFYRGKASIDIMGRPCLPWNSAIV--LQQIYHAHRSDALQLGLGKHNYCRNPDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (covalent) #status experimental
(covalent) #status experimental
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27.4%; Score 152; DB 1; Length 812; 37.8%; Pred. No. 2.5e-08; tive 11; Mismatches 34; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 27.1%; Score 150; DB 2; Length 123; Best Local Similarity 37.5%; Pred. No. 6.7e-09;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       F,315/Binding site: carbohydrate (Asn) (covalent) #status e
F,365/Binding site: carbohydrate (Ser) (covalent) #status e
F,624,667,762/Active site: His, Asp, Ser #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      438 ADKSPWCYT---TDPRVRWEFCNLKKCSETPEQVPAAP 472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12; Mismatches
from GB/EMBL/DDBJ
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R, Schaller, J.; Rickli, E.E.
Enzyme 40, 63-69, 1988
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A;Molecule type: protein
A;Residues: 1-123 <SCH>
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A/Accession: $28200

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C/Superfamily: plasmin; kringle homology; plasminogen (fragments) serine proteinase; z

F)1-37,38-117,118-460/Product: plasminogen (fragments) #status experimental cAPT>

F)1-37/Domain: activation poptide (fragment) #status experimental cAPT>

F)1-18/Domain: kringle homology cKR4>

F)18-460/Product: miniplasminogen #status experimental cMIN>

F)18-460/Product: miniplasminogen #status experimental cMIN>

F)18-460/Domain: kringle homology cKR5>

F)226-460/Domain: plasmin chain B #status experimental cBCH>

F)21-453/Domain: trypsin homology cTRY>

F)221-4315,410/Active site: His, Asp, Ser #status predicted
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A; Accession: A25835
A; Molecule type: protein
A; Residues: 27-334, D, 336-515, H, 517-554, L, 556-812 <SCH>
A; Ralinowski, D. P.; Sadler, J.E.; Davie, E.W.
Biochemistry 23, 4243-4250, 1984
A; Title: Characterization of a complementary deoxyribonucleic acid coding for human and A; A; Reference number: 145961; MUID:85023311; PMID:6148961
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                      N;Contains: miniplasminogen
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Date: 28-Oct-1994 #sequence_revision 01-Nov-1996 #text_change 17-Mar-1999
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C)Species: Bos primigenius taurus (cattle)
C)Date: 30-Sep-1987 #sequence revision 28-Apr-1995 #text_change 18-Jun-1999
C)Accession: S45046; A25835; I45961; S03736
R)Bergolund, L., Andersen, M.D.; Petersen, T.E.
submitted to the EMBL Data Library, May 1994
A;Description: Cloning and characterizatin of the bovine plasminogen cDNA.
A;Reference number: S45046
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                                                                                                                                                                                                                                                                                                                                                                                                      A;Molecule type: protein
A;Residues: 1-37;38-117 <SCH>
R;Schaller, J.; Straub, C.; Kaempfer, U.; Rickli, E.E.
Protein Seq. Data Anal. 5, 21-25, 1992
A;Title: Complete amino acid sequence of ovine miniplasminogen.
A;Ritle: Complete amino acid sequence of ovine miniplasminogen.
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R, Schaller, J.; Rickli, E.E.
Enzyme 40, 63-69, 1988
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C; Species: Rattus norvegicus (Norway rat)
C; Species: Rattus norvegicus (Norway rat)
C; Species: Rattus norvegicus (Norway rat)
C; Species: 24-1992 #sequence_revision 17-Apr-1993 #text_change 16-Jul-1999
C; Accession: A40522
R; Kanalas, J.J.; Makker, S.P.
J. Biol. Chem. 264, 10825-10829, 1991
A; Title: Identification of the rat Heymann nephritis autoantigen (GP330) as a receptor shreference number: A40522; MUID:91250378; PMID:1645711
A; Reference number: A40522; MUID:91250378; PMID:1645711
A; Reference number: A40522; MUID:91250378; PMID:1645711
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27.1%; Score 150; DB 2; Length 169;
Best Local Similarity 34.3%; Pred. No. 9.1e-09;
Matches 37; Conservative 14; Mismatches 31; Indels 2
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A40522
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(EC 3.4.21.73) (uPA)

us-09-880-503-9.rsp

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[5]
SEQUENCE FROM N.A.
Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Poel C.L., Yi Q.,
Nickerson D.A.;
Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
Holmes W.E., Pennica D., Blaber M., Rey M.W., Guenzler W.A.,
Steffens G.J., Heyneker H.L.;
"Cloning and expression of the gene for pro-urokinase in Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE=85203359; PubMed=3886571;
Jacobs P., Cravador A., Loriau R., Brockly F., Colau B., Chuchana P., van Elsen A., Herzog A., Bollen A.;
"Molecular cloning, sequencing, and expression in Escherichia coli '
"Molecular clonings economicase con and expression in Escherichia coli '
human preprourokinase cDNA.";
DNA 4:139-146(1985).
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MEDLINE=22388257, PubMed=12477932;*
MEDLINE=22388257, PubMed=12477932;*
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shennen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE=85215647; PubMed=2987867;
Riccio A., Grimaldi G., Verde P., Sebastio G., Boast S., Blasi F.,
"The human urokinase-plasminosen activator gene and its promoter."
Nucleic Acids Res. 13:2759-2771(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE=86056954; PubMed=2415429;
Magai M., Hiramatsu R., Kaneda T., Hayasuke N., Arimura H.,
Nishida M., Suyama T.;
"Molecular Clothing of CDNA coding for human preprourokinase.";
Gene 36:183-188(1985).
                                                                                                                                                                                                                                                                                UROK HUMAN STANDARD; PRT; 431 AA. P00749; Q15844; Q16618; Q969W6; 21-UUL-1986 (Rel. 01, Created) 20-MAR-1987 (Rel. 04, Last sequence update) Urokinase-type plasminogen activator precursor (U-plasminogen activator).
                                                                                                                                                                                                           ALIGNMENTS
           HGFL MOUSE
RORZ HUMAN
RORZ MOUSE
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SEQUENCE FROM N.A.
NCBI TaxID=9606;
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MEDLINE=89127526; PubMed=2536903;
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STRUCTURE BY NMR OF 67-155

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MEDLINE-97337920; PubMed-9194591;

MEDLINE-97337920; PubMed-9194591;

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EMBL; D11143; BAA01919.1; --
EMBL; X02760; CAAA6535.1; --
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Urokinase-type plasminogen activator precursor (EC 3.4.21.73) (uPA)
(U-plasminogen activator).
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Papio.
                                                     ;
0
               100.0%; Score 554; DB 1; Length 431; 100.0%; Pred. No. 6.4e-55; ive 0; Mismatches 0; Indels
                                                                                                                                                                                           128 RRRPWCYVQVGLKPLVQECMVHDCADGKKPSSPPEE 163
                                                                                                                                                                 61 RRRPWCYVQVGLKPLVQECMVHDCADGKKPSSPPEE 96
                                                                                                                                                                                                                                                                                                     433 AA
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InterPro; IRR006209; EGF 11ke.
InterPro; IRR006209; EGF 11ke.
InterPro; IRR000001; Kringle.
InterPro; IRR0000134; Kringle.
Ffam; Pr00011; Kringle; 1.
Pfam; Pr00019; kringle; 1.
Pfam; Pr00019; kringle; 1.
Prints; PR00029; CHYMOTRYPSIN.
PriNTS; PR00029; CHYMOTRYPSIN.
Pr0Dom; PD000395; Kringle; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL, X51935; CA36200.1; -. PIR, S14687; UKBAY. HSSP; P00749; 1LMW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Expon, PD000395; Kringle, 1.
SMART, SM0181; EGF; 1.
SMART; SM00130; KR; 1.
SMART; SM00020; Tryp, SPc; 1.
PROSITE; PS00022; EGF_1; 1.
       Query Match
Best Local Similarity 100.0
Matches 96; Conservative
                                                                                                                                                                                                                                                                                                     STANDARD;
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P16227;
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UROK_PAPCY
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67 KTCYEGNGHFYRGKASTDTMGRSCLAWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDN 126
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MEDLINE=88087954; PubMed=6096812;
Magamine Y., Pearson D., Altus M.S., Reich E.;
"cDMA and gene nuclectide sequence of porcine plasminogen activator.";
Nucleic Acids Res. 12:9525-9541(1984).
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Urokinase-type plasminogen activator precursor (EC 3.4.21.73) (uPA)
Planinogen activator).
PROSITE; PS01186; EGF 2; FALSE_NEG.
PROSITE; PS00021; KRINGLE 1; 1.
PROSITE; PS50070; KRINGLE 2; 1.
PROSITE; PS500104; TRYPSIN DON; 1.
PROSITE; PS00134; TRYPSIN DIS; 1.
PROSITE; PS00135; TRYPSIN SER; 1.
PROSITE; PS00135; TRYPSIN SER; 1.
PROSITE; PS00135; TRYPSIN SER; 1.
PROSITE; PS01155; TRYPSIN SER; 1.
PROSITE; PS01155; TRYPSIN SER; 1.
PROSITE; PS01155; TRYPSIN SER; 1.
SIGNAL 20 POTENTIAL.
                                                                                                                                                                                                                                             UROKINASE-TYPE PLASMINOGEN ACTIVATOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae, Sus.
                                                                                                                                                                                                                                                                 CHAIN A (BY SIMILARITY).
SHORT A CHAIN (A1) (BY SIMILARITY).
CHAIN B (BY SIMILARITY).
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Submitted (DEC-1986) to the PIR data bank.
-!- CATALYTIC ACTIVITY Specific cleavage of Arg-|-Val bond plasminogen to form plasmin.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 519; DB 1; Length 433;
                                                                                                                                                                                                                                                                                                                                                                                                CONNECTING PEPTIDE.
SERINE PROTEASE.
BY SIMILARITY.
BY SIMILARITY.
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INTERCHAIN (BY SIMILARITY).
BY SIMILARITY.
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BY SIMILARITY.
CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 RRRPWCYVQVGLKPLVQECMVHDCADGKKPSSPPEE 96
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1; Mismatches
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13-AUG-1987 (Rel. 05, Last seq
28-FEB-2003 (Rel. 41, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              48595 MW;
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94.8%;
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SEQUENCE FROM N.A.
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                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                     MENCHS; SULLAIL:

R INTERPRO; IPR001314; Chymotrypsin.

R INTERPRO; IPR001214; Chymotrypsin.

R INTERPRO; IPR001254; Ser_protease_Try.

R INTERPRO; IPR001254; Ser_protease_Try.

R INTERPRO; IPR001251; trypsin.; 1.

R PRINTS; PR00125; trypsin.; 1.

R RANT; PR00135; trypsin.; 1.

R RANT; SM00130; KRIMOLE.

R SMART; SM00130; KRIMOLE.

R SMART; SM00130; KRIMOLE.

R RANT; SM00130; KRIMOLE.

R RANT; SM00130; KRIMOLE.

R ROSITE; PS00121; RINGLE.

R ROSITE; PS00135; TRYPSIN. ToM; 1.

R ROSITE; PS00135; TRYPSIN. ToM; 1.

R ROSITE; PS00135; TRYPSIN. TSR; 1.

R ROSITE; PS00135; TRYPSIN. TSR; 1.

R ROSITE; PS00135; TRYPSIN. TSR; 1.

R ROSITE; PS00135; TRYPSIN. TSR; 1.

R ROSITE; PS00135; TRYPSIN. TSR; 1.

R ROSITE; PS00135; TRYPSIN. TSR; 1.

R ROSITE; PS00135; TRYPSIN. TSR; 1.

R ROSITE; PS00135; TRYPSIN. TSR; 1.

R ROSITE; PS00135; TRYPSIN. TSR; 1.

R ROSITE; PS00135; TRYPSIN. TSR; 1.

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Pred. No. 8.4e-42;
8; Mismatches 10; Indels 9
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CONNECTING PEPTIDE.
CONNECTING PEPTIDE.
SELINE PROTEASE.
N.LINKED (GLCNAC. .).
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-> H (IN REF. 1; CAA26511).
-> GS (IN REF. 1; CAA25806)
EE32FCEF501321EE CRC64;
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CHAIN B (BY SIMILARITY)
EGF-LIKE.
-!- SIMILARITY: Contains 1 kringle domain.
-!- SIMILARITY: Contains 1 EGF-like domain.
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Best Local Similarity 74.5.5
Best Local Similarity 74.5.5
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288
442 AA;
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MEROPS; S01.231; -.
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130 ORRPWCYVOIGLKOFVOFCMVODCSVGKSPSSPREK 165
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 plasminogen to form plasmin.
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EMBL; X85801; CAA59796.1; -.
PIR; JNO560; JNO560.
HSSP; P00749; 1LMW.
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Best Local Similarity
Lag 72; Conserve
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181
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UROK BOVIN

ID UROK BOVIN

STANDARD; PRT; 433 AA.

10 0.5589; Q28209;

DT 01-FEB-1994 (Rel. 28, Created)

DT 01-FEB-1994 (Rel. 28, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DT Cokinase-type plasminogen activator precursor (EC 3.4.21.73) (uPA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ravn P., Berglund L., Petersen T.E.; "Cloning and characterization of the bovine plasminogen activators and tPA.";
                                               UROKINASE-TYPE PLASMINOGEN ACTIVATOR.
CHAIN A (BY SIMILARITY).
SHORT A CHAIN (A1) (BY SIMILARITY).
EGF-LIKE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
Bovidae, Bovinae, Bos
Plasminogen activation, Hydrolase, Serine protease, Glycoprotein,
Kringle, EGF-like domain, Zymogen, Signal.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Int. Dairy J. 5:605-617(1995).
-!- CATALYTIC ACTIVITY: Specific cleavage of Arg-|-Val bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 427; DB 1; Length 432;
Pred. No. 1.3e-40;
                                                                                                                                KRINGLE.
CONNECTING PEPTIDE.
CONNECTING PEPTIDE.
SERINE PROTEASE.
BY SIMILARITY.
BY SIMILARITY.
INTERCHAIN (BY SIMILARITY).
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SEQUENCE FROM N.A.
TISSUE-Aortic endothelium;
MEDIJINE-9216119; PubMed-8385052;
Kraetzschmar J., Haendler B., Kojima S., Rifkin D.B.,
Schleuning W.-D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RRRPWCYVQVGLKPLVQECMVHDCADGKKPSSPPEE 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7; Mismatches
                Kringle; EGF-like domain; Zymogen;
SIGNAL 19 POTEN
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77.18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                             432 AA;
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CHAIN B (BY SIMILARITY).
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CONNECTING PEPTIDE.
INDUCTION: By retinoic acid.
SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
SIMILARITY: Contains 1 kringle domain.
SIMILARITY: Contains 1 EGF-like domain.
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InterPro; IPR001314; Chymotrypsin.
InterPro; IPR0012014; EGF like.
InterPro; IPR00100011; Kringle.
InterPro; IPR001254; Ser protease_Try.
Pfam; PP000631; Kringle; I.
PRINTS; PR00122; CHYMOTRYPSIN.
PRINTS; PR00122; CHYMOTRYPSIN.
PROMT; PR00139; Kringle; I.
SMART; SM00130; KR; I.
PROSITE; PS01020; EGF_1; I.
PROSITE; PS01021; EGF_1; I.
PROSITE; PS01021; EGF_1; I.
PROSITE; PS01021; KRINGLE_1; I.
PROSITE; PS01021; KRINGLE_2; I.
PROSITE; PS00134; TRYPSIN_DOM; I.
PROSITE; PS00134; TRYPSIN_DOM; I.
PROSITE; PS00134; TRYPSIN_DOM; I.
PROSITE; PS00134; TRYPSIN_SER; I.
PROSITE; PS01135; TRYPSIN_SER; I.
PROSITE; PS01135; TRYPSIN_SER; I.
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PROSITE; PS01136; TRYPSIN_SER; I.
PROSITE; PS01136; TRYPSIN_S
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9; Mismatches
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UROK_MOUSE

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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                            48268 MW;
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433 AA;
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                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=88163489; VubMed=2831940;
MEDLINE=88163489; VubMed=2831940;
MEDGEN S.U.F., Heckel J.L., Reich E., Degen J.L.;
Fine murine urokinase-type plasminogen activator gene.";
Biochemistry 26:8270-8279 (1987).
-! CATALYTIC ACTIVITY: Specific cleavage of Arg-|-Val bond in plasminogen to form plasmin.
-! SUBUNIT: FOUND IN HIGH AND LOW MOLECULAR MASS FORMS. EACH CONSISTS OF TWO CHAINS, A AND B. THE HIGH MOLECULAR MASS FORM CONTAINS A MOLECULAR MASS FORM TO YIELD A SHORT AI CHAIN (BY SIMILARITY).
-! SIMILARITY: CENTAINS IN EXINGLE Gomain.
-! SIMILARITY: Contains 1 EGF-like domain.
                                                             01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Urokinase-type plasminogen activator precursor (EC 3.4.21.73) (uPA)
PLAU.
                                                                                                                                                                                              Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCEI_TaxID=10090;
                                                                                                                                                                                                                                                        SECUENCE FROM N.A. MEDLINE=8179414; PubMed=2985383; MEDLINE=81179414; PubMed=2985383; Belin D. Vassalli U.-D., Combepine C., Godeau F., Nagamine Y., Reich E., Kocher H.P., Duvoisin R.M.; "Cloning, nucleotide sequencing and expression of cDNAs encoding mouse urokinase-type plasminogen activator."; Eur. J. Biochem. 148:225-232(1985).
                                                        433 AA
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PS00134; TRYPSIN HIS; FALSE NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL, X02389; CAA66231.1; -
EMBL, M17922; AA40639.1; -
PR, A29420; UKMS.
HSSP, P00749; IKDU.
MEDOPS; S01.231; -
MED, MG197611; Plau.
InterPro; IPR001314; Chymotrypsin.
InterPro; IPR006209; EGF 15ke.
InterPro; IPR006209; EGF 15ke.
InterPro; IPR006209; EGF 15ke.
InterPro; IPR006209; EGF 15ke.
InterPro; IPR006209; EGF 15ke.
InterPro; IPR006209; EGF 15ke.
Ffam; PP00011; Kringle; 1.
Pfam; PP00011; Kringle; 1.
Pfam; PP00011; Kringle; 1.
Pfam; PP00011; Kringle; 1.
Pfam; PP00011; Kringle; 1.
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SMART; SM00130; KR; 1.
SMART; SM00130; KR; 1.
PROSITE; PS00120; EGF_1; 1.
PROSITE; PS00186; EGF_2; FALSE NEG.
PROSITE; PS00021; KRINGLE 1; 1.
PROSITE; PS50070; KRINGLE 1; 1.
                                                          PRT;
                                                        STANDARD;
                                                                                                                                                                               musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                      UROK MOUSE
P06869;
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1 KTCYEGNGHFYRGKASTDIMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDN 60
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Ann. N.Y. Acad. Sci. 667:395-403(1992).
-!- FUNCTION: PROBABLY ESSENTIAL TO SUPPORT THE FEEDING HABITS OF THIS EXCLUSIVELY HAEMATOPHAGOUS ANIMAL. PROBABLE POTENT THROMBOLYTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Salivary plasminogen activator beta precursor (EC 3.4.21.68) (DSPA
PROSITE; PS00135; TRYPSIN_SER; 1.
Jamaninogen activation; Hydrolase; Serine protease; Glycoprotein; Kringle; EGF-like domain; Zymogen; Signal.
SIGNAL
                                                                                                                    UROKINASE-TYPE PLASMINOGEN ACTIVATOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Desmodus rotundus (Vampire bat).
Wakaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Chiroptera, Microchiroptera, Phyllostomidae,
Desmodontinae, Desmodus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE-Salivary gland;
MEDLINE-S20139036; PubMed=1937019;
Kraetzschmar J. Haendler B., Langer G., Boidol W., Bringmann P.,
Alagon A., Donner P., Schleuning W.D.;
The plasminogen activator family from the salivary gland of the
vampire bat Desmodus rotundus: cloning and expression.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; DB 1; Length 433;
1.7e-38;
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                                                                                                                                             CHAIN A (BY SIMILARITY)
SHORT A CHAIN (A1).
CHAIN B (BY SIMILARITY)
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01-FEB-1996 (Rel. 33, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  73.6%; Score 408;
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81 TCYKDQGVTYRGTWSTSESGAQCINWNSNLLTRRTYNGRRSDAITLGLGNHNYCRNPDNN 140

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R SWART; SW00181; EGF; 1.

R SWART; SW00181; EGF; 1.

R SWART; SW00181; EGF; 1.

R RSART; SW0020; TRYP SPC; 1.

R PROSITE; PS01186; EGF 2; 1.

R PROSITE; PS00021; KRINGLE 2; 1.

R PROSITE; PS01186; EGF 2; 1.

R PROSITE; PS01186; EGF 2; 1.

R PROSITE; PS0118; TRYPSIN IDOM; 1.

R PROSITE; PS0118; TRYPSIN ISER; 1.

R PROSITE; PS0118; TRYPSIN ISER; 1.

R PROSITE; PS0118; TRYPSIN ISER; 1.

R PROSITE; PS0118; TRYPSIN ISER; 1.

R PROSITE; PS0118; TRYPSIN ISER; 1.

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CATALYTIC ACTIVITY: Specific cleavage of Arg- |-Val bond in plasminogen to form plasmin.
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                                                                                                               -:- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
-:- SIMILARITY: Contains 1 kringle domain.
-:- SIMILARITY: Contains 1 EGF-like domain.
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InterPro; IPR006209; BGF like.
InterPro; IPR006210; IBGF.
InterPro; IPR000001; Kringle.
InterPro; IPR001254; Ser_protease_Try.
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Pfam; PF0001; Kringle; 1.
Pfam; PF0008; trypsln; 1.
PRINTS; PR0072; CHYMOTRYPSIN.
PRINTS; PR00018; KRINGLE.
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PIR; JS0599; JS0599.
HSSP; P98119; IA51.
MEROPS; S01.239; -.
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Best Local Similarity 50.08
Matches 42; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Plasminogen activators from the saliva of Desmodus rotundus (common vampire bat): unique fibrin specificity.";
Ann. N.Y. Acad. Sci. 667:395-403 (1992).
-!- FUNCTION: PROBABLY ESSENTIAL TO SUPPORT THE FEEDING HABITS OF THIS EXCLUSIVELY HAEMATOPHAGOUS ANIMAL. PROBABLE POTENT THROMBOLYTIC
                                                                                                                                                                                     01-APR-1990 (Rel. 14, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Salivary plasminogen activator alpha 2 precursor (EC 3.4.21.68) (DSPA alpha-2) (BAT-PA) (T-plasminogen activator).
Desmodus rotundus (Vampire bat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -:- SUBBUTT: MORDER:
--- DOWAIN THE FIBRONECTIN TYPE-I DOMAIN MEDIATES BINDING TO FIBRIN,
AND THE KRINGLE DOMAIN APPARENTLY MEDIATES FIBRIN-INDUCED
STIMULATION OF ACTIVITY.
--- SIMILARITY: BELONGS TO PEPTIDASE FAMILY SI.
--- SIMILARITY: Contains 1 EGF-like domain.
--- SIMILARITY: Contains 1 fibronectin type I domain.
--- SIMILARITY: Contains 1 fibronectin type I domain.
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ENZYME REGULATION: ACTIVITY TOWARD PLASMINOGEN IS STIMULATED IN
THE PRESENCE OF FIBRIN I.
                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
TISSUB-Salivary gland;
MEDLINE=92039036; PubMed=1937019;
Kraetzschnar J., Haendler B., Langer G., Boidol W., Bringmann P.,
Alagon A., Donner P., Schleuning W.D.;
The plasminogen activator family from the salivary gland of the
vampire bat Desmodus rotundus: cloning and expression.";
Gene 105:229-237(1991).
                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Chiroptera, Microchiroptera, Phyllostomidae,
Desmodontinae, Desmodus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.

TISSUB=Salivary gland;
MRDLINE=90036867; PubMed=250950;
Gardell S.G., Duong L.T., Diehl R.E., York J.D., Hare T.R.,
Register R.B., Jacobs J.W., Dixon R.A.F., Friedman P.A.;
"Isolation, characterization, and cDNA cloning of a vampire bat salivary plasminogen activator.";
J. Biol. Chem. 264:17947-17952(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHARACTERIZATION.
MEDLINE=93339059; bubMed=1309059;
Schleuning W.-D., Alagon A., Boidol W., Bringmann P., Petri T.,
Kraetzschmar J., Haendler B., Langer G., Baldus B., Witt W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CATALYTIC ACTIVITY: Specific cleavage of Arg- |-Val bond in
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                             141 SKPWCYVIKASKFILEFCSVPVCS 164
62 RRPWCYVQVGLKPLVQECMVHDCA 85
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117 N -> H (IN REF. 2).
135 M -> R (IN REF. 2).
53719 MW; 17486555C0E5077C CRC64;
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EMBL, JOSO82; AAA31596.1;
PIR, JSO598; JSO598.
HSSP; P98119; 1A51.
MEROPS; SO1.232; -.
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477 AA;
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MEDLINE=90130448; PubMed=2105315;
MEDLINE=90130448; PubMed=2105315;
PER PLOISON M., NY T.
The Structure of the TATA-less rat tissue-type plasminogen activator of TATA-less rat tissue-type plasminogen activator of TATA-less rat tissue-type plasminogen activator of TATA-less rat tissue-type plasminogen activator of TATA-less rat tissue-type plasminogen activator of TATA-less rat tissue-type plasminogen activator of TATA-less rat tissue-type plasminogen activator of TATA-less rat tissue-type plasminogen predict of TATA-less rat tissue-type plasminogen activator of TATA-less rat tissue-type plasminogen activator of TATA-less rat tissue-type plasminogen predict activator of TATA-less rat tissue-type plasminogen rate activator of TATA-less rate tissue-type plasminogen rate activator of TATA-less rate tissue-type plasminogen rate activation activator of TATA-less rate activator of TATA-less r

Rattus norvegicus (Rat). Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

NCBI TaxID=10116;

SEQUENCE FROM N.A.
MEDLINE-89170114; PubMed=3148445;
NY T., Leonardsson G., Hsueh A.J.W.;
Cloning and characterization of a cDNA for rat tissue-type plasminogen activator.";
DNS 7:671-677(1988).

01-FEB-1991 (Rel. 17, Created)
01-NOV-1991 (Rel. 20, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Tissue-type plasminogen activator precursor (EC 3.4.21.68) (tPA)
(t-PA) (t-plasminogen activator).

559 AA

STANDARD;

TPA RAT P19637;

TPA_RAT

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                                                                                                                                                                                                                                                                                                                                                                                              -!- SUBCELLULAR LOCATION: SECRETED; EXTRACELLULAR.
-!- PTM: THE SINGLE CHAIN, ALMOST FULLY ACTIVE ENZYME, CAN BE FURTHER PROCESSED INTO A TWO-CHAIN FULLY ACTIVE FORM BY A CLEAVAGE AFTER ARG-308 CATALYZED BY PLASMIN, TISSUE KALLIKREIN OR FACTOR XA.
-!- MISCELLANEOUS: BINDS TO THE KRINGLE STRUCTURE OF THE FIBRIN A CHAIN. BINDING TO FIBRIN ENHANCES ITS CATALYTIC ACTIVITY.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY $1.
-!- SIMILARITY: Contains 1 fibronectin type I domain.
-!- SIMILARITY: Contains 2 kringle domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; M23697; AAA41812.1; --
EMBL; M31197; AAA42261.1; --
EMBL; M31186; AAA42261.1; JOINE
EMBL; M31186; AAA42261.1; JOINE
EMBL; M31186; AAA42261.1; JOINE
EMBL; M31189; AAA42261.1; JOINE
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A19618;
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EMBL;
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2 TCYEGNGHFYRGKASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNR

12; Mismatches 30; Indels

42; Conservative

Matches

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61

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123 TCFEGQGITYRGTWSTAENGAECINWNSSALSQKPYSARRPNAIKLGLGNHNYCRNPDRD 182
                                                                                                                                             STANDARD;
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TISSUE-TYPE PLASMINOGEN ACTIVATOR A
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7DBD3809C1D1C921 CRC64;
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CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
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                                                                                                        InterPro; IPR000001; Kringle.
InterPro; IPR001254; Ser_protease_Try.
Pfam; PF00008; EGF; 1.
Pfam; PF00039; fn1; 1.
                                                   Chymotrypsin.
                                                                    IPR006209; EGF like.
IPR000083; Fibrnctnl.
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308
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InterPro, IPR006209;
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InterPro; IPR000083;
InterPro; IPR006210;
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559 AA;
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MEDLINE=86284200; PubMed=3090401;
Harris T.J., Patel T., Marston F.A., Little S., Emtage J.S.,
Patel T., Marston F.A., Little S., Emtage J.S.,
Opdenakker G., Volckaert G., Rombauts W., Billiau A., Somer P.;
"Cloning of cDNA coding for human tissue-type plasminogen activator and its expression in Escherichia coli.";
Mol. Biol. Med. 3:279-292 (1986).
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MEDIATE=84528137; PubMed=6089198;

MDIATE=84528137; Lund B.;

"The structure of the human tissue-type plasminogen activator gene: correlation of intron and exon structures to functional and structural domains.";

Proc. Natl. Acad. Sci. U.S.A. 81:5355-5359(1984).
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MEDLINE-8805470; PubMed=2824147;
Reddy V.B., Garramone A.J., Sasak H., Wei C.-M., Watkins P., Galli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Fetal lung;
MEDLINE=88262579; PubMed=3133640;
Sasaki H., Saito Y., Hayashi M., Otsuka K., Niwa M.;
Shucleotide sequence of the tissue-type plasminogen activator CDNA from human fetal lung cells.";
Nucleic Acids Res. 16:5695-5695 (1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Expression of human uterine tissue-type plasminogen activator in mouse cells using BPV vectors.";
DNA 6:461-472(1987).
                                                                                                                                                                                                                                                                             Homo sapiens (Human).
Bukaryota, Metazoa; Chordata, Craniata, Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                    PO0750; Q1510.

21-UUL-1986 (Rel. 01, Created)

21-UUL-1986 (Rel. 01, Last sequence update)

15-SRP-2003 (Rel. 42, Last annotation update)

15-SRP-2003 (Rel. 42, Last annotation update)

(t-pha) (t-phasminogen activator precursor (EC 3.4.21.69) (tPA)

ELAT.
                                   183 VKPWCYVFKAGKYTTEFCSTPAC----PKGPTED 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-86196143; PubMed=3009482;
Friezner Degen S.J., Rajput B., Reich E.;
The human tissue plasminogen activator gene.";
"The biol. Chem. 261:6972-6985(1986).
62 RRPWCYVQVGLKPLVQECMVHDCADGKKPSSPPEE 96
                                                                                                                                562 AA
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TISSUE=Umbilical vein;
MEDLINE=90192129; PubMed=2107528;
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MEDLINE=83115262; PubMed=6337343;
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MEDILINE=22388257; PubMed=12477932;
A Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
A strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Altashul S.F., Zeeberg B., Bartow K.H., Schaefer C.F., Bhat N.K.,
Altashul S.F., Zeeberg B., Bartow K.H., Schaefer C.F., Bhat N.K.,
A plokins R.F., Jordan H., Moore T., Max S.I., Wang J., Haish F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M.J., Gares M.B., Boraldo M.F., Casavant T.L., Scheetz T.E.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Brownstein M.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Moorley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergen E.J., Lu X., Gibbs R.A.,
Rahoton D.K., Muzny D.M., Sodergen E.J., Lu X., Gibbs R.A.,
Blakesley R.W., Touchman M., Madan A., Rodrigues S., Sanchez A.,
Rodriguez A.C., Grimwood J., Schwutz J., Myers R.M.,
Schnerch A., Schein J.E., Jones S.J.M., Marra M.S.,
Cherch A., Schein J.E., Jones S.J.M., Marra M.A.,
Caparation and initial analysis of more than 15,000 full-length SEGÜENCE OF 31-562 FROM N.A.
MEDLINE=91291340; PubMed=1368681;
Itagaki Y., Yasuda H., Morinaga T., Mitsuda S., Higashio K.;
Iturification and characterization of tissue plasminogen activator
secreted by human embryonic lung diploid fibroblasts, IMR-90 cells.";
Agric. Biol. Chem. 55:1225-1232(1991). Pohl G., Kaellstroem M., Bergsdorf N., Wallen P., Joernvall H.; "Tissue plasminogen activator: peptide analyses confirm an indirectly derived amino acid sequence, identify the active site serine residue, establish glycosylation sites, and localize variant differences."; "Isolation and characterization of the human tissue-type plasminogen activator structural gene including its 5' flanking region."; J. Biol. Chem. 260:11223-11230(1985). Siebert P.D., Fong K.;
"Variant tissue-type plasminogen activator (PLAT) cDNA obtained from
"Natiant tissue-type plasminogen activator (PLAT) cDNA obtained from
Numan endothelial cells.";
Nucleic Acids Res. 18:1086-1086(1990). 'Vallen P., Pohl G., Bergsdorf N., Raanby M., Ny T., Joernvall H., 'Purification and characterization of a melanoma cell plasminogen SEQUENCE OF 212-361 FROM N.A. MEDLINE-83169656; PubMed=6572897; Edlund T., Ny T., Raanby M., Heden L.-O., Palm G., Holmgren E., Josephson S., Isolation of cDNA sequences coding for a part of human tissue MEDLINE=90092112; PubMed=2513186; Pfeiffer G., Schmidt M., Strube K.-H., Geyer R.; "Carbohydrate structure of recombinant human uterine tissue MEDLINE=85289338; PubMed⇒3161893; Fisher R., Waller E.K., Grossi G., Thompson D., Tizard R.. Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002). plasminogen activator."; Proc. Natl. Acad. Sci. U.S.A. 80:349-352(1983). J. Biochem. 132:681-686(1983). MEDLINE=83209620; PubMed=6682760; TISSUE=Melanoma; MEDLINE=85000468; PubMed=6433976; Biochemistry 23:3701-3707(1984). SEQUENCE OF 33-52 AND 311-330. STRUCTURE OF CARBOHYDRATES SEQUENCE OF 1-36 FROM N.A. SEQUENCE OF 36-562. SEQUENCE FROM N.A. Schleuning W.-D. activator

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126 TCYEDQGISYRGTWSTAESGAECTNWNSSALAQKPYSGRRPDAIRLGLGNHNYCRNPDRD 185
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Byeon I.-J.L., Kelley R.F., Llinas M.; "IH NWR structural characterization of a recombinant kringle 2 domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 TCYEGNGHFYRGKASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=92106329; PubMed=1762144; Bycon I.-J., Llinas M.; Bycon I.-J., Llinas M.; Sybution structura for the tissue-type plasminogen activator kringle gonain complexed to 6-aminohexanoic acid an antifibrinolytic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Lysine 156 promotes the anomalous proenzyme activity of tPA: X-ray crystal structure of single-chain human tPA.";
EMBO J. 16:4797-4805(1997).
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Byeon I.-J.L., Kelley R.F., Llinas M.;
"Kringle-2 domain of the tissue-type plasminogen activator. 1H-NMR
assignments and secondary structure.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=92118803; PubMed=1310033; de Vos A., Ultsch M.H., Kelley R.F., Padmanabhan K., Tulinskly A., de Vos A., Ultsch M.H., Kosaiakof A.A.; "Crystal structure of the kringle 2 domain of tissue plasminogen activator at 2.4-A resolution.";
                                                                                                                                                                                                                                                                                                                                         X.BAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF CATALYTIC DOMAIN.
MEDLINE-96200985; PubMed-8613982;
Lamba D., Bauer M., Huber R., Fischer S., Rudolph R., Kohnert U.,
                                                                           MEDILINE-91159408; PubMed=1900431; Harris R.J., Leonard C.K., Guzzetta A.W., Spellman M.W.; Harris R.J., Leonard C.K., Guzzetta A.W., Spellman M.W.; Tisseue plasminogen activator has an O-linked fucose attached to threonine-61 in the epidermal growth factor domain."; Biochemistry 30:2311-2314(1991).
                                                                                                                                                                                                                                              Bang N.U.;
plasminogen activator expressed in mouse epithelial cells.";
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                                                                                                                                                                                                               MEDLINE 20144705; Pubmed=1645336; Vlahos C.J., Wilhelm O.G., Hassell T., Jaskunas S.R., Bang "Disulfide pairing of the recombinant kringle-2 domain of "plasminogen activator produced in Escherichia coli."; J. Biol. Chem. 266:10070-10072(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         K-RAY CRYSTALLOGRAPHY (3.1 ANGSTROMS) OF CATALYTIC DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF KRINGLE 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 from human tissue-type plasminogen activator.";
Biochemistry 28:9350-9360(1989).
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                     Eur. J. Biochem. 186:273-286(1989).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=97449126; PubMed=9305622;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PubMed=2558718;
                                                                CARBOHYDRATE-LINKAGE SITE THR-96.
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                                                                                                                                                                                                         DISULFIDE BONDS IN KRINGLE 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Donner P.;
"Plasminogen activators from the saliva of Desmodus rotundus (common
                                                                                                                                                                                                                                               01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
01-FEB-2003 (Rel. 41, Last annotation update)
Salivary plasminogen activator gamma precursor (EC 3.4.21.68) (DSPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FUNCTION: PROBABLY ESSENTIAL TO SUPPORT THE FEEDING HABITS OF THE EXCLUSIVELY HARMATOPHAGOUS ANIMAL. PROBABLE POTENT THROMBOLYTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Salivary gland;
MEDLINE=292039036; PubMed=1937019;
Kraetzschmar J., Handlar B., Langer G., Boidol W., Bringmann P., Alagon A., Donner P., Schleuning W.D.; the salivary gland of the 'The plasminogen activator family from the salivary gland of the vampire bat Deemodus rotundus: cloning and expression."; den 105:229-237(1991).
                                                                                                                                                                                                                                                                                                                                                                                     Desmodus rotundus (Vampire bat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Chiroptera; Microchiroptera; Phyllostomidae;
Desmodontinae; Desmodus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-53393059; PubMed-1309059;
Schleuning W.-D., Alagon A., Boidol W., Bringmann P., Petri T.,
Kraetzschmar J., Haendler B., Langer G., Baldus B., Witt W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CATALYTIC ACTIVITY: Specific cleavage of Arg- |- Val bond in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    plasminogen to form plasmin.
SUBUNIT: Monomer.
SIMILARITY: BELONGS TO PEPTIDASE FAMILY SI.
SIMILARITY: Contains 1 kringle domain.
                                                                                                                                                                                         394 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    vampire bat): unique fibrin specificity.";
Ann. N.Y. Acad. Sci. 667:395-403(1992).
-!- FUNCTION: PROBABLY ESSENTIAL TO SUPPORT
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MEROPS; S01.239; -.

MEROPS; S01.239; -.

InterPro; IPR001314; Chymotrypsin.

InterPro; IPR001254; Ser_protease_Try.

Pfam; PF00051; Kringle; 1.

Pfam; PF00051; Kringle; 1.

PRINTS; PR00139; KRINGLE;

PRODOM; PD000395; KRINGLE;

PRODOM; PR0001395; KRINGLE;

SMART; SM00130; KRINGLE;

PROSITE; PS50070; KRINGLE;

PROSITE; PS50070; KRINGLE;

PROSITE; PS50070; KRINGLE;

PROSITE; PS50070; KRINGLE;

PROSITE; PS50070; KRINGLE;

PROSITE; PS50070; KRINGLE;

PROSITE; PS50070; KRINGLE;

PROSITE; PS500740; TRYPSIN_DOM;

PROSITE; PS500134; TRYPSIN_DOM;

PROSITE; PS00134; TRYPSIN_DOM;

PROSITE; PS00134; TRYPSIN_ES;

PROSITE; PS00134; TRYPSIN_ES;

PROSITE; PS00134; TRYPSIN_ES;

PROSITE; PS00134; TRYPSIN_ESR;

PROSITE; PS00134; TRYPSIN_ESR;

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EMBL; M63990; AAA31595.1; -. PIR; JS0600; JS0600.
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TRAUSHER R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Antschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Antschul S.F., Zeeberg B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Boatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Asta S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Rachards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Vilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Tahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Milting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
                                                                                                                                                                                                                                                                                                                                                                                                         44 TCYKDQGVTYRGTWSTSESGAQCINWNSNLLIRRTYNGRMPEAVKLGLGNHNYCRNPDGA 103
                                                                                                                                                                                                                                                                                                                                                                                      2 TCYEGNGHFYRGKASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNR
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Rickles KJ., Darrow A.L., Strickland S.;
Molecular cloning of complementary DNA to mouse tissue plasminogen
activator mRNA and its expression during F9 teratocarcinoma cell
           POTENTIAL.
SALIVARY PLASMINOGEN ACTIVATOR GAMMA
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                           (BY SIMILARITY)
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Pl1214, Q31VD2,
101-UUL-1989 (Rel. 11, Created)
15-SEP-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Tissue-type plasminogen activator precursor (EC 3.4.21.68) (LPA)
(t-PA) (t-plasminogen activator).
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                                               KRINGLE.
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Kringle, Signal, Multigene family
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Best Local Similarity 45.2
Matches 38, Conservative
                                            Mus musculus (Mouse)
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394 AA;
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RAM ROGITIGNER A.C., Grinwood J., Schmutz S., Myers R.M.,
RAMINER D.E.,
RAM BULGETIES OF M.N. KETPATISHS M.I., WARKER W. R. Samilus D.E.,
RAM GONES CHANGE C.M. M. KETPATISHS M.I., WARKER W. R. Samilus D.E.,
GONESTIEL, Acad. Sci. U.S. A. 9916899-160010202.

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2 TCYEGNGHFYRGKASTDIMGRPCLPWNSAIVLQQTYHAHRSDALQLGLGKHNYCRNPDNR 61
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01-FEB-1996 (Rel. 33, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Salivary plasminogen activator alpha 1 precursor (EC 3.4.21.68) (DSPA
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TISSUE=salivary gland;
MEDLINE=92039036, PubMed=1937019;
MEDLINE=92039036, PubMed=1937019;
MEDLINE=92039036, PubMed=1937019;
MEDLINE=92039036, PubMed=1937019;
Alagon A., Donner P., Schleuning W.D.,
"The plasminogen activator family from the salivary gland of the vampire bat Desmodus rotundus: cloning and expression.";
Gene 105:229-237(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Desmodus rotundus (Vampire bat).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Chiroptera, Microchiroptera, Phyllostomidae,
Desmodontinae, Desmodus.
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MEDLINE=93393059; PubMed=1309059;
Schleuning W.-D., Alagon A., Boidol W., Bringmann P., Petri T.,
Kraetzschmar J., Haendler B., Langer G., Baldus B., Witt W.,
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63122 MW, 8CCEE2BDB94514D9 CRC64;
                                                                SERINE PROTEASE.
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            FIBRONECTIN TYPE-I.
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                                       KRINGLE 1.
KRINGLE 2.
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TCYEGNGHFYRGKASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNR
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; Pred. No. 1.7e-16;
10; Mismatches 35; Indels
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                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its modified on-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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RREOPE, S01.232, --
RIGEOPE, S01.232, --
RIGEOPE, S01.232, --
RIGEOPE, S01.232, --
RIGEOPE, PROBLEDB, P99119; --
RIGEOPE, IPROBLEDB, P69119; --
RIGEOPE, IPROBLEDB, EGF like.
RIGEOPE, IPROBLEDB, EGF.
RIGEOPE, IPROBLEDB, EGF.
RIGEOPE, IPROBLEDB, RIGGE.
RIGEOPE, IPROBLESE, SET_DIOLESE_Try.
RIGEOPE, IPROBLESE, SET_DIOLESE_Try.
REAM, PROBLES, EGF.
RIGGE, REAMORENEE, I.
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                    Desmodus rotundus (common
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Donner P.;
"Plasmingen activators from the saliva of vampire bat): unique fibrin specificity."; Ann. N.Y. Acad. Sci. 667:395-403(1992).
                                                                                               X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; M63987; AAA31591.1; -.
EMBL; M63986; AAA31592.1; -.
PIR; JS0597; JS0597.
PDB; 1A51; 23-MAR-99.
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279 ОРИСНУМКОВОГТИВУСПУРОС 300
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Best Local Similarity
Matches 39; Conservat
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487
487
566 AA;
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127 TCYEGQGVTYRGTWSTAESRVECINWNSSLLTRRTYNGRMPDAFNLGLGNHNYCRNPNGA 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                       INC. Dairy J. 5:605-617(1995).
-!- FUNCTION: CONVERTS THE ABUNDANT, BUT INACTIVE, ZYMOGEN PLASMINOGEN PLASMINOGEN TO PLASMIN BY HYDROLYZING A SINGLE ARG-VLA BOND IN PLASMINOGEN. BY CONTROLLING PLASMIN-MENDIATED PROTECLYSIS, IT PLAYS AN IMPORTANT ROLE IN TISSUE REMODELING AND DEGRADATION, IN CELL MIGRATION AND MANY OTHER PHYSIOPATHOLOGICAL EVENTS.
-!- CATALYTIC ACTIVITY: Specific cleavage of Arg-|-Val bond in plasminogen to form plasmin.
-!- SUBUNIT: HETERODIMER OF CHAIN A AND CHAIN B HELD BY A DISULFIDE
                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Kidney;
Ravn P., Berglund L., Petersen T.B.;
"Cloning and characterization of the bovine plasminogen activators uPA
and tPA.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBCELLULAR LOCATION: SECRETED; EXTRACELLULAR.

PTM: THE SINGLE CHAIN, ALMOST FULLY ACTIVE ENZYME, CAN BE FURTHER PROCESSED INTO A TWO-CHAIN FULLY ACTIVE FORM BY A CLEAVAGE AFTER ARG-314 CATALYZED BY PLASMIN, TISSUE KALLIKREIN OR FACTOR XA.
MISCELLANEOUS: BINDS TO THE KRINGLE STRUCTURE OF THE FIBRIN A CHAIN. BINDING TO FIBRIN ENHANCES ITS CATALYTIC ACTIVITY.
SIMILARITY: COLLAINS ID EGF-LIKE domain.
SIMILARITY: Contains I EGF-Like domain.
SIMILARITY: Contains I fibronectin type I domain.
                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
Bovidae, Bovinae, Bos.
MCBI_TaxID=9913,
                                                                                                                                                                           01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Tissue-type plasminogen activator precursor (EC 3.4.21.68) (tPA)
PLAT.
                                                                                                                                                 566 AA
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HSSP; P00750; IRTF.
MEROPS; S01.232;
InterPro; IPR001314; Chymotrypsin.
InterPro; IPR006209; EGF_like.
InterPro; IPR006039; Fibrnctnl.
InterPro; IPR0060103; Fibrnctnl.
InterPro; IPR000011; Kringle.
InterPro; IPR001224; Ser_protease_Try.
Pfam; PF00009; EGF; 1.
                                                                  210
                                                                                                                                                 PRT;
                                                               187 PKPWCYVIKAGKFTSESCSVPVCS
                                 62 RRPWCYVQVGLKPLVQECMVHDCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00051; kringle; 2.
Pfam; PF00089; trypsin; 1.
PRINTS; PR00722; CHYMCTRYPSIN.
PRINTS; PR00018; KRINGLE.
Probom; PD000395; Kringle; 2.
                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                               Bos taurus (Bovine).
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                                                                                                                                               TPA_BOVIN
Q28198;
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DR SMART; SM00181; EGF; 1.

DR SMART; SM00020; TryP_SPC; 1.

DR PROSITE; PS00022; TryP_SPC; 1.

DR PROSITE; PS01086; EGF_2; 1.

DR PROSITE; PS00123; FIRENDECTIN 1; 1.

DR PROSITE; PS00021; KRINGLE_1; 1.

DR PROSITE; PS00134; TRYPSIN_DOM; 1.

DR PROSITE; PS00134; TRYPSIN_DOM; 1.

DR PROSITE; PS00135; TRYPSIN_DOM; 1.

DR PROSITE; PS00135; TRYPSIN_SER; 1.

DR PROSITE; PS00135; TRYPSIN_SER; 1.

DR PROSITE; PS00136; TRYPSIN_SER; 1.

DR PROSITE; PS00136; TRYPSIN_SER; 1.

DR PROSITE; PS00136; TRYPSIN_SER; 1.

DR PROSITE; PS00136; TRYPSIN_SER; 1.

DR PROSITE; PS00136; TRYPSIN_SER; 1.

DR PROSITE; PS00136; TRYPSIN_SER; 1.

DR PROSITE; PS00136; TRYPSIN_SER; 1.

DR PROSITE; PS00136; TRYPSIN_SER; 1.

DR SIMILARITY.

22 33 BR SIMILARITY.

24 11SSUE-TYPE PLASMINOGEN ACTIVATOR B.

TISSUE-TYPE PLASMINOGEN ACTIVATOR B.

THESUE-TYPE PLASMINOGEN ACTIVATOR B.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 CYEGNGHFYRGKASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNRR 62
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01-APR-1990 (Rel. 14, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
Urohlase-type plasminogen activator precursor (EC 3.4.21.73) (uPA)
Gallus gallus (Chicken).
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HGFA HUMAN
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SMART; SM00181, EGF; 1.

SMART; SM00180; KR; 1.

R PROSITE; PS01186; EGF 2; 1.

R PROSITE; PS01186; EGF 2; 1.

R PROSITE; PS02186; KRINGLE 1; 1.

R PROSITE; PS02204; KRINGLE 2; 1.

R PROSITE; PS02204; KRINGLE 2; 1.

R PROSITE; PS02134; TRYPEIN HIS; 1.

R PROSITE; PS0135; TRYPEIN HIS; 1.

R PROSITE; PS0135; TRYPEIN JAGON 1.

R PROSITE; PS0136; TRYPEIN JAGON 1.

R PROSITE; PS0136; JAYPEIN JAGON 1.

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CONNECTING PEPTIDE.
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                                                                 SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

MEDLINE=90110185; PubMed=2295632;

Leslie N.D., Kessler C.A., Bell S.M., Degen J.L.;

Leslie N.D., Kessler C.A., Bell S.M., Degen J.L.;

The chicken urokinase-type plasminogen activator gene.";

J. Biol. Chem. 265:1339-1344(1990).

-: CATALYTIC ACTIVITY: Specific cleavage of Arg-|-val bond in plasminogen to form plasmin.

-: SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.

-: SIMILARITY: Contains 1 kingle domain.

-: SIMILARITY: Contains 1 EGF-like domain.
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BD881048DD666A55 CRC64;
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CHAIN B (BY SIMILARITY)
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EMBL, J05188; AAA49130.1; --
HSP, A35005, A35005.
HSSP, P00763; 1DPO.
MEROPS; S01.231; --
InterPro; 1PR001314; Chymotrypsin.
InterPro; 1PR006209; EGF like.
InterPro; 1PR006210; IEGF.
InterPro; 1PR001254; Scr. protease_Try.
Pfan; PF00013; kringle, 1.
Pfan; PF00018; kringle, 1.
PRINTS; PR00722; CHYMOTRYPSIN.
PRINTS; PR001039; KRINGLE.
PRODOM; PR001039; KRINGLE.
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162
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434 AA;
                                                NCBI_TaxID=9031;
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                                                                                                                                                                                    79 CYSGNGEDYRGMAEDP----GCLYWDHPSVIRWGDYHADLKNALQLGLGKHNYCRNPNGR 134
                                                                                                                         3 CYEGNGHFYRGKASIDIMGRPCLPWNSAIVLQ-QTYHAHRSDALQLGLGKHNYCRNPDNR 61
                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryoča, Metazoa, Chordata; Craniata; Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Molecular cloning and sequence analysis of the cDNA for a human serine protesse reponsible for activation of hepatocyte growth factor. Structural similarity of the protesse precursor to blood coagulation factor XII";
J. Biol. Chem. 268:10024-10028(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 40-655 FROM N.A.

Zhao S., Odell C.;

Submitted (FBE-1996) to the EMBL/GenBank/DDBJ databases.

-!- FUNCTION: ACTIVATES HEPATOCYTE GROWTH FACTOR (HGF) BY

CONVERTING IT FROM A SINGLE CHAIN TO A HETERODIMERIC FORM.

-!- SUBUNIT: DIMER OF A SHORT CHAIN AND A LONG CHAIN LINKED BY A
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01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Hepatocyte growth factor activator precursor (EC 3.4.21.-) (HGF activator) (HGFA).
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TISSUE-Liver, and Serum;
MEDLINE=93252878; PubMed=7683665;
MYyaawa K., Shimomura T., Kitamura A., Kondo J., Morimoto Y.,
DB 1; Length 434;
Query Match 35.8%; Score 198.5; DB 1; Length Best Local Similarity 54.4%; Pred. No. 6.6e-15; Matches 37; Conservative 7; Mismatches 19; Indels
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GO; GO:0005576; C:extracellular; TAS.
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EMBL; Z6923; CAA93803.1; -.
PIR; A46688, A46688.
HSSP; P00763; IDPO.
MEROPS; S01.228; -.
                                                                                                                                                                                                                                                                                                                 135 SŘPWCYTK 142
                                                                                                                                                                                                                                                      62 RRPWCYVQ 69
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Gaps

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TISSUENCE FROM N.A., AND SEQUENCE OF 19-37; 318-332.AND 359-373.

RA TISSUELINE=31003367; PubMed=1390917;

RA MEDLINE=93003367; PubMed=1390917;

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                                                                                                                                                                                                                                                                                        3 CYEGNGHFYRGKASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNRR
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Skaryvota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Hystricognathi, Caviidae, Cavia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Coaquiation factor XII precursor (EC 3.4.21.38) (Hageman factor)
(HAP) (Fragment).
                                                                                                                       Query Match 35.1%; Score 194.5; DB 1; Length 655; Best Local Similarity 40.4%; Pred. No. 2.9e-14; Matches 42; Conservative 8; Mismatches 41; Indels 13;
            N-LINKED (GLCNAC. . .) (POTENTIAL).
R -> O (IN REF. 2).
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                                                                                                                                                                                                                                                                                                                                                                      63 RPWCYVQVGLKPLVQECMVHDC-----ADGKKPSSP 93
                                      R -> Q (IN REF. 2).
2CF72F1E1B862ED7 CRC64;
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InterPro; IPR001314; EGF 2.
InterPro; IPR001881; EGF 7ca.
InterPro; IPR006209; EGF 1ike.
InterPro; IPR000083; Fibrnctnl.
                                                                   70681 MW;
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655 AA;
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            DR InterPro; IPR00114; Chyoneclysts and peptidolysis; TAS.

INTERPRO; IPR000141; Chyoneclysts and peptidolysis; TAS.

INTERPRO; IPR000141; Chyoneclysts

INTERPRO; IPR000062; FN TYPe_II.

INTERPRO; IPR000061; Firenceni.

INTERPRO; IPR000061; KITAPE_II.

INTERPRO; IPR000061; KITAPE_II.

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GO; GO:0006508; P:proteolysis and peptidolysis; TAS
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215 SCYEGRGVSYRGMARTTVSGAKCQRWAS----EATYRNMTAEQALRRGLGHHTFCRNPDN 270
                                     61 RRRPWCYVQVGLKPLVQECMVHDCADGKKPSSPPEE 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AF099017; AAF02489.1; -. EMBL; AF224724; AAF34712.1; -. HSSP; P00763; 1DPO.
                                                                                                                                                                                                                                                                                          Mus musculus (Mouse)
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ALPHA-FACTOR XIIA LIGHT CHAIN.
FIBRONECTIN TYPE-II.
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48DC6B946FB9ED59 CRC64;
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FIBRONECTIN TYPE-I.
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Interpro; IPR000562; FN Type_II.
Interpro; IPR006210; IEGF.
Interpro; IPR000001; Kringle.
Interpro; IPR001254; Ser_protease_Try
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Van Adelsberg U.S., Sengal S., Kukes A., Brady C., Barasch J.; Yang J.; Huan Y.; Huan Y.; Huan Y.; Huan Y.; Huan Y.; Huan Y.; Huan Y.; Experiment of HGF by endogenous HGF activator is required for metanephric kidney morphogenesis in vitro."; Submitted (JAN-2000) to the EMBL/Genbank/DDBAD databases.
-!- FUNCTION: ACTIVATES HERATOCYTE GROWTH FACTOR (HGF) BY CONVERTING IT FROM A SINGLE CHAIN TO A HETERODIMERIC FORM (BY SIMILARITY).
-!- SUBUNIT: DIMER OF A SHORT CHAIN AND A LONG CHAIN LINKED BY A DISULFIDE BOND (BY SIMILARITY).
-!- SUBCURIAR LOCATION: SECRETED AS AN INACTIVE SINGLE-CHAIN PRECURSOR AND IS THEN ACTIVATED TO A HETERODIMERIC FORM (BY
                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                          HGFA_MOUSE STANDARD; PRT; 653 AA.
09R0891, 09UR081.
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 41, Last annotation update)
28-FRBE-2003 (Rel. 41, Last annotation update)
4Pepatocyte growth factor activator precursor (EC 3.4.21.-) (HGF
                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=BALB/c;
Itoh H., Kataoka H., Koono H.;
"Mouse hepatrocyte growth factor activator.";
Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
-!- SIMILARITY: Contains 2 EGF-like domains.
-!- SIMILARITY: Contains 1 fibronectin type I domain.
-!- SIMILARITY: Contains 1 fibronectin type II domain.
-!- SIMILARITY: Contains 1 kringle domain.
271 DTRPWCFVWMGNRLSWEYCDLAQCQYPPQPTATPHD 306
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MEROPS; SQ1.228; -...
MGD, MGI:1859281; Hgfac.
InterPro; IPR0001314; Chymotrypsin.
InterPro; IPR000742; EGF 2;
InterPro; IPR000083; Fibrictn1.
InterPro; IPR000509; FGF_like.
InterPro; IPR000509; Fibrictn1.
InterPro; IPR000501; Kingle.
InterPro; IPR0001254; Ser_protease_Try.
Pfam; PF00039; fn1; 1...
Pfam; PF00039; fn1; 1...
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PF00089; trypsin; 1.
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TCYEGNGHFYRGKASTDTMGRPCLPWNSATVLQQTYHAHRSD-ALQLGLGKHNYCRNPDN

343 RPWCYV 348

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                                 R PRINTS; PROGUES, KRINGLE.

R PRODOM; PD000995; EN Type_II; 1.

R PRODOM; PD000995; EN Type_II; 1.

R PRODOM; PD000995; EN Type_II; 1.

R PRODOM; PD000995; FN2; 1.

R RAMAR; SM00018; EGF; 2.

R SMART; SM00020; FN2; 1.

R PROSITE; PS01022; EGF_I; 2.

R PROSITE; PS01023; FIBRONECTIN_2; 1.

R PROSITE; PS01023; FIBRONECTIN_2; 1.

R PROSITE; PS01024; TRYPSIN L); 1.

R PROSITE; PS01014; TRYPSIN LOOM; 1.

R PROSITE; PS01014; TRYPSIN HIS; 1.

R PROSITE; PS01015; TRYPSIN HIS; 1.

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CLEAVED IN ACTIVE FORM (BY SIMILARITY).
HEPATOCYTE GROWTH FACTOR ACTIVATOR SHORT
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EGF-LIKE 2.
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PR00722; CHYMOTRYPSIN. PR00013; FNTYPEII.
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MEDLINE=96133302; PubMed=8528215;
Schloesser M., Hofferbert S., Bartz U., Lutze G., Lammle B., Engel W.;
"The novel acceptor splice site mutation 11396(G-->A) in the factor
"If gene causes a truncated transcript in cross-reacting material
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "cDNA sequence coding for human coagulation factor XII (Hageman).", Nucleic Acids Res. 14:3146-3146(1986).
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MEDLINE=86033830; PubMed=3877053;

Cool D.E., Edgell C.-J.S., Louie G.V., Zoller M.J., Brayer G.D.,

McGillivray R.T.A.;

"Characterization of human blood coagulation factor XII cDNA.

Prediction of the primary structure of factor XII and the tertiary structure of beta-factor XIIa.";

J. Biol. Chem. 260:13666-13676(1985).
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McMullen B.A., Fujikawa K.;
"Amino acid sequence of the heavy chain of human alpha-factor XIIa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A., AND VARIANTS ALA-207; ASP-545 AND HIS-605. Rieder M.J., Armel T.Z., Carrington D.P., Ozuna M., Kuldanek S.A., Rajkumar N., Toth E.J., Yi Q., Nickerson D.A.; Submitted (AUG-2002) to the EMBL/Genbank/DDBJ databases.
                                                                                                                                                                                                                                                                Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates; Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Characterization of a cDNA coding for human factor XII (Hageman
                            P00748; P78339;
21-JUL-1986 (Rel. 01, Created)
01-CTT-1989 (Rel. 12, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Coaquiation factor XII precursor (EC 3.4.21.38) (Hageman factor)
(HAP).
                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE-88007593; PubMed=2888762;
Cool D.E., McGillivray R.T.A.;
"Characterization of the human blood coagulation factor XII ge
Intron/exon gene organization and analysis of the 5'-flanking
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 4-615 FROM N.A.
MEDLINE-86176794; PubMed=3754331;
Tripodi M., Citarella F., Guida S., Galeffi P., Fantoni A.,
Cortese R.;
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MEDLINE=83291041; PubMed=6604055;
Fujikawa K., MCMUllan B.A.;
"Amino acid acquence of human beta-factor XIIa.";
J. Biol. Chem. 258:10924-10933(1983).
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MEDLINE=86216049; PubMed=3011063;
Que B.G., Davie E.W.;
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Blochemistry 25:1525-1528(1986)
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   HUMAN
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                                                                                                                                                                                                      "Coagulation factor XII (Hageman factor) Washington D.C.: inactive factor XIIa results from Cys-571-->Ser substitution.";
Proc. Natl. Acad. Sci. U.S.A. 86:8319-8322(1989).
                                                                                                                                                                                                                                                                 VARIANT LOCARNO PRO-372.
MEDLINE=94325559; PubMed=8049433;
Hovinga J.K., Schaller J., Stricker H., Wuillemin W.A., Furlan M.
Laemmle B.;
                                      CARBOHYDRAIE-LINKAGE SITE THR-109.
MEDLINE=92184750; PubMed=1544894;
Harris R.J., Ling V.T., Spellman M.W.;
"O-linked fuccose is present in the first epidermal growth factor domain of factor XII but not protein C.";
J. Biol. Chem. 267:5102-5107(1992).
                                                                                                                                                                            Miyata T., Kawabata S.-I., Iwanaga S., Takahashi I., Alving B.,
Saito H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; M31315; AAA70225.1; EMBL; AF538691; AAA70225.1; EMBL; M1723; AAA51986.1; EMBL; M1746; AAB59490.1; EMBL; M1746; AAB59490.1; JOINED. EMBL; M13147; AAB59490.1; JOINED. EMBL; M13147; AAB59490.1; JOINED. EMBL; M13147; AAA51203.1; FRHIZ. MSCPS; POOT63; LDPC. MSCPS; SO1.21; Genew; HGNC:3530; F12.
 negative patients.";
Hum. Mol. Genet. 4:1235-1237(1995).
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VARIANT WASHINGTON D.C. SER-590.
MEDLINE=90046788; PubMed=2510163;
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GO; GO:0003805; F:blood coagulation factor XI activity; TAS.
DR GO; GO:0003805; F:blood coagulation factor XII activity; TAS.
DR InterPro; IRR001314; Chymorrypain.
DR InterPro; IRR001314; Chymorrypain.
DR InterPro; IRR000805; Fb.Drodton1.
DR InterPro; IRR000805; Fb.Drodton1.
DR InterPro; IRR000805; Fb.Drodton1.
DR InterPro; IRR000801; Fb.Drodton1.
DR InterPro; IRR000801; Fr.Ingle.
DR InterPro; IRR000081; EGF; 2.
DR Fdam; PR00009; Fd; 2.
DR Ffam; PR00009; Fd; 2.
DR Ffam; PR00009; Fd; 2.
DR Ffam; PR00009; Frygain; 1.
DR Ffam; PR00009; Frygain; 1.
DR Ffam; PR00009; FW179e-II; 1.
DR FRINTS; PR00019; FW179e-II; 1.
DR FRINTS; PR00019; FW179e-II; 1.
DR FRINTS; PR00019; FW1; 1.
DR FROOTE; PR00019; FW1; 1.
DR SWART; SW00019; FW1; 1.
DR SWART; SW00019; FW1; 1.
DR SWART; SW0019; FW1; 1.
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CHARGE RELAY SYSTEM (BY SIMILARITY).
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Pred. No. 1.3e-11;
6; Mismatches 24; Indels 5
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ALPHA-FACTOR XIIA LIGHT CHAIN.
BETA-PACTOR XIIA PART 1.
BETA-FACTOR XIIA PART 2.
FIBRONECTIN TYPE-II.
FIBRONECTIN TYPE-II.
FIBRONECTIN TYPE-I.
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PRO-RICH.
SERINE PROTEASE.
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Best Local Similarity 40.9
Matches 36; Conservative
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                                                                 DOMAIN
SEQUENCE
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Tomlinson J.E., McLean J.W., Lawn R.M.;
"Rhesus monkey apolipoprotein(a). Sequence, evolution, and sites of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS; PRO0012; Typerii, I.
PRINTS; PRO0013; KRINGLE.
PRINTS; PRO00139; KRINGLE.
SMART; SM00130; KRINGLE.
SMART; SM00130; KRINGLE.
SMART; SM00120; Tryp_SPC; 1.
PROSITE; PS50240; TRYPSIN_DOM; 1.
PROSITE; PS50240; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_HIS; FALSE NEG.
PROSITE; PS00135; TRYPSIN_HIS; FALSE NEG.
Hydrolase; Serine procease; Lipid transport; Plasma; Glycoprotein; Maringle; Repeat; Atherosclerosis.
                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae,
Cercopithecinae, Macaca.
                            01.JAN-1990 (Rel. 13, Created)
U-JAN-1990 (Rel. 13, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Apolipoprotein(a) (EC 3.4.21.-) (Apo(a)) (Lp(a)) (Fragment)
               PRT; 1420 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KRINGLE 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR01314; Chymotrypsin.
InterPro; IPR00101; Kringle.
InterPro; IPR0101254; Ser protease_Iry.
Pfam; PF00051; Kringle; Il.
Pfam; PF00089; trypsin; 1.
                                                                    Macaca mulatta (Rhesus macaque)
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              STANDARD;
                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                               MEROPS; S01.226;
                                                                                                    NCBI_TaxID=9544;
            APOA MACMU
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1068 CYHGNGQSYRGIFSTIVIGRICQSWSSMIPHQHKRIPENHPNDDLIM-----NYCRNPDA 1122
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                                                                                                                                                                                                                                                                                                                                                                                   28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Kremen protein 1 precursor (Kringle-containing protein marking the eye
and the nose) (Dickkopf receptor).
KREMENI OR KREMEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A., DEVELOPMENTAL STAGE, AND TISSUE SPECIFICITY. TISSUE=Brain, and Kidney;
MEDLINE=21167372; PubMed=11267660;
Nakamura T., Aoki S., Kitajima K., Takahashi T., Matsumoto K., Nakamura T.;
                                                                                                                                                                                  12;
                                                                                                                                                      Length 1420;
             KRINGLE 5.
KRINGLE 6.
KRINGLE 6.
KRINGLE 9.
KRINGLE 9.
KRINGLE 10.
SERINE PROTEASE.
                                                                                                                                                                                31; Indels
                                                                                                                                                  29.1%; Score 161; DB 1;
40.9%; Pred. No. 3.8e-10;
live 9; Mismatches 31
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277 355 KRING
391 469 KRING
505 587 KRING
619 697 KRING
725 803 KRING
83 917 KRING
953 1031 KRING
1067 1145 KRING
1191 1420 SERING
1420 AA; 158367 MW; B
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HSSP; P00747; 1CEA.
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
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28-FEB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Kremen protein I precursor (Kringle-containing protein marking the eye and the nose) (Dickkopf receptor).
KREMENI OR KREMEN.
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
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(POTENTIAL).
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                                                                                                                                                                                                                                                                      POTENTIAL.
KREBEN PROTEIN 1.
EXTRACELLULAR (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
KRINGLE.
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                                                                                                                                                                                                                                                      Transmembrane, Kringle
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N-LINKED (GLCNAC...) (
N-LINKED (GLCNAC...) (
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              C:integral to membrane; NAS
                           InterPro; IPR000859; CUB domain.
InterPro; IPR000859; CUB domain.
InterPro; IPR000801; Kringle.
InterPro; IPR000891; WsC.
InterPro; IPR000891; WsC.
InterPro; IPR00081; Kringle.
IPR00051; Kringle; 1.
IPR00051; Kringle; 1.
IPR00051; Kringle; 1.
IPR00061; Kringle; 1.
IPR00061; Kringle; 1.
IPR0017E; P8000180; CUB; 1.
IPR0SITE; P800180; CUB; 1.
IPR0SITE; P800180; CUB; 1.
IPR0SITE; P800180; CUB; 1.
IPR0SITE; P800021; KRINGLE 1; 1.
IPR0SITE; P800021; KRINGLE 1; 1.
IPR0SITE; P800021; KRINGLE 1; 1.
IPR0SITE; P800021; KRINGLE 1; 1.
IPR0SITE; P800021; KRINGLE 1; 1.
IPR0SITE; P800021; KRINGLE 1; 1.
IPR0SITE; P800021; KRINGLE 1; 1.
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IPR0SITE; P800021; KRINGLE 1; 1.
IPR0SITE; P800021; KRINGLE 1; 1.
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IPR0SITE; P800021; KRINGLE 1; 1.
IPR0SITE; P800021; KRINGLE 1; 1.
IPR0SITE; P800021; KRINGLE 1; 1.
IPR0SITE; P800021; KRINGLE 1; 1.
IPR0SITE; P800021; KRINGLE 1; 1.
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293
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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       32 CFTANGADYRGTQSWTALQGGKPCLFWNE--TFQHPYNTLKYPNGEGGLGEHNYCRNPDG 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CYEGNGHFYRGKASTDTM--GRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDN 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kremen protein 1 precursor (Kringle-containing protein marking the eye
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Receptor for Dickkopf protein. Cooperates with Dickkopf
-!- to block Mut/bera-catenin signaling (By similarity).
-!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
-!- SIMILARITY: Contains 1 CUB domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Xenopus laevis (African clawed frog).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
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(POTENTIAL)
(POTENTIAL)
(POTENTIAL)
(POTENTIAL)
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EXTRACELLULAR (POTENTIAL).
POTENTIAL.
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                                                                    EMBL; AB065090; BAB62003.1; -.
GO; GO:0016021; C:integral to membrane; ISS.
InterPro; IPR000859; CUB_domain.
InterPro; IPR000859; CUB_domain.
InterPro; IPR000801; Kringle.
InterPro; IPR00289; WSC.
Pfam; PF00431; CUB; 1.
Pfam; PF00451; kringle; 1.
Pfam; PF00051; kringle; 1.
Propom, PD000395; Kringle; 1.
SMART; SM00130; KR: 1.
PROSITE; PS010180; CUB; 1.
PROSITE; PS01021; KRINGLE.
PROSITE; PS01021; KRINGLE.
PROSITE; PS01021; KRINGLE.
PROSITE; PS01021; KRINGLE.
PROSITE; PS01021; KRINGLE.
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15-SEP-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
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MEDLINE=88039109; PubMed=3670400;
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                                                                                                                        SERINE PROTEASE ACTIVITY.
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                                                                                                                                                                                                                                                                                    Utermann G.;
                                                                    plasminogen.
 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its mode by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 CYEGNGHFYRGKASTDTM--GRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDN 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30 CYTVNGADYRGTQNQTSLDGGKPCLFWNE--TFQHPYNTLKYPNGEGGLGEHNYCRNPDG 87
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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1-AUG-1988 (Rel. 08, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Apolipoprotein(a) precursor (EC 3.4.21.-) (Apo(a)) (Lp(a)).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EXTRACELLULAR (POTENTIAL).
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 -!- SIMILARITY: Contains 1 kringle domain.
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InterPro; IPR000859; CUB_domain.
InterPro; IPR00081; Kringle.
InterPro; IPR000289; WSC.
Pfam; PF00431; CUB; I.
Pfam; PF01082; WSC; I.
Pfam; PF01082; WSC; I.
PRINTS; PR00018; KRINGLE.
ProDom; PD000395; Kringle; I.
SMART; SM00130; KR; I.
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Please G.W. Toolahamon, E.W. Kanang W.-J., Eaton D.L., Chen E.Y.,

Flease G.W. Scanu A.M. Iawn R.M.;

Karon Sequence of human apolipoprotein(a) is homologous to

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Best Local Similarity 34.2%;
Matches 40; Conservative
         4369
4412
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                                                               4548 AA;
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                     APOLI POPROTEIN (A).

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MEDLINE=20057165; PubMed=10591208; MEDLINE=20057165; PubMed=10591208; MEDLINE=20057165; PubMed=10591208; MEDLINE=20057165; PubMed=10591208; MEDLINE=20057165; PubMed=10591208; MEDLINE=20057165; PubMed=10591208; MEDLINE=20057165; PubMed=10591208; MEDLINE D. J. Ainscough R., Almeida J.P., Babbage A.K., Ragguley C., Bailey J., Baridgeman A.M., Buck D., Burgess J., Baridgeman A.M., Buck D., Burgess J., Baridgen V.E., Carler N.P., Chen Y., Clark G., Colley V.E., Corby W.R., Corville G.J., Cox A.V., Davis J., Dawson E., Achan P.D., Dockree C., Dodsworth S.J., Durbin R.M., Ellington A.G., Rans K.L., Fey J.M., Fleming K., French L., Garner A.A., Brans K.L., Fey J.M., Fleming K., French L., Garner A.A., Gilbert J.G.R., Goward M.E., Grafham D.V., Griffiths M.N.D., Hall C., All R., Johnes M.C., Leversha M.A., Lloyd C., Lloyd D.M., All R., Langford C.F., Leversha M.A., Lloyd C., Lloyd D.M., Martyn I.D., Mashreghi-Mohammadi M., Matthews L.H., Mccann O.T., McClay J., McJaren S., McMurray A.A., Milne S.A., Mortimore B.J., Odell C.N., Pavitt R., Pearce A.V., Pearson D., Phillimore B.J., Odell C.N., Pavitt R., Ramsay H., Ramsey Y., Rogers L., Ross M.T., Soct C.E., Sehra H.K., Skuce C.D., Smalley S., Smith M.L., Soderlund C., Spragon L., Steward C.A., Sulston J.E., Swann R.M.,
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Q96MGB; Q9BYO; Q9UGBS; Q9UGUI;
CP6FEB-2003 (Rel. 41, Created update)
28-FEB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
15-SEP-2003 (Rel. 42, Last annotation update)
and the nose) (Dickkopf receptor).
KREMENIO R KREMEN.
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Tashiro H., Yamazaki M., Watanabe K., Kumagai A., Itakura S.,

Tashiro H., Yamazaki M., Watanabe K., Sugiyama T., Itie R.,

Otsuki T., Sato H., Wakamater A., Ishii S., Yamamoto J., Isono Y.,

Rawai Hio Y., Saito K., Nishikwa T., Kimura K., Yamashita H.,

Murakawa K., Nakamura Y., Sekine M., Kikuchi H., Kanda K., Waqatsuma M.,

Rawakami B., Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K.,

Isogai T.,

Isogai T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 CYEGNGHFYRGXASTDIMGRPCLPWNSATVLOQTYHAHRSDAL---QLGLGKHNYCRNPD
                                                                                                                                                                                                                                                                                                                                             Score 157, DB 1; Length 4548; Pred. No. 3.7e-09; 9; Mismatches 36; Indels 32; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----ADGKKPSSPPEE 96
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
W.-> R (LOSS OF LYSINE-SEPHAROSE BINDING).
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Nakamura T., Nakamura T.;
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                        /FTId=VAR 006633.
501313 MW; 96921BE96A465C5F CRC64;
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Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
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Navidin W., Williams On M., Williams On M., Williams On M., Williams On M., Williams On M., Williams On M., Williams On M., Williams On M., Williams On M., Williams On M., Williams On M., Williams On M., Williams On M., Williams On M., Williams On M., Williams On M., Williams On M., Williams On M., Williams On M., Williams On M., Williams On M., Williams On M., Williams On M., Williams On M., Williams On M., Williams On M., Williams On M., Williams On M., Williams On M., Williams On M., Williams On M., Williams On M., Williams On M., Williams On M., Williams On M., Williams On M., Williams On M., Williams On M., Williams On M., Williams On M., Williams On M., Williams On M., Williams On M., Williams On M., Williams On M., Williams On M., Williams On M., Williams On M., Williams On M., Williams On M., Williams On M., Williams On M., Williams On M., Williams On M., Williams On M., Williams On M., Williams On M., Williams On M., Williams On M., Williams On M., Williams On M., Williams On M., Williams On M., Williams On M., Williams On M., Williams On M., Williams On M., Williams On M., Williams On M., Williams On M., Williams On M., Williams On M., Williams On M., Williams On M., Williams On M., Williams On M., Williams On M., Williams On M., Williams On M., Williams On M., Williams On M., Williams On M., Williams On M., Williams On M., Williams On M., Williams On M., Williams On M., Williams On M., Williams On M., Williams On M., Williams On M., Williams On M., Williams On M., Williams On M., Williams On M., Williams On M., Williams On M., Williams On M., Williams On M., Williams On M., Williams On M., Williams On M., Williams On M., Williams On M., Williams On M., Williams On M., Williams On M., Williams On M., Williams On M., Williams On M., Williams On M., Williams On M., Williams On M., Williams On M., Williams On M., Williams On M., Williams On M., Williams On M., Williams On M., Williams On M., Williams On M., Williams On M., Williams On M., Williams On M., Williams On M., Williams On M., Williams On M., Wi
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3 CYEGNGHFYRGKASTDIM--GRPCLPWNSAIVLQQIYHAHRSDALQLGLGKHNYCRNPDN 60
                                                                                                                                                                                                                        MEDIINE-1942/182; PubMed=8186251; Shibuya Y., Semba U., Okabe H., Kambara T., Yamamoto T.; Shibuya Y., Semba U., Okabe H., Kambara T., Yamamoto T.; Perimary Structure of bovine Hageman factor (blood coagulation factor XII): comparison with human and guinea pig molecules."; Biophys. Acta 1206:63-70(1994).
                                                                                                VSD -- AIQDSEVTSLIWSQGQPRSI (in isoform
                                                                                                                                                                                                                                                                                                                                                                                                   Bos taurus (Bovine).
Sukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Boyidae; Boyinae; Bos.
                                     (POTENTIAL)...) (POTENTIAL)...) (POTENTIAL)...) (POTENTIAL)...) (POTENTIAL)...) (POTENTIAL)...)
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01-FEB-1996 (Rel. 33, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Coagulation factor XII precursor (EC 3.4.21.38) (Hageman factor)
                                                                                       (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 10-21; 350-364 AND 525-550.
MEDLINE=77182112; Pubmed=861210;
PUjkawa K., Walsh A., Davie W.E.;
"Isolation and characterization of bovine factor XII (Hageman Isolation and characterization of bovine factor XII
                                                                                                                                                                  Score 156; DB 1; Length 475;
Pred. No. 4.4e-10;
8; Mismatches 26; Indels
                                                                                                                            MISSING (IN REF. 1).
I -> V (IN REF. 2).
B7E86FD80F96A0A4 CRC64;
CYTOPLASMIC (POTENTIAL)
                                                                  (GLCNAC.
(GLCNAC.
                                                                                                                     /FTId=VSP 003900.
                                                          (GLCNAC
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                                       N-LINKED
                                                          N-LINKED
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                                                N-LINKED
                                                                    N-LINKED
          KRINGLE
                                                                                                                             29 30 Mi
206 206 I
475 AA; 51898 MW;
                                                                                                                                                                  28.2%;
                                                                                                                                                                              Best Local Similarity 44.1
Matches 30; Conservative
                                                                                                                                                                                                                                                                                                                       STANDARD;
61 RRRPWCYV 68
                                                                                                                                                                                                                                                                     92 DVSPWCYV 99
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 TISSUE=Liver;
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AC P98140;
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2 TCYE--GNGHFYRGKASTDTMGRPCLPWNSATVLQQTY-HAHRSDALQLGLGKHNYCRNP 58
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MEDLINE-85023111; PubMed-6148961;
Malinowski D.P., Sadler J.E., Davie E.W.;
"Characterization of a complementary deoxyribonucleic acid coding for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CARBOHYDRATE-LINKAGE SITES.
MEDLINE=88185329; PubMed=3356193;
MEDLINE=88185329; PubMed=3356193;
Marti T., Schaller J., Rickli E.E., Schmid K., Kamerling J.P.,
Gerwig G.J., van Halbeek H., Vliegenthart J.F.;
"The N- and O-linked carbohydrate chains of human, bovine and porcine
plasminogen. Species specificity in relation to sialylation and
fucosylation patterns";
Eur. J. Blochem. 1773:57-63(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 27-812, AND CARBOHYDRATE-LINKAGE SITES.
MEDLINE=82203906; PubMed=3846522;
Schaller J., Moser P.W., Dannegger-Muller G.A.K., Rosselet S.J.,
Rampfer U., Rickli B.E.,
"Complete amino acid sequence of bovine plasminogen. Comparison with
BY SIMILARITY.
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C-LINKED (CDCO) (BY SIMILARITY).
N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Liver;
Berglund L., Andersen M.D., Petersen T.E.;
"Cloning and characterization of the bovine plasminogen cDNA.";
Int. Dairy J. 5:593-603(1995).
                                                                                                                                                                                                       28.1%; Score 155.5; DB 1; Length 593; 38.4%; Pred. No. 6.3e-10;
                                                                                                                                                                                                                                9; Mismatches 37; Indels
                                                                                                                                                                                                                                                                                                                                                                                             PLMN BOVIN STANDARD; PRT; 812 AA. P06868; Q28162; 01-JAN-1988 (Rel. 06, Created) 01-NOV-1997 (Rel. 35, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update) Plasminogen precursor (EC 3.4.21.7).
                                                                                                                                                                                                                                                                                                         59 DNRRRPWCYVQVGLKPLVQECMVHDC 84
                                                                                                                                                                                                                                                                                                                         DNDTRPWCFIWKGDRLSWNYCRLAPC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    human plasminogen.";
Eur. J. Biochem. 149:267-278(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           human and bovine plasminogen.";
Biochemistry 23:4243-4250(1984).
                                                                                                                                                                                65148 MW;
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hes 33; Conservative
   SEQUENCE FROM N.A.
TISSUE=Liver;
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   8
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PROSITE: PS01025; EGF 1; FALSE NEG.
PROSITE: PS01025; FGF 2; FALSE NEG.
PROSITE: PS01025; FIBRONECTIN I; 1.
PROSITE: PS00023; FIBRONECTIN I; 1.
PROSITE: PS00021; FIBRONECTIN 2; 1.
PROSITE: PS00070; KRINGLE 1; 1.
PROSITE: PS00170; KRINGLE 1; 1.
PROSITE: PS00170; KRINGLE 2; 1.
PROSITE: PS00170; FRYPSIN DOM; 1.
PROSITE: PS00135; TRYPSIN HIS; 1.
Glycoprotain; Blood coagulation; Plasma; Kringle; Serine protease; Hydrolase; Fibrinolysis; EGF-like domain; Repeat; Zymogen; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY).
SIMILARITY).
SIMILARITY).
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ALPHA-FACTOR XIIA HEAVY CHAIN.
ALPHA-FACTOR XIIA LIGHT CHAIN.
FIBRONECTIN TYPE-II.
 -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY SI.
-!- SIMILARITY: Contains 2 EGF-like domains.
-!- SIMILARITY: Contains 1 fibronectin type I domain.
-!- SIMILARITY: Contains 1 fibronectin type II domain.
-!- SIMILARITY: Contains 1 kringle domain.
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FIBRONECTIN TYPE-I.
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KRINGLE.
PRO-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EGF-LIKE
                                                                                                                                                                                                                                                                                                                                                                                                                                            SMART; SM00181; EGF; 2.
SMART; SM00058; FN1; 1.
SMART; SM00059; FN2; 1.
SMART; SM00130; KR; 1.
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This SWISS-FROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                             -!- ENZYME REGULATION: CONVERTED INTO PLASMIN BY PLASMINOGEN
ACTIVATORS, BOTH PLASMINOGEN AND ITS ACTIVATOR BEING BOUND TO
FIBERIN. CANNOT BE ACTIVATED WITH STREPTOXINASE.
-!- PTM: N-LINKED GLYCANS CONSITO FO FAL-GALRAC DISACCHARIDE MITH IS
O-LINKED GLYCANS CONSIST OF FAL-GALRAC DISACCHARIDE MITH IS
MODIFIED WITH UP TO 2 SITALIC ACID RESIDUES (MCROHETEROGENEITY)
INMEDIATELA AFTER DISSOCIATION FROM THE CLOT.
-!- SIMILARITY: BELONGS TO PEPTIDASE PAMILY SI. PLASMINOGEN SUBFAMILY
-!- SIMILARITY: CORTAINS 5 KRINGLE GOMENIES
FUNCTION: PLASMIN DISSOLVES THE FIBRIN OF BLOOD CLOTS AND ACTS AS AS PROFEDCIVITE FACTOR IN A VARIETY OF OTHER PROCESSES INCLUDING EMBRYONIC DEVELOPMENT. TISSUE EMMODELING, TUMOR INVASION, AND INFLAMMATION; IN OVULATION IT WEAKENS THE WALLS OF THE GRAAFIAN FOLLICLE. IT ACTIVATES THE URCKINASE-TYPE PLASMINGGEN ACTIVATOR, COLLAGENASE SAND SEVERAL COMPLEMENT ZYMOGENS, SUCH AS CI AND CS. IT CLEAVES FIBRIN, FIBRONECTIN, THROMBOSPONDIN, CALAMININ AND VON WILLEBRAND FACTOR.

CATALYTIC ACTIVITY: PREFERENTIAL CHARGES AND SACHALYDIN, FIBRONECTIN, THROMBOSPONDIN, CATALYTIC ACTIVITY: PREFERENTIAL CHARGES AND SACHALYDIN, FIBRONECTIN, THROMBOSPONDIN, CATALYTIC ACTIVITY: PAREFERENTIAL CHARGES AND SACHALYDIN, FIBRONECTIN, THROMBOSPONDIN, CATALYTIC ACTIVITY: PAREFERENTIAL CONVETES FIBRIN INTO SOUNDIE.
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RESP, POOT47; 2PK4.

RESP, POOT47; 2PK4.

RESP, POOT47; 2PK4.

RESP, POOT47; 2PK4.

RESP, POOT3314; Chymotrypsin.

RICEPPO; IPRO01314; Chymotrypsin.

RICEPPO; IPRO013069; Pan_app.

RICEPPO; IPRO01266; Prothrombin.

RICEPPO; IPRO01266; Prothrombin.

RICEPPO; IPRO01254; Ser_protease_Try.

RESP, PFOONS9; trypsin; 1.

RESP, PRO0122; CHYMOTRYPSIN.

RESPONS1; KRINGLE.

RESPONS1; KRINGLE.

RESPONS1; KRINGLE.

RESPONS1; RESPONS1; KRINGLE.

RESPONS1TE; PSO0136; KRINGLE.

RESPONS1TE; PSO0136; TRYPSIN_DOM; 1.

RESPONS1TE; PSO0136; TRYPSIN_DOM; 1.

RESPONS1TE; PSO0136; TRYPSIN_DOM; 1.

RESPONSITE; PSO0136; TRYPSIN_ESS.

RESPONSITE; PSO0136; TRYPSIN_SER; 1.

RESPONSITE; PSO0136; TRYPSIN_SER; 1.

RESPONSITE; PSO0136; TRYPSIN_SER; 1.

RESPONSITE; PSO0136; TRYPSIN_SER; 1.

RESP, PROSITE; PSO0136; TRYPSIN_SER; 1.

RESP, PROSITE; PSO0136; TRYPSIN_SER; 1.

RESP, PROSITE; PSO0136; TRYPSIN_SER; 1.

RESP, PROSITE; PSO0136; TRYPSIN_SER; 1.

RESP, PROSITE; PSO0136; TRYPSIN_SER; 1.

RESP, PROSITE; PSO0136; TRYPSIN_SER; 1.

RESP, PROSITE; PSO0136; TRYPSIN_SER; 1.

RESP, PROSITE; PSO0136; TRYPSIN_SER; 1.

RESP, PROSITE; PSO0136; TRYPSIN_SER; 1.

RESP, PROSITE; PSO0136; TRYPSIN_SER; 1.

RESP, PROSITE; PSO0136; TRYPSIN_SER; 1.

RESP, PROSITE; PSO0136; TRYPSIN_SER; 1.

RESP, PROSITE; PSO0136; TRYPSIN_SER; 1.

RESP, PROSITE; PSO0136; TRYPSIN_SER; 1.

RESP, PROSITE; PSO0136; TRYPSIN_SER; 1.

RESP, PROSITE; PSO0136; TRYPSIN_SER; 1.

RESP, PROSITE; PSO0136; TRYPSIN_SER; 1.

RESP, PROSITE; PSO0136; TRYPSIN_SER; 1.

RESP, PROSITE; PSO0136; TRYPSIN_SER; 1.

RESP, PROSITE; PSO0136; TRYPSIN_SER; 1.

RESP, PROSITE; PSO0136; TRYPSIN_SER; 1.

RESP, PROSITE; PSO0136; TRYPSIN_SER; 1.

RESP, PROSITE; PSO0136; TRYPSIN_SER; 1.

RESP, PROSITE; PSO0136; TRYPSIN_SER; 1.

RESPRESEDENTE; PSO0136; TRYPSIN_SER; 1.

RESP, PROSITE; PSO0136; TRYPSIN_SER; 1.

RESP, PROSITE; PSO0136; TRYPSIN_SER; 1.

RESP, PROSITE; PSO0136; TRYPSIN_SER; 1.

RESP, PROSITE; PSO0136; TRYPSIN_SER; 1.

RESP, PROSITE; PSO0136; TRYPSIN_SER; 1.

RESP, PROSITE; 
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LIGHT CHAIN
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N-LINKED (GLCNAC.../FTIG=CAR 000014.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PLASMINOGEN
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KRINGLE 4.
KRINGLE 5.
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EMBL; K02935; AAA30714.1; -.
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                 384 CYHGNGQSYRGTSSTTITGRKCQSWSS-----MTPHRHLKTPENYPNAGL-TMNYCRNPD 437
                                                                                                                                                                                       3 CYEGNGHFYRGKASTDTMGRPCLPWNSATVLQQTYHAH---RSDALQLGLGKHNYCRNPD 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                products.
-!-ENZYME REGULATION: CONVERTED INTO PLASMIN BY PLASMINOGEN
ACTIVATORS, BOTH PLASMINOGEN AND ITS ACTIVATOR BEING BOUND TO
FIBRIN. CANNOT BE ACTIVATED WITH STREPTOKINASE.
-!-INTECELLANBOUS: PLASMIN IS INACTIVATED BY ALPHA-2-ANTIPLASMIN
-!-SIMILARITY: BELONGS TO PEPTIDASE PAMILY SI. PLASMINOGEN SUBFAMILY.
-!- SIMILARITY: CONTAINS 5 kringle domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                   Rattus norvegicus (Rat).
Eukaryota, Metazoa; Chordata, Craniata, Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kanalas J.J., Makker S.P.;
"Identification of the rat Heymann nephritis autoantigen (GP330) as
                                                                                                                                                               16;
                                                                                                                                    Length 812;
                                                                                                                                                             34; Indels
          CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
N -> D (IN REF. 2).
Q -> H (IN REF. 2).
T -> K (IN REF. 3).
T -> K (IN REF. 3).
W, 38A6AA691E220946 CRC64;
                                                                                                                                                                                                                                                            60 NRRRPWCYVQVGLKPLV--QECMVHDCADGKK--PSSP 93
                                                                                                                                  , DB 1;
2.2e-09;
 FTIG=CAR 000015
                                                                                                                                                                                                                                                                                                                                                               01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Plasminogen (EC 3.4.21.7) (Fragment).
                                                                                                                                               1 Similarity 37.8%; Fred. No. 2.2e-(37; Conservative 11; Mismatches
                                                                                                                                                                                                                                                                                                                                        PRT; 169 AA
                                                                                                                                  27.4%; Score 152; 37.8%; Pred. No. 2
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MEDLINE=91250378; PubMed=1645711;
                                                                                                        91216 MW;
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72 AA;
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3 CYEGNGHFYRGKASTDTMGRPCLPWNSATVLQQTYHAHRSDALQL---GLGKHNYCRNPD 59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              synthesis.";
J. Biol. Chem. 264:5957-5965(1989).
J. Biol. Chem. 264:5957-5965(1989).
J. Biol. Chem. 264:5957-5965(1989).
J. PUNCTION: PLASMIN DISSOLVES THE FIBRIN OF BLOOD CLOTS AND ACTS AS A PROTECLYTIC FACTOR IN A VARIETY OF OTHER PROCESSES INCLUDING EMBRYONIC DEVELOPMENT, TISSUE REMODELING, TUMOR INVASION, AND INFLAMMATION, IN OVULATION IT WEAKENS THE WALLS OF THE GRAAFIAN FOLLICLE. IT ACTIVATES THE UROKINASE TYPE PLASMINGEN ACTIVATOR, COLLAGENASES AND SEVERAL COMPLEMENT ZYMOGENS, SUCH AS C1 AND C5. IT CLEAVES FIBRIN, FIBRONECTIN, THROMBOSPONDIN, LAMININ AND VON WILLEBRAND FACTOR.
-!- CATALYTIC ACTIVITY: PREFETENDIAL CHARACTER LIBERIAL ACTIVITY: PREFETENDIAL CONVERTS fibrin into soluble
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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SEQUENCE FROM N.A.
MEDLINE=89174660; PubMed=2925643;
MEDLINE=0 J.E., McLean J.W., Lawn R.M.;
"Rhesus monkey apolipoprotein(a). Sequence, evolution, and sites of
           RECORDS, SOL.23.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae,
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                                                                                                                                                                                                                                                                                                                                                                                                                     27.1%; Score 150; DB 1; Length 169; 34.3%; Pred. No. 7e-10;
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KRINGLE 4 (BY SIMILARITY).
KRINGLE 5 (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                           18401 MW; 77A54214C49D010C CRC64;
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01-0CT-1989 (Rel. 12, Last sequence update)
01-0CT-1989 (Rel. 12, Last annotation update)
Plasminogen precursor (EC 3.4.21.7).
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NCBL_TaxID=9544;
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C. HIGGELANDOS: PLASTIC STATUTE ACCOUNT OF STEAD COLD. TO HIGGELANDOS: PLASTIC STATUTOR BRING BADDE ACCOUNT TO HIGGELANDOS: PLASTIC STATUTOR FOR THE CACTULATION. HIGGELANDOS: PLASTIC STATUTOR FOR THE CACTULATION. HIGGELANDOS: PLASTIC STATUTOR FOR THE CACTULATION. HIGGELANDOS: IN THE STEAD COLD. TO HIGGELANDOS: IN THE STEAD COLD. THE INHIBITION. HIGGELANDOS: IN THE STEAD COLD. THE STATUTOR. HIGGELANDOS: IN THE STEAD COLD. THE STATUTOR. HIGGELANDOS: IN THE STATUTOR. HIGGELANDOS: IN THE STATUTOR. HIGGELANDOS: IN THE STATUTOR. HIGGELANDOS: IN THE STATUTOR. HIGGELANDOS: IN THE STATUTOR. HIGGELANDOS: IN THE STATUTOR. HIGGELANDOS: IN THE STATUTOR. HIGGELANDOS: IN THE STATUTOR. HIGGELANDOS: IN THE STATUTOR. HIGGELANDOS: IN THE STATUTOR. HIGGELANDOS: IN THE STATUTOR. HIGGELANDOS: IN THE STATUTOR. HIGGELANDOS: IN THE STATUTOR. HIGGELANDOS: IN THE STATUTOR. HIGGELANDOS: IN THE STATUTOR. HIGGELANDOS: IN THE STATUTOR. HIGGELANDOS: IN THE STATUTOR. HIGGELANDOS: IN THE STATUTOR. HIGGELANDOS: IN THE STATUTOR. HIGGELANDOS: IN THE STATUTOR. HIGGELANDOS: IN THE STATUTOR. HIGGELANDOS: IN THE STATUTOR. HIGGELANDOS: IN THE STATUTOR. HIGGELANDOS: IN THE STATUTOR. HIGGELANDOS: IN THE STATUTOR. HIGGELANDOS: IN THE STATUTOR. HIGGELANDOS: IN THE STATUTOR. HIGGELANDOS: IN THE STATUTOR. HIGGELANDOS: IN THE STATUTOR. HIGGELANDOS: IN THE STATUTOR. HIGGELANDOS: IN THE STATUTOR. HIGGELANDOS: IN THE STATUTOR. HIGGELANDOS: IN THE STATUTOR. HIGGELANDOS: IN THE STATUTOR. HIGGELANDOS: IN THE STATUTOR. HIGGELANDOS: IN THE STATUTOR. HIGGELANDOS: IN THE STATUTOR. HIGGELANDOS: INTERCTOR. HIGGELANDOS: INTERCTOR. HIGGELANDOS: INTERCTOR. HIGGELANDOS: INTERCTOR. HIGGELANDOS: INTERCTOR. HIGGELANDOS: INTERCTOR. HIGGELANDOS: INTERCTOR. HIGGELANDOS: INTERCTOR. HIGGELANDOS: INTERCTOR. HIGGELANDOS: INTERCTOR. HIGGELANDOS: INTERCTOR. HIGGELANDOS: INTERCTOR. HIGGELANDOS: INTERCTOR. HIGGELANDOS: INTERCTOR. HIGGELANDOS: INTERCTOR. HIGGELANDOS: INTERCTOR. HIGGELANDOS: INTERCTOR. HIGGELANDOS: INTERCTOR. HIGGELANDOS: INTERCTOR. HIGGELANDOS: INTERCTOR. HIGGELANDOS: INTE
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KRM2 HUMAN STANDARD; PRT; 462 AA.

AC QBNCW0; QBN2J4; QBNCW1; Q96GLB; Q9BTP9;

DT 15-SEP-2003 (Rel. 42, Created)

DT 15-SEP-2003 (Rel. 42, Last annotation update)

DT 15-SEP-2003 (Rel. 42, Last annotation update)

DF Kremen protein 2 precursor (Kringle-containing protein marking the eye and the nose) (DICKkopf receptor 2).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE-Ovarian carcinoma;
Isogai T., Ota T., Nishikawa T., Hayashi K., Otsuki T., Sugiyama T., Suzuki Y., Ota T., Nishikawa T., Farato K., Suzuki Y., Nagai K., Sugano S., Ishii S., Kawai-Hio Y., Saito K., Yamamoto J., Wakamatsu A., Nakamura Y., Kojima S., Nagahari K., Masuho Y., Ono T., Okano K., Yoshikawa Y., Aotsuka S., Sasaki N., Hattori A., Okumura K., Iwayanagi T., Ninomiya K.;
"NEDO human cDNA sequencing project.";
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
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ISSUGBARAIN, and Uterus;
MEDLINE=22380557; Pubmed=12477932;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Atlausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetcow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                               .) (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Merazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; DB 1; Length 810; 4.7e-09;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Human Kremen2 and Wnt signaling.";
Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A75E1C51A1A0F24A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       431 ADKGPWCFT---TDPSVRWEYCNLKKCSGTEGSVAAPPP 466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         60 NRRRPWCYVQVGLKPLV--QECMVHDCA--DGKKPSSPP 94
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COLLINKED (GALN)
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                                                                                        SIMILARITY.
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90255 MW;
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Best Local Similarity 36.4%
Matches 36; Conservative
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Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheerz T.E.,
A Brownstein M.J., Ugdin T.B., Toshiyuki S., Carninci P., Prange C.,
A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A Willalon D.K., Muzny D.W., Sodergren E.J., Lu X., Gibbs R.A.,
Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Whiting M., Madan A., Youchman J.W., Green E.D., Dickson M.C.,
A Rodriguez A.C., Grimwood J., Schwutz J., Myers R.M.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
A Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                       and mouse CDNA sequences."

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

-!- FUNCTION: Receptor for Dickkopf protein. Cooperates with Dickkopf protein. Cooperates with Dickkopf brotein. Cooperates with Dick wat/beta-catenin signaling. Forms a ternary complex with Dkkl and LRP6 and induces rapid endocytosis and removal of the Wnt receptor LRP6 from the plasma membrane (By similarity).

-!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS01180; CUB; 1.
PROSITE; PS000021; KRINGLE 1: 1.
PROSITE; PS50070; KRINGLE 2: 1.
Wht signaling pathway; Glycoprotein; Kringle; Signal; Transmembrane; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL.
KREMEN PROTEIN 2.
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Name=3; Synonyms=Kremen2b;
IsoId=Q8NCW0-3; Sequence=VSP_050511, VSP_050512;
Name=4; Synonyms=Kremen2c;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Isoid=08NCW0-4; Sequence=VSP_050513, VSP_050514; SIMILARITY: Contains I CUB domain. SIMILARITY: Contains 1 kringle domain. SIMILARITY: Contains 1 WSC domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Name=2; Synonyms=Kremen2a;
IsoId=Q8NCW0-2; Sequence=VSP_050509, VSP_050510;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Event=Alternative splicing, Named isoforms=4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IsoId=Q8NCW0-1; Sequence=Displayed;
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EMBL, AB086355, BAC00823.1; --
EMBL, AB086355, BAC00824.1; --
EMBL, AB086357, BAC00825.1; --
EMBL, AK077669, BAB55281.1; --
EMBL, BC003333, AAH03533.1; --
EMBL, BC003333, AAH03533.1; --
EMBL, BC009383, AAH0383.1; --
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InterPro; IPR000001; Kringle.
InterPro; IPR002889; WSC.
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Pfam; PF00051; kringle; 1.
Pfam; PF01822; WSC; 1.
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ProDom; PD000395; Kringle;
SMART; SM00042; CUB; 1.
SWART; SM00130; KR; 1.
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(POTENTIAL).		·	·	·	(GLCNAC) (POTENTIAL).	SCLLAPGKGPPALGASRGPRRSWAVWYQQPR -> CGALGQ	GLRADRWWGAGAPEGNRARKELLGS (in isoform		150509.	isoform 2).	150510.	ARVFSTVTAVSVLLLLLGLLRPLRRRSCLLAPGKGPPALG	ASRGPRRSWAVWY -> GAVCWLREKGPRRWGLPGAPGEAG	LCGINSPEGWPCPAPPGTPRLRVLPRATGL (in		50511.	i isoform 3).	150512,	ARVFSTVTAVSVLLLLLLGLLRPLRRRSCLLAP -> GEAG			5,0513			Migning (in pot 3, paginore)	I NOT . Z. DACTIOOD .	A -> D (in Ref. 2; BAC11365).	7A9AA68 CRC64;	.; DB 1; Length 462;		les 26; Indels 5; Gaps 2;	CYEGNGHFYRGKASTDIMGRPCLPWNSATVLQQIYHAHRSDALQLGLGKHNYCRNPD 59	CFQVNGADYRGHQNRTGPRGAGRPCLFWDQTQQHSYSSASDPHGRWGLGAHNFCRNPD 93
CYTOPLASMIC KRINGLE.	cub.	_	_		N-LINKED (G	SCLLAPGKGPP	GLRADRWWGAG	2).	/FTId=VSP 050509.	Missing (in isoform	/FTId=VSP 050510.	ARVFSTVTAVS	ASRGPRRSWAV	LCGTNSPEGWP	isoform 3).	/FTId=VSP 0	Missing (in isoform	/FTId=VSP 050512	ARVFSTVTAVS	ARDGSESGSRP	4).	/FTIA=VSD 050513	Mind of the Annual Control	FITSTANG (IN IBOLO)	di barasin	HT SHTEETH	A -> D (1D	; CE3301591	Score 148.5;	Dred No 30-00.	9; Mismatches	IMGRECLEWNSA	SAGRPCLFWDQT
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Search completed: December 3, 2003, 14:40:10 Job time : 3.08464 secs

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Q9xt70 oryctolagus
Q8mkb1 oryctolagus
Q9u99 homo sapien
Q91vp2 mus musculu
Q8ng20 homo sapien
Q8sq23 sus scrofa
Q8sq23 mus musculu
Q14520 homo sapien
Q9c04 mus musculu
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Dichek D.A.;

"Increased expression of urokinase during atherosclerotic lesion growth.";

"Increased expression of urokinase during atherosclerotic lesion growth.";

"Increased expression of urokinase during atherosclerotic lesion growth.";

Proc. Natl. Acad. Sci. U.S.A. 99.10665-10670(2002).

"Increpro: IRRONGSTO PERTIDASE FAMILY S1.

"InterPro: IRRONGSTO PERTIDASE FAMILY S1.

"InterPro: IRRONGSTO FEG LIKe.

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                                                                                                                            Gaps
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Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
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                                                                     Score 495; DB 4; Length 154;
Pred. No. 2.4e-51;
0; Mismatches 1; Indels
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Glycoprotein, Kinase, Kringle.
SEQUENCE 154 AA: 17305 MW; A3CCF2FCFF505572 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-07T-2002 (TrEMBLrel. 22, Created)
01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   433 AA
                                                                                                                                                                                                                                                                                                              128 RRRPWCYVQVGLKLLVQECMVHDCADG 154
                                                                                                                                                                                                                                                                         61 RRRPWCYVQVGLKPLVQECMVHDCADG 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Urokinase-type plasminogen activator
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Oryctolagus cuniculus (Rabbit).
                                                                       Query Match . 89.4%;
Best Local Similarity 98.9%;
Matches 86; Conservative
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PRINTS; PR000139; KRINGLE.
PRINTS; PR000139; KRINGLE.
SMART; SM001030; KR, 1.
SMART; SM001002; TYPP, SPC; 1.
PROSITE; PS00022; EGF 1.; 1.
PROSITE; PS00002; TRYPSIN DA; 1.
PROSITE; PS00134; TRYPSIN DA; 1.
PROSITE; PS00134; TRYPSIN DA; 1.
PROSITE; PS00134; TRYPSIN DA; 1.
PROSITE; PS00135; TRYPSIN DA; 1.
PROSITE; PS00135; TRYPSIN SER; 1.
PROSITE; PS00135; TRYPSIN SER; 1.
PROSITE; PS00135; TRYPSIN SER; 1.
PROSITE; PS00135; TRYPSIN SER; 1.
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0.1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
0.1-MAY-2003 (TrEMBLrel. 23, Last annotation update)
0.1-MAR-2003 (TrEMBLrel. 23, Last annotation update)
0.1-MAR-2003 (TremBlrel. 23, Last annotation update)
0.2 Urokinase plasminogen activator (Fragment).
0.2 Laurus (Bovine).
0.2 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
0.3 Mammalia; Eutheria; Cetariodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Lagomorpha, Leporidae, Oryctolagus.
NCBI_TaxID=9986;
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Sugiki M., Yoshida E., Anai K., Maruyama M.;
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
                                                                           Last sequence update)
Last annotation update)
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433
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InterPro; IPR006209; EGF like.
InterPro; IPR000001; Kringle.
InterPro; IPR001254; Ser protease_Try.
Pfam; PF00051; Kringle; 1.
Pfam; PF00089; trypsin; 1.
                                                                  01-OCT-2002 (TrEMBLrel. 22, Last seq
01-WAR-2003 (TrEMBLrel. 23, Last ann
Urokinase-type plasminogen activator
                                                 -OCT-2002 (TrEMBLrel. 22, Created)
                                                                                                                                                                                      Oryctolagus cuniculus (Rabbit)
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us-09-880-503-9.rspt

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129 QKRPWCYVQIGLRQFVQECMVHDCSLSKKPSSSVDQ 164
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
TISSUE=Lung;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEROPS; S01.231;
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Q9XT70
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STRAIN-C57BL/6J; TISSUB=Ovary;
MEDLINE223346683; PubMed=12466851;
The FANTOM Consortium Research Group Phase I & II Team;
the RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation of 60,70 full-length CDNAs.";
Nature 420:563-573(2002).
EMBL; AK054349; BAC35743.1; -...
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
1-MAR-2003 (TrEMBLrel. 23, Last annotation update)
1-MAR-2003 (TrEMBLrel. 23, Last annotation update)
1-MAS musculus (Mouse).

Eukaryota, Metazoa; Chordata, Craniata, Vertebrata; Euteleostomi;
Mammalia; Eutheria, Rodentia; Sciurognathi; Muridae; Musinae;
MUCB_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              76.2%; Score 422; DB 6; Length 157; 75.0%; Pred. No. 1.3e-42; ative 9; Mismatches 15; Indels
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                                                                                                        TISSUE=Skeletal muscle;
MEDLINE=21071388; PubMed=11204721;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Glycoptctein; Kinase; Kringle.
NON TER 157 157
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Best Local Similarity 75.0%
To 72; Conservative
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                                                                           SEQUENCE FROM N.A.
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MINCEPS JOLISTIA SURROUTIAN CHYMOLITYPEIN.

RINGEPPO IPRO001314; Chymolitypein.

RINGEPPO IPRO00124; Sir protease_Try.

R Pfam; PR00051; kringle; 1.

R Pfam; PR00052; CHYMOTRYESIN.

R RNINTS; PR00022; CHYMOTRYESIN.

R PROMO130; KR; III.

R RAART; SM00130; KR; III.

R RAART; SM00130; KR; III.

R ROSITE; PS00121; KRINGLE 1; I.

R ROSITE; PS00120; KRINGLE 2; I.

R ROSITE; PS00134; TRYPSIN DOM; 1.

R ROSITE; PS0134; TRYPSIN HIS; 1.

R Glycoprotein; Hydrolase; Kinase; Kringle; Protease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20 MGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVGLKPLVQEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                              01-NOV-1999 (TrEMBLrel. 12, Created)
1-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NAP-2003 (TrEMBLrel. 12, Last annotation update)
Urokinase-type plasminogen activator (Fragment).
Urokinase-type plasminogen activator (Fragment).
Urokinase-type plasminogen activator (Fragment).
Urokinase-type plasminoulus (Rabbit).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tissue-type plasminogen activator.

Tissue-type plasminogen activator.

Suyctcolagus cuniculus (Rabbit).

Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;

Mammalia, Eutheria, Lagomorpha, Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 337.5; DB 6; Length :
Pred. No. 2.4e-32;
6. Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
Sugiki M., Yoshida E., Anai K., Maruyama M.;
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    214 AA; 24314 MW; 69975C41C32B0D7E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-077-2002 (TrEMBLrel. 22, Created)
01-077-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                    214 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            60.9%;
78.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     80 MVHDCADGKKPSSPP 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 KVHD-SSGKKPALPP 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    59; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
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R PFAMY; PR00089; trypein; 1.

R PRINTS; PR00722; CHYMOTRYBSIN.

R PRINTS; PR0001395; KRINGLE.

R SMART; SM00181; EGF; 1.

R SMART; SM00181; EGF; 1.

R PROSITE; PS00022; EGF_1; 1.

R PROSITE; PS00002; EGF_1; 1.

R PROSITE; PS0001; KRINGLE 1; 2.

R PROSITE; PS0001; KRINGLE 2; 2.

R PROSITE; PS00134; TRYPSIN HDS; 1.

R PROSITE; PS00134; TRYPSIN HDS; 1.

R PROSITE; PS00135; TRYPSIN HS; 1.

R PROSITE; PS00135; TRYPSIN HS; 1.

R PROSITE; PS00135; TRYPSIN SER; 1.

R PROSITE; PS00135; TRYPSIN SER; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62 RRPWCYVQVGLKPLVQECMVHDCADG 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 47.7
hes 41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
TISSUE=Breast tumor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Serine protease.
SEQUENCE 516 A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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Q91VP2
                    g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 CYEGNGHFYRGKASTDIMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNRR 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09809;
01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Similar to plasminogen activator, tissue.
Similar to plasminogen activator, companies.
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Primates; Catarrhini, Hominidae, Homo.
C. -i - SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.

RELLA ANGOSOUS AAKA OZAOLI; -

INTERPRO, IPROGLOUS; -

RICERPO, IPROGLOUS; ESF LIKE.

RICERPO, IPROGLOUS; FIDENCEIL.

RICERPO, IPROGLOUS; FIDENCEIL.

RICERPO, IPROGLOUS; FIDENCEIL.

RICERPO, IPROGLOUS; FIDENCEIL.

RICERPO, IPROGLOUS; FIDENCEIL.

RICERPO, IPROGLOUS; FIDENCEIL.

RICERPO, IPROGLOUS; KINGLE.

REAM: PROGLOS; KINGLE.

REAM: PROGLOS; KINGLE.

REAM: PROGLOS; KINGLE.

REAM: SMART; SMOOLS; KINGLE.

REAM: SMART; SMOOLS; FNI; I.

REAM: SMART; SMOOLS; FNI; I.

REAM: SMART; SMOOLS; FNI; I.

REAM: PROSLIE; PSOOLS; FRINGLE.

REAM: PROSLIE; PSOOLS; KRINGLE.

REAM: PROSLIE; PSOOLS; KRINGLE.

REAM: PROSLIE; PSOOLS; KRINGLE.

REAM: REAM: MINGLE PSOOLS; KRINGLE.

REAM: REAM: MINGLE PSOOLS; KRINGLE.

REAM: REAM: MINGLE PSOOLS; KRINGLE.

REAM: REAM: REAM: MINGLE PSOOLS; KRINGLE.

REAM: REAM: REAM: REAM: MINGLE PSOOLS; KRINGLE.

REAM: REAM: REAM: REAM: MINGLE PSOOLS; KRINGLE.

REAM: REAM: REAM: REAM: MINGLE PSOOLS; KRINGLE.

REAM: REAM: REAM: REAM: MINGLE PSOOLS; KRINGLE.

REPOSLIE; PSOOLS; KRINGLE.

REPOSLIE; PSOOLS; KRINGLE.

REPOSLIE; PSOOLS; KRINGLE.

REPOSLIE; PSOOLS; KRINGLE.

REPOSLIE; PSOOLS; KRINGLE.

REPOSLIE; PSOOLS; KRINGLE.

REPOSLIE; PSOOLS; KRINGLE.

REPOSLIE; PSOOLS; KRINGLE.

REPOSLIE; PSOOLS; KRINGLE.

REPOSLIE; PSOOLS; KRINGLE.

REPOSLIE; PSOOLS; KRINGLE.

REPOSLIE; PSOOLS; KRINGLE.

REPOSLIE; PSOOLS; KRINGLE.

REPOSLIE; PSOOLS; KRINGLE.

REPOSLIE; PSOOLS; KRINGLE.

REPOSLIE; PSOOLS; KRINGLE.

REPOSLIE; PSOOLS; KRINGLE.

REPOSLIE; PSOOLS; KRINGLE.

REPOSLIE; PSOOLS; KRINGLE.

REPOSLIE; PSOOLS; KRINGLE.

REPOSLIE; PSOOLS; KRINGLE.

REPOSLIE; PSOOLS; KRINGLE.

REPOSLIE; PSOOLS; KRINGLE.

REPOSLIE; PSOOLS; KRINGLE.

REAM: REAM: REAM: REPOSLIE; REPOSLOUS; KRINGLE.

REAM: REAM: REAM: REAM: REPOSLUSS; KRINGLE.

REAM: REAM: REAM: REAM: REPOSLUSS; KRINGLE.

REAM: REAM: REAM: REAM: REAM: REAM: REAM: REAM: REAM: REAM: REAM: REAM: REAM: REAM: REAM: REAM: REAM: REAM: REAM: REAM: REAM: REAM: REAM: REAM: REAM: REAM: REAM: REAM: REAM: REAM: REAM: REAM: REAM: REA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    564 AA; 62726 MW; 459D8BAC6D4A937C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     277 KPWCHVLKNRKLVIEYCDVPQCATCGLRQDKQPQ 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         63 RPWCYVQVGLKPLVQECMVHDCAD-GKKPSSPPE 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Serine protease
SEQUENCE 564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  09BU99
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61
                                                                                                       2 TCYEGNGHFYRGKASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNR
                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse).
Wataryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A STRANSPERGER L. CHROLY

SUBMITTED UNITED TO THE EMBL/GENBANK/DDBJ databases.

SUBMITTED UNITED TO THE EMBL/GENBANK/DDBJ databases.

--- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.

--- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.

REBBL; BC011256; AAH11256.1; ---
REBL; BC011256; AAH11256.1; ---
REPLS; PR001314; Chymotrypsin.

RICEPPO; IPR001314; Chymotrypsin.

RICEPPO; IPR001314; Chymotrypsin.

RICEPPO; IPR000083; Fibrrochil.

RICEPPO; IPR000083; Fibrrochil.

RICEPPO; IPR000081; Kringle.

REPRINTS; PR000139; fin; 1.

REPRINTS; PR000139; KR1NGLE.

REPRINTS; PR00139; KR1NGLE.

REPRINTS; PR00130; KR1NGLE.

REPRINTS; PR00130; KR1NGLE.

REPRINTS; PR00130; KR1NGLE.

REPRINTS; PR00130; KR1NGLE.

REPRINTS; PR00130; KR1NGLE.

REPRINTS; PR00130; KR1NGLE.

REPRINTS; PR00130; KR1NGLE.

REPRINTS; PR00130; KR1NGLE.

REPRINTS; PR00130; KR1, 1.

REPROSITE; PS01186; EGF_1; 1.

REPROSITE; PS01186; EGF_1; 1.
                               40.8%; Score 226; DB 4; Length 516;
47.7%; Pred. No. 1.4e-18;
Live 9; Mismatches 36; Indels
516 AA; 57370 MW; BAB31901FDC96800 CRC64;
                                                                                                                                                                                                                                                                                                                    091VP2;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Similar to plasminogen activator, tissue.
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PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SMART; SM00058; FN1; 1
SMART; SM00130; KR; 1.
       sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
Matches 42; Conserva
                                                                                                                  SEQUENCE FROM N.A.
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       임
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8 CYFGNGSAYRGTHSLTESGASCLPWNSMILIGKVYTAQNPSAQALGLGKHNYCRNPDGDA 67
                                                                                                                                                                                                                                                                                                                         2 TCYEGNGHFYRGKASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNR 61
                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metažoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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PROSITE; PS01253; FIBRONECTIN 1; 1.
PROSITE; PS00021; KRINGLE 1; 2.
PROSITE; PS50070; KRINGLE 2; 2.
PROSITE; PS50240; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN HIS; 1.
PROSITE; PS00135; TRYPSIN SER; 1.
EGF-like domain; Glycoprotein; Hydrolase; Kringle; Protease;
                                                                                                                                                                                                                                   Length 559;
                                                                                                                                                                                                                              39.5%; Score 219; DB 11; Length 55
46.0%; Pred. No. 1.1e-17;
tive 11; Mismatches 36; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Doub.;
"Production of kringle fragment.";
"Production of kringle fragment.";
submirted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARIY: CONTAINS 1 KRINGLE DOWAIN.
EMBL, AF282882; AAM52248.1;
-InterPro; JRR000001; Kringle.
Fram: PF00051; kringle;
PRODOM; PR00018; KRINGLE.
ProDom; PD000395; Kringle; 1.
                                                                                                                                                                                     559 AA; 63122 MW; 8CCEE2BDB94514D9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SMART; SM00130; KR; 1.
PROSITE; PS00021; KRINGLE 1; 1.
PROSITE; PS50070; KRINGLE 2; 1.
Glycoprotein; Kringle.
SEQUENCE 90 AA; 9804 MW; A33887F9FDF4C7B1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OBEZWI:
01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Neonatal thrombolytic agent alpha-form (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             90 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                             183 LKPWCYVFKAGKYTTEFCSTPACPKGK 209
                                                                                                                                                                                                                                                                                                                                                                                                                    62 RRPWCYVQVGLKPLVQECMVHDCADGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            63 RPWCYVQVGLKPLVQECMVHDCA 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       68 KPWCYT-TNPRKLYDYCDVPQCA 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Plasminogen/activator kringle.
                                                                                                                                                                                                                                   39.5%
Query Match
Best Local Similarity 46.0%
Matches 40; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 49.4
Matches 41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9606;
                                                                                                                                                                  Serine protease
SEQUENCE 559 A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q8NG20 3
Q8NG20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     O9BZW1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 10
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48 CYFGNGSAYRGTHSLTESGASCLPWNSMILIGKVYTAQNPSAQALGLGKHNYCRNPDGDA 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 CYEGNGHFYRGKASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNRR 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
T-plasminogen activater.
T-plasminogen activater.
Sus scrofa (Pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalyais Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
[11]
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 39.4%; Score 218.5; DB 4; Length 395; 44.7%; Pred. No. 8.5e-18; tive 10; Mismatches 41; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SMART; SM00020; Tryp_SPC; 1.
PROSITE; PS01253; FIBRONECTIN 1; 1.
PROSITE; PS50070; KRINGLE 1; 1.
PROSITE; PS50040; KRINGLE 2; 1.
PROSITE; PS50340; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN MIS; 1.
PROSITE; PS00135; TRYPSIN MIS; 1.
ROSITE; PS0135; TRYPSIN SER; 1.
ROSITE; PS0135; TRYPSIN SER; 1.
ROSITE; PS0135; TRYPSIN SER; 1.
ROSITE; PS0135; TRYPSIN SER; 1.
                                                                                                                                                                         Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.

Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.

--- SIMILARITY: BELONGS TO PEPTIDASE PAMILY S1.

EMBL; AFZ60825; AAK11956.1; ---
R HSSP; P007550; 1PR2.

R InterPro; IPR001083; Fibrnctn1.

R InterPro; IPR001083; Fibrnctn1.

R InterPro; IPR001254; Ser_protease_Try.

R Pfam; PF00015; Kringle; 1.

R Pfam; PF00089; Kringle; 1.

R Pfam; PR00018; KRINGLE.

R PRINTS; PR00725; CHYMOTRYESIN.

R PRINTS; PR00725; CHYMOTRYESIN.

R PRINTS; PR00018; KRINGLE.

R PRINTS; PR000185; KRINGLE.

R PRINTS; PR000185; KRINGLE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE 395 AA; 44323 MW; 3FBD4A2F0B7C11C8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             108 KPWCHVLKNRRLTWEYCDVPSCSTCGLRQYSQPQ 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63 RPWCYVQVGLKPLVQECMVHDCAD-GKKPSSPPE 95
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151 CYVGDGYSYRGKVSKTVNQNPCLYWNSHLLLQETYNMFMEDAETHGIAEHNFCRNPDGDH 210
                                                                                                                                                                                                                                                            3 CYEGNGHFYRGKASTDIMGRPCLPWNSAIVLQQIYHAHRSDALQLGLGKHNYCRNPDNRR 62
                                                                                                                                                                                                                           4; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Purification and characterization of a novel hyaluronan-binding protein (PHBP) from human plasma: it has three EGF, a kringle and a serine protease domain, similar to hepatocyte growth factor activator.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE=9642501; PubMed=8827452;
Choi-Miura N.H., Tobe T., Sumiya J., Nakano Y., Sano Y., Mazda T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryoča; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
   PROSITE; PS01186; EGF_2; 2.
PROSITE; PS00021; KRINGLE_1; 1.
PROSITE; PS50040; KRINGLE_1; 1.
PROSITE; PS50240; TRYPSIN DOM: 1.
PROSITE; PS00134; TRYPSIN DOM: 1.
PROSITE; PS00135; TRYPSIN SER; 1.
HYDOTHERICAL PROTEIN; SER; 1.
KRINGLE; PS00135; Serine Gomain; Glycoprotein; Hydrolase; SEQUENCE 517 AA; 57326 MM; 3855A42035A5EAS9 CRC64;
                                                                                                                                                                                    37.9%; Score 210; DB 11; Length 517;
43.5%; Pred. No. 1.2e-16;
tive 14; Mismatches 34; Indels 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         014520; 000663;
01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NAR-1903 (TEMBLrel. 03, Last annotation update)
HGF activator like protein (Hyaluronan binding protein 2).
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (MAR-1995) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                       211 KPWCFVKVNSEKVKWEYCDVTVC---PVPDTP 239
                                                                                                                                                                                                                                                                                                                                 63 RPWCYVQVGLKPLVQE-CMVHDCADGKKPSSP 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEROPS; SOT. 033; --.
Genew; HGNC:4799; HABP2.
InterPro; IPRO01314; Chymctrypsin.
InterPro; IPRO01214; Chymctrypsin.
InterPro; IPRO01259; EGF_like.
InterPro; IPRO01254; Ser_protease_Try.
Pfam; PF00009; EGP; 3.
Pfam; PF00089; trypsin; 1.
Pfam; PF00089; trypsin; 1.
PRINTS; PR00121; KRINGLE.
ProDom; PD000395; KRINGLE.
ProDom; PD000395; KRINGLE.
PROSITE; PS00022; EGF_l; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Biochem. 119:1157-1165(1996).
                                                                                                                                                                                                       Best Local Similarity 43.5%
Matches 40; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
TISSUE=Colon, and Kidney;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kitamura N.
                                                                                                                                                                                        Query Match
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Q14520
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
R InterPro; IPR001024; Ser_Drotease_Try.

R Pfam; PF000039; EGF; 1.

R Pfam; PF000039; fn1; 1.

R Pfam; PF000039; Lrypsin; 1.

R Pfam; PF000039; Lrypsin; 1.

R Pfam; PF000039; Lrypsin; 1.

R Pfam; PF000039; Lrypsin; 1.

R SWART; SW00103; EGF; 1.

R SWART; SW001030; Tryp SPc; 1.

R SWART; SW001030; Tryp SPc; 1.

R PROSITE; PS01020; EGF_2; 1.

R PROSITE; PS01021; EGF_2; 1.

R PROSITE; PS01021; KRINGIE_1; 2.

R PROSITE; PS01031; TRYPSIN_DOM; 1.

R PROSITE; PS01031; TRYPSIN_HIS; 1.

R PROSITE; PS01031; TRYPSIN_HIS; 1.

R PROSITE; PS01031; TRYPSIN_HIS; 1.

R PROSITE; PS01031; TRYPSIN_HIS; 1.

R PROSITE; PS01031; TRYPSIN_HIS; 1.

R PROSITE; PS01031; TRYPSIN_HIS; 1.

R PROSITE; PS01031; TRYPSIN_HIS; 1.

R PROSITE; PS01031; TRYPSIN_HIS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 38.1%; Score 211; DB 6; Length 562; Best Local Similarity 43.2%; Pred. No. 9.9e-17; Matches 38; Conservative 10; Mismatches 40; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Strausberg R.;
Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
-:- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
-:- SIMILARITY: CONPAINS 1 KRINGLE DOMAIN.
EMBL; BC031775; AAH31775.1;
                                                                                                                                                                                                                                                                                                                                                                  Serine protease.
SEQUENCE 562 AA; 63668 MW; F9E6B4C77CB101E8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-0CT-2002 (TrEMBLrel. 22, Created)
01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical protein.
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       186 SKPWCYIFKAEKYSPDFCSTPACTKEKE 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001314; Chymotrypsin.
InterPro; IPR00181; EGF_Ca.
InterPro; IPR006209; EGF_like.
InterPro; IPR006210; IEGF.
InterPro; IPR006010; Kringle.
InterPro; IPR001001; Kringle.
InterPro; IPR001001; Kringle; Irpfam; PF00108; EGF; 2.
Pfam; PF00108; Kringle; I.
Pfam; PF00108; Kringle; I.
Pfam; PF00108; Kringle; I.
PRINTS; PR00122; CHYMOTRYPSIN.
PRINTS; PR00129; Kringle; I.
SMART; SM0130; Kringle; I.
SMART; SM0130; Kringle; I.
SMART; SM0130; Kringle; I.
SMART; SM0130; Kringle; I.
SMART; SM0130; Kringle; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62 RRPWCYVQVGLKPLVQECMVHDCADGKK 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q8K0D2
Q8K0D2;
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101 OPWCHVWKDRQLTWEYCDVPQC 122
63 RPWCYVQVGLKPLVQECMVHDC 84
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                                                                                                                                                                            PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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XX DELINE=97199025; PubMed=9047000;

XX DELINE=97199025; PubMed=9047000;

XY DELINE=97199025; PubMed=9047000;

XY DELINE=97199025; PubMed=9047000;

XY DELINE=97199025; PubMed=9047000;

XY DELINE=97199025; PubMed=9047000;

XY DELINE=97199025; PubMed=9047000;

XY DELINE=9704; PERSON STRIPS

XY DELINE=9705; PROFOUS STRIPS

XY DELINE=9705; PROFOUS STRIPS

XY DELINE=9705; PROFOUS STRIPS

XY DELINE=9705; PROFOUS STRIPS

XY DELINE=9705; PROFOUS STRIPS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Archosauria, Aves, Neognathae, Galliformes, Phasianidae, Phasianinae,
                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Gaps
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ش
                                                                                                                                                                                                                                                36.0%; Score 199.5; DB 4; Length 560; 40.2%; Pred. No. 2.4e-15; tive 15; Mismatches 40; Indels 3
PROSITE; PS01186; EGF_2; 2.
PROSITE; PS00021; KRINGLE 1; 1.
PROSITE; PS50070; KRINGLE 2; 1.
PROSITE; PS50134; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN DOM; 1.
PROSITE; PS00135; TRYPSIN EM; 1.
EGF-like domain; Glycoprotein; Hydrolase; Kringle; Protease; Serine procease.
Serine Docease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match

34.5%; Score 191; DB 13; Length 202;
Best Local Similarity 43.9%; Pred. No. 7.8e-15;
Matches 36; Conservative 7; Mismatches 39; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23148 MW; 049DB42941D83AFC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1996 (TrEMBLrel. 01, Last sequence update) 01-MAR-2003 (TrEMBLrel. 23, Last annotation update) Tissue-type plasminogen activator (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               :|||::::|
254 KPWCFIKVTNDKVKWBYCDVSACSAQDVAYPEESPTE 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                  63 RPWCYVQVGLKPLVQE-CMVHDCA--DGKKPSSPPEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (TrEMBLrel. 01, Created)
                                                                                                                                                                                                                                                                                                  39; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gallus gallus (Chicken).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          202 AA; 231
                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 39; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            [1]
SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1996
01-NOV-1996
01-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          090675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 CYEGNGHFYRGKASIDIMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNRR 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HISTORY PROUPLY LAMI.

INTERPRO! PROUPLY LAMI.

INTERPRO! PROUPLY EGF_2.

INTERPRO! PROUPLY EGF_2.

INTERPRO! PROUPLY EGF_2.

INTERPRO! PROUPLY EGF_1.

INTERPRO! PROUPLY EGF_1.

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INTERPROUPLY EGF_1.

INTERPRO! PROUPLY ENTYELI.

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INTERPRET. TRYPEIN EGF_1.

INTERPRO. TRYPEIN EGF_1.

INTERPRO. TRYPEIN EGF_1.

INTERPRET. TRYPEIN EGF_1.

INTERPRET. TRYP
                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBL_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Strausberg R.;
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
-!- SIMILARITY: CONTAINS 1 KRINGLE DOMAIN.
EMBL, BCO19375; AAH19376.1; -.
HSSP; P00761; 1AN1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length
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SEQUENCE 653 AA, 70553 MW, FE18D90174ED6FDD CRC64;
                                                                                      01-WAR-2002 (TrEMBLrel. 20, Created)
01-WAR-2002 (TrEMBLrel. 20, Last sequence update)
01-WAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical 70.6 kpa protein.
Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     33.9%; Score 188; DB 11; 53.0%; Pred. No. 6.6e-14; ive 6; Mismatches 25;
     653 AA
PRT;
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae, Sus. NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Promise Pronous; Int; 1.

Refam; Pronous; Int; 1.

Refam; Pronous; Int; 1.

Refam; Pronous; Lrypain; 1.

Refam; Pronous; Lrypain; 1.

Refam; Pronous; Rivyesin; 1.

Refam; Pronous; Rivyesin; 1.

Refam; Pronous; Rivyesin; 1.

Refam; Refam; Refam; Rivgel; 1.

Refam; Refam; Refam; Rivgel; 1.

Refam; Refam; Refam; 1.

Refam; Refam; Refam; 1.

Refam; Refam; Refam; 1.

Refam; Refam; Refam; 1.

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                                                                                                                                                                                                                                                                                                                                                                                    Takahashi T., Kihara T.;
Takahashi T., Kihara T.;
"Poroine liver factor XII.";
Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY SI.
-!- SIMILARITY: CONTAINS 1 KRINGLE DOMAIN.
EMBL; AB02245; BAA37148.1; -.
                                                                                                - MAY-1999 (TrEMBLrel. 10, Created)
- MAY-1999 (TrEMBLrel. 10, Last sequence update)
- MAR-2003 (TrEMBLrel: 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPPR001314; Chymotrypsin.
InterPro; IPR00042; 26F 2.
InterPro; IPR006509; EGF 11ke.
InterPro; IPR000631; Fibrnctni.
InterPro; IPR000652; WI Type_II.
InterPro; IPR006501; WI Type_II.
InterPro; IPR006501; Kringle.
InterPro; IPR000001; Kringle.
Fam; PP00008; EGF; 2.
Pfam; PP00009; EGF; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
32.2%
Best Local Similarity 41.2%
Matches 42, Conservative
                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                              Sus scrofa (Pig).
                                                                                                     01-MAY-1999
01-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEROPS; S01
                                                 097507
RESULT 18
                           097507
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         60
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                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
33.8%; Score 187.5; DB 11; Length 597;
Best Local Similarity 37.7%; Pred. No. 6.9e-14;
Matches 40; Conservative 10; Mismatches 39; Indels 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS01253; FIBRONECTIN 1; 1.
PROSITE; PS00023; FIBRONECTIN 2; 1.
PROSITE; PS00021; KRINGLE 1; 1.
PROSITE; PS50070; KRINGLE 2; 1.
PROSITE; PS50134; TRYPSIN DOM; 1.
PROSITE; PS00135; TRYPSIN LIS; 1.
PROSITE; PS00135; TRYPSIN SER; 1.
EGF-like domain; Glycoprotein; Hydrolase; Kringle; Protease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   272 DTRPWCFVWSGDRLSWDYCGLEQCQTPTFAPLVVPESQEESPSQAP 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 RRRPWCYVQVGLKPLVQECMVHDC------ADGKKPSSPP 94
                                                                                                                                                                                                                                                                                                                                                                                                                                  Schloesser M., Schwager S., Engel W.; Schloesser M., Schwager S., Engel W.; Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases. -! - SIMILARITY: BELONGS TO PEPTIDASE FAMILY SI. -! - SIMILARITY: CONTAINS I KRINGLE DOMAIN. EMBL, X99571; CAA67891.1; -. HSRP, F0076.0; 1077.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            597 AA; 65638 MW; F3AC07C37D0C0FBA CRC64;
                                                                                                                      Created)
Last sequence update)
Last annotation update)
                                                                          597 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MGD; MGI:1891012; F12.
INTERPRO; IPRO01314; Chmotrypsin.
INTERPRO; IPRO02039; EGF like.
INTERPRO; IPRO02039; F1brnctn1.
INTERPRO; IPRO0203; F1brnctn1.
INTERPRO; IPRO02001; KINPE_II.
INTERPRO; IPRO0210; IRGF.
INTERPRO; IPRO021054; Ser_protease_Try.
Pfam; PF00009; EGF; 2.
Pfam; PF00019; fn1; 1.
Pfam; PF00019; fn1; 1.
Pfam; PF00010; Kringle; 1.
Pfam; PF00010; Kringle; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRINTS, PROGOZS, CHYMOTRYPSIN, PRINTS, PROGOZS, CHYMOTRYPSIN, PRINTS, PROGOZS, CHYMOTRYPSIN, PRINTS, PROGOGS, ENTYPEII.
PRODOM, PD000395, RN Type II; 1.
SMART; SM00181, EGF, 2.
SMART; SM00181, EGF, 2.
SMART; SM00181, EGF, 1.
SMART; SM00180, RN; 1.
SMART; SM00180, RR; 1.
SMART; SM00180, RR; 1.
PROSITE; PS01186, EGF 1; 2.
PROSITE; PS01186, EGF 2; 1.
PROSITE; PS01186, EGF 2; 1.
PROSITE; PS01186, EGF 2; 1.
PROSITE; PS01283; FIBRONECTIN 2; 1.
                                                                    PRT;
                                                                                                                            05,
23,
                                                                       PRELIMINARY;
                                                                                                                   01-JAN-1998 (TrEMBLrel.
01-JAN-1998 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
                                                                                                                                                                                                                                                     Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                               NCBI TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Serine protease
SEQUENCE 597
                                                                                                                                                                                                                                                                                                                                                                                                                  ISSUE=Liver;
                                                                                                                                                                                                      Factor XII.
                                                                                                   035727;
                                                                       035727
                   RESULT 17
035727
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217 CYSDRGLSYRGMAQTTLSGAPCQPWAS----EATYWNMTAEQALNWGLGDHAFCRNPDND 272 3 CYEGNGHFYRGKASTDTMGRPCLPWNSATVLQQTY-HAHRSDALQLGLGKHNYCRNPDNR 61 Gaps 32.2%; Score 178.5; DB 6; Length 616; 41.2%; Pred. No. 8.5e-13; tive 7; Mismatches 40; Indels 13; 273 TRPWCFVWRGDQLSWQYCRLARCQAPIGEAPPILTPTQSPSE 314 62 RRPWCYVQVGLKPLVQECMVHDCAD--GKKP-----SSPPE 95

RESULT 19

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452 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
(TrEMBLrel.
                                                                                                                                                                                                                                                                                         Best Local Similarity
Matches 42, Conserva
                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                            NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                               Query Match
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                                                                                 Gallus
                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 22
Q90Y90
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
                                                                                                                                                                                                                                                                                                                3 CYEGNGHFYRGKAS-TDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNR 61
                                                                                                                                                                                                                                                                                                                                     29 CFTVNGRDYRGTVSQAGPEGTPCLYWNQTT--QHLYNAQSDPDGELGLGNHNYCRNPDAD 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 TCYEGNGHFYRGKASTDTMGRPCLPWNSATVLQQTY-HAHRSDALQLGLGKHNYCRNPDN
                                                                                                                                                            SEQUENCE FROM N.A.

MEDLINE=2208873; PubMed=12421700;

Davidson G., Mao B., Del Barco Barrantes I., Niehrs C.;

Davidson G., Mao B., Del Barco Barrantes I., Niehrs C.;

Comparison interact with Dickkopfi to regulate anteroposterior CNS patterning.";

Davelopment 129:5587-5596 (2002).

ERMBL, AVISO813; AAN64661.1; --

SEQUENCE 421 AA, 46274 MW; 74D04DB1682CD15F CRC64;
                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                           Xenopus laevis (African clawed frog).
Vebaryota; Metazoa, Chordata; Craniata; Vertebrata; Buteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homó sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                          3;
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                                                                                                                                                                                                                                                               31.1%; Score 172.5; DB 13; Length 421; S0.7%; Pred. No. 2.9e-12; cive 4; Mismatches 26; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ouery Match 30.8%; Score 170.5; DB 4; Length 615; Best Local Similarity 48.5%; Pred. No. 7.7e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.

Wada H., Nishioka J., Nakatani K., Kasai Y., Abe Y., Nobori T
"Molecular chracterization of coagulation factor XII-Mie.";
"Dumitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.

EMBL, AB098845; BAC23095.1; -.
SEQUENCE 615 AA; 67735 MW; 030508870A0C7EDB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6; Mismatches 24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
1-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Coagulation factor XII-Mie.
                                   Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            947 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                           615 AA.
             421 AA
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                        Q8AXX3;
01-MAR-2003 (TrEMBLrel. 23,
01-MAR-2003 (TrEMBLrel. 23,
01-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                                                                                                                                                                          34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           33; Conservative
             PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 RRRPWCYV 68
                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                            62 RRPWCYV 68
                                                                                                                                                                                                                                                                                                                                                                           : | | | | | 87 VQPWCYV 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI TaxID=9606;
                                                                                                                                       NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                    Query Match
                                                                      Kremen2.
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QBAXY6,
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Q81225;
              Q8AXX3
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Q81ZZ5
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Q8AXY6
ID Q8AXY
AC Q8AXY
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463 RTCYSGNGOFYQGWANVTASGIPCQKWS-----DQAPHLHRRTPQVFPELSDA----- 510
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=21167372; PubMed=11267660;
A Nakamura T., Aoki S., Kitajima K., Funakoshi H., Takahashi T.,
A Matsumoto K., Nakamura T.;
A Matsumoto K., Nakamura T.;
A Matsumoto K., Prometric R.;
A Matsumoto K., Prometric R.;
A matsumoto K., Prometric R.;
Containing transmembrane protein.";
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01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
Muscle-specific receptor tyrosine kinase MuSK.
Gallus gallus (Chicken).
Eukaryosi, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-20538710; PubMed=11083926; Ip F.C., Glass D.G., Gies D.R., Cheung J., Lai K.O., Fu A.K., Yancopoulos G.D., Ip N.Y.; "Cloning and characterization of muscle-specific kinase in chicken."; Mol. Cell. Neurosci. 16:661-673 (2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        52 HNYCRNP-DNRRRPWCYVQVGLKPLV--QECMVHDCADG-----KKPSS-----PP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Edenopus laevis (African clawed frog).

Busaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Bartachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
Xenopodinae, Xenopus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30.1%; Score 167; DB 13; Length 947; llarity 35.9%; Pred. No. 3.3e-11; Conservative 8; Mismatches 29; Indels 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gies D., Glass D.J., Yancopoulos G.D.,
Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AN143173, AAN05008.1, -.
Receptor; Kinase.
SEQUENCE 947 AA, 105588 MW, E6C3FCC5796CC8BE CRC64:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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ProDom; PD000395; Kringle;
SMART; SM00142; CUB; 1.
SMART; SM00100; KR; 1.
PROSITE; PS01180; CUB; 1.
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157 DTGPWCFT---MDPSVRWEYCNLTRCSD 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00021; KRINGLE 1; 1.
PROSITE; PS50070; KRINGLE 2; 1.
Glycoprotein; Kringle; Lipoprotein.
NON TER 11 113
SEQÜENCE 113 AA; 12685 MW; F3D6
                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HSSP; P00747; IPMK.
InterPro; IPR00001; Kringle.
Pfam; PP00051; kringle; 1.
PRINTS; PR00018; KRINGLE.
ProDom; PD000395; Kringle; 1.
SMART; SM00130; KR; 1.
                                                                                                                                                                               Apolipoprotein(a) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 34.8
ses 39; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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                                                                                       Q9UIR5
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018783
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                                                                                                                                                            3 CYEGNGHFYRGKASIDIM--GRPCLPWNSAIVLQQIYHAHRSDALQLGLGKHNYCRNPDN 60
                                                                                                                                                                                      3 CYEGNGHFYRGKASTDTMGRPCLPWNSATVLQ--QTYHAHRSDALQLGLGKHNYCRNPDN 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12; Gaps
                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cox L.A., Jett C., Hixson J.E.;
"Molecular Basis of the Apolipoprotein (a) Null Phenotype: A Splice
Site Mutation is Associated with Deletion of a Single Exon in a Null
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Papio hamadryas (Hamadryas baboon).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae,
Cercopithecinae, Papio.
                                                                                                                           4,
                                                                                     28.5%; Score 158; DB 13; Length 452; 44.1%; Pred. No. 1.7e-10; ive 9; Mismatches 25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 454;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28.5%; Score 158; DB 6; Length 454 39.8%; Pred. No. 1.7e-10; ive 10; Mismatches 31; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SMART; SMO0130; KR; 2: SEAST; SMO0130; KR; 2: SMART; SMO0130; KR; 2: SEC, 1: SROOT20; Tryp_SPc; 1: PROSITE; PS00021; KRINGLE 2; 2: PROSITE; PS50240; TRYPSIN DOM; 1: PROSITE; PS00135; TRYPSIN DOM; 1: Glycoprotein; Hydrolase; Kringle; Lipoprotein; Protease; Serine protease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
-!- SIMILARITY: CONTAINS 2 KRINGLE DOMAINS.
EMBL; AF029691; AAB97886.1; -.
HSSP; P00747; 2PK4.
PROSITE; PS00021; KRINGLE_1; 1.
PROSITE; PS5070; KRINGLE_2; 1.
Glycoprotein; Kringle.
SEQUENCE 452 AA; 50188 MW; ED24BCD1AF4564E2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    454 AA; 50041 MW; 974E30744C187B2F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                            Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR001314; Chymotrypsin.
InterPro; IPR0010114; Kringle.
InterPro; IPR0010254; Ser protease_Try.
Pfam; PF00051; Kringle; 2.
Pfam; PF00089; trypsin; 1.
PRINTS; PR00125; CHYMOTRYPSIN.
PRINTS; PR001018; KRINGLE.
ProDom; PD000395; Kringle; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 RRRPWCYVQVGLKPLV--QECMVHDCAD 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Apolipoprotein a (Fragment).
BABAPOA.
                                                                                                                                                                                                                                                                                                                                                                       046506;
01-JUN-1998 (TrEMBLrel. 06,
01-JUN-1998 (TrEMBLrel. 06,
01-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 39.88
Matches 35, Conservative
                                                                                                                           30; Conservative
                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                    61 RRRPWCYV 68
                                                                                                                                                                                                                                                                  88 DVSPWCYI 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                          Best Local Similarity
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                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Allele."
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                                                                                                                           Matches
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9 RQCYHGNGQSYRGTFSTTVTGRICQSWSSMTPHRHQRTPENYPNDGLTM-----NYCRNP 63
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MEDLINE=98004511; PubMed=9342350;
Lawn R.M., Schwartz K., Patthy L.;
Convergent evolution of apolipoprotein(a) in primates and hedgehog.";
Proc. Natl. Acad. Sci. U.S.A. 94:11992-11997(1997).
-:- SIMILARITY: CONTAINS 5 KRINGLE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 KTCYEGNGHFYRGKASTDTMGRPCLPWNSATV -- LQQTYHAHRSDALQLGLGKHNYCRNP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=21181705; PubMed=11285247;

Ogorelkova M., Kraft H.G., Ehnholm C., Utermann G.;

"Single nucleotide polymorphisms in exons of the apo(a) kringles IV
"Single nucleotide polymorphisms in exons of the apo(a) kringles IV
types 6 to 10 domain affect Lp(a) plasma concentrations and have
different patterns in Africans and Caucasians.";
Hum. Mol. Genet. 10.815-824(2001).
-!- SIMILARITY: CONTAINS 1 KRINGLE DOMAIN.
-!- SIMILARITY: CONTAINS 1 KRINGLE DOMAIN.
--- EMBL, AF158663; AAF03680.1; ---
EMBL, AF158662; AAF03680.1; ---
--- TOTALENDED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Macropus eugenii (Tammar wallaby).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Metatheria, Diprotodontia, Macropodidae, Macropus.
                                                                                                                                                                                                        Homo sapiens (Human).
Bukaryota; Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCSI TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       64 DADTGPWCFT---MDPSIRWEYCNLTRCSDTEGTVVAPPTVIQVPSLGPPSE 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 59 DNRRRPWCYVQVGLKPLV--QECMVHDCADG------KKPS-SPPEE 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28.3%; Score 157; DB 4; Length 113; 34.8%; Pred. No. 4.8e-11; Live 13; Mismatches 36; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 113 AA; 12685 MW; F3D65681D9B5253A CRC64;
                                                     01-WAY-2000 (TrEMBLrel. 13, Created)
01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-WAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-07N-1998 (TrEMBLrel. 05, Created)
01-07N-1998 (TrEMBLrel. 05, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
113 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         806 AA
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316 CYNGSGADYRGMASTTKSGHQCQPW----ALQHP-HSHRLSSTEFPELG-GGHAYCRNPG 369
                                                                                                                                                                                                                                                                                                                                                   3 CYEGNGHFYRGKASTDIMGRPCLPWNSAIVLQQIYHAHR---SDALQLGLGKHNYCRNPD 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 CYEGNGHFYRGKASTDIMGRPCLPWNSAIVLQQIYHAHR---SDALQLGLGKHNYCRNPD 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=C57BL/6J; TISSUE=Heart;
STRAIN=223846813; PubMed=12466851;
The FANTOM Consortium.
The FANTOM Consortium Research Group Phase I & II Team;
the RIKEN Genome Exploration Research Group Phase I & II Team;
"halysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
No full-length cDNAs.";
Nature 420:563-573 (2002).
EMBL; AK084752; BAC39273.1; -.
SEQUENCE 944 AA; 105037 MW; 8708ADD4CBIBIF36 CRC64;
SMART; SM00219; TyrKc; 1.

PROSITE; PS50038; FZ; 1.

PROSITE; PS500021; KRINGLE_1; 1.

PROSITE; PS50010; KRINGLE_2; 1.

PROSITE; PS500109; PROTEIN_KINASE_DOM; 1.

PROSITE; PS00109; PROTEIN KINASE_TYR; 1.

Hypothetical protein; ATP-binding; Glycoprotein; Kringle; Transferase.

NON TER 1 1 1

SEQÜENCE 801 AA; 89201 MW; 3AS928326C8B885D CRC64;
                                                                                                                                                                                                                                                27.7%; Score 153.5; DB 11; Length 944;
41.9%; Pred. No. 1.4e-09;
tive 9; Mismatches 32; Indels 13; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Receptor tyrosine kinase-like orphan receptor 2.
Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  227 GOMEGPWCFTÓ-NKNVRVELCDVPPCSPRDGSK 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       370 GOMEGPWCFTÓ-NKNVRVELCDVPPCSPRDGSK 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                   60 NRRR-PWCYVQVGLKPLVQECMVHDCA--DGKK 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        60 NRRR-PWCYVQVGLKPLVQECMVHDCA--DGKK 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             944 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 41.9
Matches 39; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 28
Q8BSP6
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     슝
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ch 27.8%; Score 154; DB 6; Length 806;
1 Similarity 35.5%; Pred. No. 9.9e-10;
33; Conservative 11; Mismatches 25; Indels 24; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                            MENCEPS: S01.233; -.

MENCEPS: S01.233; -.

RILGEPEO: IPRO00001; Kringle.

RILGEPEO: IPRO00001; Kringle.

RILGEPEO: IPRO03004; Pan_app.

RILGEPEO: IPRO03066; Pan_app.

RILGEPEO: IPRO03066; Pan_app.

RILGEPEO: IPRO03066; Pan_app.

R. PÉTAN; PRO00021; Kringle; 5.

R. PÉTAN; PRO00039; LYPSIN; 1.

R. PRINTS; PRO00039; RRINGLE.

R. PRINTS; PRO00039; RRINGLE.

R. PRINTS; PRO00039; RRINGLE.

R. PROMO130; KR; 4.

R. SMART; SMO00130; KR; 4.

R. SMART; SMO00130; KR; 4.

R. SMART; SMO00130; KR; 4.

R. SMART; PSO0021; KRINGLE 1; 5.

R. PROSITE; PSO0021; TYPEIN DOM; 1.

R. PROSITE; PSO0134; TRYPEIN DOM; 1.

R. PROSITE; PSO0134; TRYPEIN DOM; 1.

R. PROSITE; PSO0134; TRYPEIN DOM; 1.

R. PROSITE; PSO0134; TRYPEIN SR; 1.

R. PROSITE; PSO0134; TRYPEIN SR; 1.

R. PROSITE; PSO0134; TRYPEIN SR; 1.

R. PROSITE; PSO0134; TRYPEIN SR; 1.

R. PROSITE; PSO0134; TRYPEIN SR; 1.

R. PROSITE; PSO0134; TRYPEIN SR; 1.

R. PROSITE; PSO0134; TRYPEIN SR; 1.

R. PROSITE; PSO0134; TRYPEIN SR; 1.

R. PROSITE; PSO0134; TRYPEIN SR; 1.

R. PROSITE; PSO0134; TRYPEIN SR; 1.

R. PROSITE; PSO0134; TRYPEIN SR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Strausberg R.;
Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: CONTAINS I KRINGLE DOMAIN.
EMBL, BC030848, AAH30848.1; -.
InterPro; IPR000024; Fz domain.
InterPro; IPR00001; Kringla.
InterPro; IPR000719; Proc kinase.
InterPro; IPR001299; Ser_thrinase.
InterPro; IPR001295; Tyr_pkinase.
Pfam; PF01392; Fz 1.
Pfam; PF00059; pkinase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q8KOQ8.
01-0CT-2002 (TrEMBLrel. 22, Created)
01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical protein (Fragment).
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  420 CRNPDGDKSPWCYT---MDPTVRWEFCNLEKCS 449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     55 CRNPDNRRRPWCYVQVGLKPLV--QECMVHDCA 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            801 AA
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PRINTS; PRO109; TYRKINASE.
Probom; PD000395; Kringle; 1.
Probom; PD000001; Prot_kinase; 1.
SMART; SM00130; KR; 1.
SMART; SM00220; S_TKC; 1.
EMBL; AF012297; AAB65760.1; -.
HSSP; P00747; SHPG.
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Best Local Similarity
Matches 33; Conservat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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Q8WMR1
                  RESULT 30
Q8WMR1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 CYEGNGHFYRGKASTDIMGRPCLPWNSAIVLQOIYHAHRSDALQLGLGKHNYCRNPDNRR 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11 CYHGDGOSYRGSFSTIVTGRICOSWSSMI---PHWHQRITEXYPNGGLIRNYCRNPDAEI 67
SEQUENCE FROM N.A.
STRAIR-CSTBL/GA1/ IISSUB=Forelimb;
MEDLINE=22354683; PubMed=12466851;
The FANTOM Consortium,
The RIKEN Genome Exploration Research Group Phase I & II Team;
The RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
Nature 420:563-573 (2002).
BMBL; AR031112; BAC27258-11;
SEQUENCE 944 AA; 105053 MW; 1BBD416BE3170401 CRC64;
                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                          13;
                                                                                                                                                          27.7%; Score 153.5; DB 11; Length 944; 41.9%; Pred. No. 1.4e-09; ive 9; Mismatches 32; Indels 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27.6%; Score 153; DB 4; Length 113; 39.3%; Pred. No. 1.5e-10; tive 8; Mismatches 35; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            113 113
113 AA; 12815 MW; 4F80ADF8708548CB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                      01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                       370 GOMEGPWCFTQ-NKNVRVELCDVPPCSPRDGSK 401
                                                                                                                                                                                                                                                                             60 NRRR-PWCYVQVGLKPLVQECMVHDCA--DGKK 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00051; kringle; 15.

Probon; PR00018; KRINGLE.

Probom; PR000185; KRINGLE.

SMART; SM00130; KR; 1.

PROSITE; PS00021; KRINGLE 1; 1.

PROSITE; PS50070; KRINGLE 2; 1.

Glycoprotein; Kringle; Lipoprotein.

NON TER 113 113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                68 RPWCYT---MDPSVRWEYCNLTRC 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Apolipoprotein(a) (Fragment).
                                                                                                                                                                         Local Similarity 41,9
nes 39; Conservative
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hes 33; Conservative
                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                             Query Match
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                                                                                                                                                                                       Matches
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    SORTARARYCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 CYEGNGHFYRGKASTDTMGRPCLPWNSATVLQQTYHAHRSDAL-----QLGLGKHNYCRN 57
                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. Price Associated B., Chan R., Kisker O., Pirie-Shepherd S.R., Coffman K.T., Resnick D., Chan R., Kisker O., Folkman J., Waters D.J.; "Angiostatin is Detectable in the Urine of Dogs with Spontaneous Bone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13; Gaps
                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Rissipedia; Canidae; Canis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match

27.3%; Score 151.5; DB 6; Length 359;
Best Local Similarity 44.3%; Pred. No. 8e-10;
Matches 31; Conservative 5; Mismatches 21; Indels 13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cancer.";
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
SIMILARITY: CONTAINS 4 KRINGLE DOMAINS.
EMBL, AY069985; AALS8519.1;
InterPro; IPR000001; Kringle.
InterPro; IPR00366; Prothrombin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NON_TER 359 359
SEQUENCE 359 AA, 41172 MW, 776D35F4AB0BDD9E CRC64;
                       QBWMR.;
QBWMR.;
01-WAR-2002 (TrEMBLrel. 20, Created)
01-WAR-2002 (TrEMBLrel. 20, Last sequence update)
PLAR-2003 (TrEMBLrel. 23, Last annotation update)
Plasminogen (Fragment).
Canis familiaris (Dog).
PRT; 359 AA
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Job time : 12.8119 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS00021; KRINGLE_1; 4. PROSITE; PS50070; KRINGLE_2; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PERMY PRODOSI; KRINGLE, 4.
PRINTS; PRODOSI; KRINGLE.
PRINTS; PRO1505; PROTHROMBIN.
PRODOM; PD000395; Kringle; 4.
SMART; SM00130; KR; 4.
PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               334 PDADKSPWCY 343
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Glycoprotein; Kringle.
NON_TER 1 1
NON_TER 359 359
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Human ovarian anti
Delta 1-46 urokina
Human prourokinase
Bi functional uroki
Human prourokinase
Bifunctional uroki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human uPA kringle
Human uPA amino te
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human colon cancer
                                                                                                             .; Search time 15.1223 Seconds (without alignments) 1007.637 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                  96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Description
                                                                                                                                                                                                                                  1 KTCYEGNGHFYRGKASTDTM.....QECMVHDCADGKKPSSPPEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | SIDS1/gcgdata/geneseq/geneseqp-embl/AA1980_DAT:
| SIDS1/gcgdata/geneseq/geneseqp-embl/AA1981_DAT:
| SIDS1/gcgdata/geneseq/geneseqp-embl/AA1982_DAT:
| SIDS1/gcgdata/geneseq/geneseqp-embl/AA1983_DAT:
| SIDS1/gcgdata/geneseq/geneseqp-embl/AA1984_DAT:
| SIDS1/gcgdata/geneseq/geneseqp-embl/AA1984_DAT:
| SIDS1/gcgdata/geneseq/geneseqp-embl/AA1985_DAT:
| SIDS1/gcgdata/geneseq/geneseqp-embl/AA1986_DAT:
| SIDS1/gcgdata/geneseq/geneseqp-embl/AA1987_DAT:
| SIDS1/gcgdata/geneseq/geneseqp-embl/AA1987_DAT:
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/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA2003.DAT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /AA1993.1
/AA1994.1
/AA1995.1
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/AA1997.1
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| SIDSI | gogdata/gensesq/gensesqp_embl/AA|
| SIDSI | gogdata/gensesq/gensesqp_embl/AA|
| SIDSI | gogdata/gensesq/gensesqp_embl/AA|
| SIDSI | gogdata/gensesq/gensesqp_embl/AA|
| SIDSI | gogdata/gensesq/gensesqp_embl/AA|
| SIDSI | gogdata/gensesq/gensesqp_embl/AA|
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| SIDSI | gogdata/gensesq/gensesqp_embl/AA|
| SIDSI | gogdata/gensesq/gensesqp_embl/AA|
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| SIDSI | gogdata/gensesq/gensesqp_embl/AA|
| SIDSI | gogdata/gensesq/gensesqp_embl/AA|
| SIDSI | gogdata/gensesq/gensesqp_embl/AA|
| SIDSI | gogdata/gensesq/gensesqp_embl/AA|
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                               1107863 seqs, 158726573 residues
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                                                                                                                 2003, 14:33:02
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Listing first 45 summaries
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AAE16549
AAG75492
ABP41795
AAR68854
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AAR66266
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ALIGNMENTS

Cines DB, Higazi AA; WPI; 2002-122240/16.

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20-JUN-2000; 2000US-212874P.
                                                                                                                                                                                         13-JUN-2001; 2001WO-US18976
                                                                 and connecting peptide
                                                                            Query Match
Rest Local Similarity
                                                                                                                                                                              WO200197752-A2.
                                                                                                                                    09-APR-2002
                                                                                                                                                                                   27-DEC-2001.
                                                                       Sequence
                                                                                                                              AA::16549;
                                                                               Best Loca
Matches
                                                                                                                  RESULT 2
AAE16549
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urokinase-type plasminogen acuporation computation is used to modulate the contractility and angiogenic activity of a mammalian muscle, endothelial cell or tissue. The composition is used for treating stroke, hypotension, hypertension, atherosclerosis, heart attack, microvascular occlusions, thrombotic microangiopathies, surgically induced thrombotic disorders, angiogenic disorders, pulmonary fibrosis, asthma, tumour cell angiogenesis, pulmonary fibrosis, asthma, tumour cell invasion, tumour cell angiogenesis, tumour cell metastasis, glaucoma, diabetic retinopathy, wound healing, clotting disorder, uterine such as asthma, adult respiratory disease or condition such as asthma, adult respiratory distress syndrome, primary pulmonary associated with chronic intrapulmonary fibrin formation. The present sequence is human urokinase-type plasminogen activator (upA) amino terminal fragment (ATF) and connecting peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           48 KTCYEGNGHFYRGKASTDIMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDN 107
                                                                                                                                                                        The invention relates to a composition comprising one or more domains of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 KTCYEGNGHFYRGKASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDN
                                                  treating atherosclerosis, asthma, hypertension, glaucoma, impotence, comprising domains from urokinase-type plasminogen activator
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; colon cancer; colon cancer antigen; diagnosis; detection;
                            Composition for modulating muscle cell and tissue contractility
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 554; DB 23; 100.0%; Pred. No. 4.2e-45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human colon cancer antigen protein SEQ ID NO:6256.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             colorectal carcinoma; chromosome 10.
                                                                                                                         24; Fig 1H; 117pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAG75492 standard; Protein; 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28-SEP-2000; 2000WO-US26524.
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96; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              143 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29-SEP-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
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Matches 9
                                                                                                                         Claim
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                                                                                                                                                                                        The invention relates to a composition comprising one or more domains of urckinase-type plasminogen activator (uPA). The composition is used to modulate the contractility and angiogenic activity of a mammalian muscle, endothelial cell or tissue. The composition is used for treating stroke, hypotension, hypertension, atherosclerosis, heart attack, microvascular occlusions, thrombotic microangiopathies, surgically induced thrombotic disorders, pulmonary fibrosis, asthma, tumnour cell invasion, tumnour cell angiogenesis, tumnour cell metastasis, glaucoma, diabetic retinopathy, wound healing, clotting disorder, uterine contraction disorder, male impotence, respiratory disease or condition such as asthma, adult respiratory distress syndrome, primary pulmonary hypertension, microvascular thrombotic occlusion, and a disorder associated with chronic intrapulmonary fibrin formation. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; urokinase-type plasminogen activator; uPA; therapy; hypertension; stroke, hypotension; stroke, hypotension; astroke, thrombotic disorder; microvascular occlusion; angiogenic disorder; pulmonary fibrosis; asthma; tumour cell metastasis; glaucoma; diabetic retinopathy; wound healing; clotting disorder; uterine contraction disorder; respiratory disease; adult respiratory distress syndrome; amino terminal fragment; ATF; male impotence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 KTCYEGNGHFYRGKASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDN 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 KTCYEGNGHFYRGKASTDIMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKGKHNYCRNPDN 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                          Composition for modulating muscle cell and tissue contractility for treating atherosclerosis, asthma, hypertension, glaucoma, impotence, comprising domains from urokinase-type plasminogen activator -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human uPA amino terminal fragment (ATF) and connecting peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 554; DB 23;
100.0%; Pred. No. 2.9e-45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 RRRPWCYVQVGLKPLVQECMVHDCADGKKPSSPPEE 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 RRPWCYVQVGLKPLVQECMVHDCADGKKPSSPPEE 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAE16549 standard; Protein; 143 AA,
                                                                                                                                                Claim 25; Fig 1I; 117pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             96 AA;
N-PSDB; AAD27083
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Nucleic acids encoding 4277 human colon cancer-associated polypeptides, useful for preventing, diagnosing and/or treating colorectal cancers

WPI; 2001-235357/24.

N-PSDB; AAH34897.

UYPE-) UNIV PENNSYLVANIA

Cines DB, Higazi AA;

WPI; 2002-122240/16. N-PSDB; AAD27082.

Claim 11; Page 7707-7708; 9803pp; English.

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Gaps

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Length 143;

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AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon cancer-associated mucleic acid molecules (N) and proteins (P), where the proteins are collectively known as colon cancer antigens. The colon cancer antigens have cytostatic activity and can be used in gene therapy and treatment of diseases associated with inappropriate perpension. For example, N and P may be used in the prevention, associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of P by expressing inactive proteins or to supplement the patients own production of P. Additionally, N may be used to produce the colon cancer-associated Ps, by inserting the nucleic acids into a host cell and culturing the cell to express the proteins. N and P can be used in the prevention, diagnosis and treatment of colorectal carcinomas and cancers. AAH37196 to AAH37204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    74 KTCYEGNGHFYRGKASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDN 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour; ovarian cancer; breast cancer; tumour; reproductive system disorder; infertility; pregnancy disorder; anovulation; polycystic ovary syndrome; PCOS; ovarian cyst; dysmenorrhoea; endocrine disorder; infection; inflammatory condition; immune disorder; blood disorder; infection; cardiovascular disorder; respiratory disorder; neurological disorder; gastrointestinal disorder; urinary system disorder; drug screening; gene therapy; chromosome mapping; forensic analysis; antibody preparation; cytostatic; immunomodulatory; neuroprotective; antiinflammatory; gynaecological; reproductive; chromosome 10q24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 KTCYEGNGHFYRGKASTDIMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                           present invention.
N.B. Pages 666 to 682 and page 7053 of the sequence listing were missing at time of publication, meaning no sequences are present for SEQ ID NO:1027 to 1052, 7921 and 7922.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ·,
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 337;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 554; DB 22; 100.0%; Pred. No. 9.4e-45;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
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Best Local Similarity 100..
Loc 96; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                               337 AA;
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ABP41795
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The invention relates to 2175 novel human ovarian antigens (ABB41054-ABB43228) and to cDNAs encoding them (ABG54131-ABG56305), and also concompasses polypeptides 90% identical and polymuclectides 95% identical to the sequences of the invention. The invention additionally relates to recombinant vectors and host cells comprising human ovarian antigens to recombinant vectors and host cells comprising human ovarian antigens of ovarian antigens comprising human ovarian antigens and the use of ovarian antigen polymucleotides and polymptides in diagnosing, treating, prognosing or preventing various ovary and/or breast related disorders. Such conditions include ovarian cancer and breast cancer, and metastatic tumours of ovarian or breast origin, reproductive system disorders (e.g., infertility, disorders of pregnancy, anovulation, polycystic ovary syndrome, ovarian cysts, and dysmenorrhoea), endocrine disorders, incertions (e.g., chlamydia, HV, toxoplasmosis, and toxic shock syndrome), inflammatory conditions (e.g., mastitis, cophoritis and varianties), immune disorders (e.g., congenital and acquired chorders), inclammatory conditions (e.g., mastitis, sophoritis and conditions (e.g., mastitis, sophoritis and conditions disorders), conditions (e.g., mastitis, sophoritis and conditions (e.g., anaemia), cardiovascular disorders, neurological disorders, gastrointestinal disorders, or and unimary system disorders. Ovarian antigen polypeptides and conditions (e.g., anaemia), cardiovascular disorders or compounds which modulate ovarian antigen expression or activity. The polymucleotides may also be used in screening for compounds which confidential in disease diagnosis, drug targeting and phenotyping. The present sequence represents a human ovarian antigen of the invention.

Consequence represents a human ovarian antigen of the invention of the printed or specification, but was obtained in electronic format directly from MIPO configuration, but was obtained in electronic format directly from WIPO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 KTCYEGNGHFYRGKASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDN 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human, des-epidermal growth factor homologous plasminogen activator; uPA; liver membrane; reduced affinity; EGF homologous; thrombosis; thrombolytic; increased half-life; urokinase.
                   Isolated nucleic acid molecules encoding novel ovarian polypeptides,
                                             (e.g.
                          ovarian cancer), immune disorders, cardiovascular disorders and neurological diseases -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 554; DB 23; Length 337; 100.0%; Pred. No. 9.4e-45;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                   English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAR68854 standard; protein; 365 AA
                                                                                                                                SEQ ID No 2927; 2922pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Beet Local Similarity 100.00
Thes 96; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (engineered)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (updated)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Delta 1-46 urokinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              337 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Misc-difference 1
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AAR68854
à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       셤
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New variants of human prourokinase (hPUK) comprise a hPUK deficient in (i) at least part of the first loop region of the epidermal growth factor (EGF) domain; (ii) at least part of the epidermal growth least part of the second loop; or (iii) at least part of the third loop. The hPUK variants show an increased blood half-life comparable to that of the whole EGF domain-deficient hPUK variant and urokinase while retaining the same properties as those of hPUK. They have potent thrombolytic activity and very little tendency to cause spontaneous bleeding. The present sequence represents a specific variant appear in the specification and has been created using the wild-type hPUK sequence and the junction sequence after deletion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 KTCYEGNGHFYRGKASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDN 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15 KTCYEGNGHFYRGKASTDIMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDN 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    fibrinolysis; thrombin inhibition; thrombolytic; anti-thrombotic;
urokinase; variant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 554; DB 11; Length 378; 100.0%; Pred. No. 1.1e-44; ive 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                    Human pro-urokinase variants - deficient in loop regions c
epidermal growth factor, showing long blood half-life, as
fibrinolytic agent
                                                                                                                                                                                                                                                                          Kawabe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RRRPWCYVQVGLKPLVQECMVHDCADGKKPSSPPEE 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 RRRPWCYVQVGLKPLVQECMVHDCADGKKPSSPPEE 96
                                                                                                                                                                                                                                                                        Kasai S,
                                                                                                                                                                                                                                                                   H, Amatsuji Y, Hirose M,
1, Tanabe T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAR66266 standard; protein; 386 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Page -; 22pp; English
                                                                                                                                  89JP-0126433.
86JP-0156936.
                                                                           90EP-0109472
                                                                                                                90JP-0042020
                                                                                                                                                                         87JP-0036495
                                                                                                                                                                                          89JP-0126434
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(first entry)
                                                                                                                                                                                                                                 (GREC ) GREEN CROSS CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           96; Conservative
                                                                                                                                                                                                                                                                                                                               WPI; 1990-350146/47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               378 AA;
                                                                                                                                                                                                                                                                                                                                             N-PSDB; AAT61672
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                                                                         18-MAY-1990;
                                                                                                                                                       03-JUL-1986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25-MAR-2003
17-AUG-1995
                                                                                                                                       .8-MAY-1989;
                                                                                                                                                                                        18-MAY-1989;
                                      22-NOV-1990
                                                                                                                                                                         18-FEB-1987
  EP398361-A.
                                                                                                                                                                                                                                                                                          Morita M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAR66266;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                        Airmura
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 7
AAR66266
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 KTCYEGNGHFYRGKASTDIMGRPCLPWNSAIVLQQTYHAHRSDALQLGLGKHNYCRNPDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 KTCYEGNGHFYRGKASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human, prourokinase, hPUK; variant, half-life, increase, EGF,
epidermal growth factor domain; deletion, thrombolysis, fibrinolysis.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Amino acid residues 1-46 contain the EGF region of human urokinase. Deletion of this region results in a plasminagen activator with reduced affinity for liver cell membranes; the mutant protein is not cleared from the circulation as rapidly as is wild-type tPA. The specification only gives the sequence around the deletion and not the full-length sequence of "delta 1-46 urokinase"; the sequence in AAR68854 has been obtained by amending a previously according to the description given in Example 3. (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                       New modified plasminogen activator cpds. - having regions removed to reduce affinity for liver membranes and increase circulation half-life.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 554; DB 16; Length 365; ilarity 100.0%; Pred. No. 1e-44; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10..378
/note= "residues 43-411 of native hPUK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human prourokinase variant lacking entire EGF domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "residues 1-9 of native hPUK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "corresponds to TAC codon"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62 RRRPWCYVQVGLKPLVQECMVHDCADGKKPSSPPEE 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 RRRPWCYVQVGLKPLVQECMVHDCADGKKPSSPPEE
have been deleted"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW13635 standard; Protein; 378 AA
                                                                                                                                                                                                          (AMHP ) AMERICAN HOME PROD CORP.
                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page ?; 26pp; English.
                                                                                                              88US-0150267.
                                                                                                                                                 87US-0008795.
88US-0150267.
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Matches 96; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        365 AA;
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                                                                                                              29-JAN-1988;
                                                                                                                                                   30-JAN-1987;
29-JAN-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               04-JUN-1997
                                    US5376547-A
                                                                       27-DEC-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
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RESULT 6 AAW13635

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 KTCYEGNGHFYRGKASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDN
                                                                                                                                                                                                                                                                                                                                                                                              Bifunctional urokinase derivatives corresponding to the formula M4-X1-Y1 are claimed (see features table). Sequences AAR66244-R66266 are specific examples of such derivs. Which have both improved fibrinolytic and thrombin-inhibiting activities, compared to known plasminogen activators or thrombin inhibitors. The proteins are useful as thrombolytic agents, e.g. for treatment of arterial occlusions, deep vein thrombosis, cardiac and cerebral infarction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
         /label= M4
/note= "unglycosylated prourokinase(Ser47-Leu411)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels 0;
                                                                                                                                                                                                                                                                                                                                    New bifunctional urokinase derivs and related plasmids - with improved fibrinolytic and thrombin inhibiting activities, for treating cardiac and cerebral infarct, pulmonary embolism, etc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 386;
                                                                                                                                                                                                                                                                                     Steffens GJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human prourokinase variant lacking EGF domain loops 1 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 100.0%; Score 554; DB 16; Best Local Similarity 100.0%; Pred. No. 1.1e-44; Matches 96; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                    Schneider J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RRPWCYVQVGLKPLVQECMVHDCADGKKPSSPPEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and pulmonary embolism. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 RRRPWCYVQVGLKPLVQECMVHDCADGKKPSSPPEE
                                                                                                                                                                                                                                                                                                                                                                             Example 1; Page 11 and Fig 1; 34pp; German.
                                                                            151..222
247..316
279..295
306..334
365..366
/label= X1
/noce="peptide bond"
366..386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW13636 standard; Protein; 389 AA
                                                                                                                                                                                                                                                                                    Heinzel-Wieland R, Saunders DJ,
                                                                                                                                                                                                                          93DE-4323754.
                                                                                                                                                                                                                                             93DE-4323754
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                                                                                                                                                                                                                                                                 (CHEF ) GRUENENTHAL GMBH.
                                                                                                                                                                                                                                                                                                                  WPI; 1995-015191/03.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     386 AA;
                                     Distriction bond Distriction bond Distriction bond Distriction bond Distriction bond Distriction bond Distriction bond Distriction bond Distriction bond Distriction bond Distriction bond Distriction bond Distriction bond
                              Disulfide-bond
                                                                                                                                                                                                                          15-JUL-1993;
                                                                                                                                                                                 DE4323754-C1
                                                                                                                                                                                                     01-DEC-1994
                                                                                                                                                                                                                                                                                               Wnendt S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW13636;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 KTCYEGNGHFYRGKASTDIMGRPCLPWNSAIVLQQIYHAHRSDALQLGLGKHNYCRNPDN 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New variants of human prounckinase (hPUK) comprise a hPUK deficient in (i) at least part of the first loop region of the epidermal growth factor (EGF) domain; (ii) at least part of the first loop and at loop. The hPUK variants show an increased blood half-life comparable to that of the whole EGF domain-deficient hPUK variant and urokinase while retaining the same properties as those of hPUK. They have potent thrombolytic activity and very little tendency to cause spontaneous bleeding. The present sequence represents a specific sequence does not appear in the specification and has been created using the wild-type hPUK sequence and the junction sequence after deletion, both of which are given (in Fig 1 and on page 8,
Human, prourokinase, hPUK; variant, half-life, increase, EGF, epidermal growth factor domain; deletion; thrombolysis, fibrinolysis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human pro-urokinase variants - deficient in loop regions c
epidermal growth factor, showing long blood half-life, as
fibrinolytic agent
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                                                                                                                                                                                                                                                                note= "residues 33-411 of native hPUK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kawabe H;
                                                                                                                                                                                                        /note= "residues 1-10 of native hPUK'
                                                                                                                                                                                                                                                                                                                      /note= "corresponds to TAC codon"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kasai S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Airmura H, Amatsuji Y, Hirose M,
Morita M, Tanabe T;
                                                                                                                                                           location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 6; Page -; 22pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             89JP-0126433.
86JP-0156936.
87JP-0036495.
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96; Conservative
                                                                                                                                                                                                                                       11..389
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                                                                                 Homo sapiens
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18-FEB-1987;
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Key Region

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Bifunctional urokinase derivatives corresponding to the formula M4-X1-Y1 are claimed (see features table). Sequences AAR66244-R66266 are specific examples of such derives, which have both improved fibrinolytic and thrombin-inhibiting activities, compared to known plasminogen activators or thrombin inhibitors. The proteins are useful as thrombolytic agents, e.g. for treatment of arterial and pulmonary embolism. (Updated on 25-WAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                          1..365
|label= M4
|note= "unglycosylated prourokinase(Ser47-Leu411)"
                                                                                                                                                                                                                                              fibrinolysis, thrombin inhibition, thrombolytic, anti-thrombotic,
urokinase, variant, mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New bifunctional urokinase derivs and related plasmids - with improved fibrinolytic and thrombin inhibiting activities, for treating cardiac and cerebral infarct, pulmonary embolism, etc
                 RRRPWCYVQVGLKPLVQECMVHDCADGKKPSSPPEE 97
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RRRPWCYVQVGLKPLVQECMVHDCADGKKPSSPPEE
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                                                                                                                                                                                                                   Bifunctional urokinase variant M14.
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                                                                                                           AAR66247 standard; protein; 390
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/label= X1
372..390
/label= Y1
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(first entry)
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6 . . 80
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17-AUG-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                              'note= "unglycosylated prourokinase(Ser47-Leu411)"
                                                                                                                                     fibrinolysis; thrombin inhibition; thrombolytic; anti-thrombotic; urokinase; variant; mutein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and pulmonary embolism. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 1; Page 10 and Fig 1; 34pp; German.
                                                                                                                                                                                                                  Location/Qualifiers
1..365
/label= M4
                                                                                                         Bifunctional urokinase variant M12.
   AAR66245 standard; protein; 390 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Heinzel-Wieland R, Saunders DJ,
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/label= X1
372..390
/label= X1
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17-AUG-1995
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Best Local S
Matches 96
                                  AAR66245;
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Steffens GJ;

100.0%; Score 554; DB 16; Length 390; Query Match

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Length 392;

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RESULT 11 AAR66254

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1 KTCYEGNGHFYRGKASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDN
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 occlusions, deep vein thrombosis, cardiac and cerebral infarction and pulmonary embolism. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                       fibrinolysis; thrombin inhibition; thrombolytic; anti-thrombotic;
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                                                                                       100.0%; Score 554; DB 16; 100.0%; Pred. No. 1.1e-44;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                           Bifunctional urokinase variant M22.
                                                                                                                                                                                                                                                                                                         AAR66255 standard; protein; 392 AA
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/label= M4
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247..316
279..295
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366..371
/label= X1
372..392
/label= X1
                                                                                                                                                                                                                                                                                                                                                                                                                                                        urokinase; variant; mutein
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                                                                      Query Match
Best Local Similarity
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                Gaps
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/label= M4
/note= "unglycosylated prourokinase(Ser47-Leu411)"
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100.0%; Pred. No. 1.1e-44;
live 0; Mismatches 0;
                                                                                                                       RRRPWCYVQVGLKPLVQECMVHDCADGKKPSSPPEE 97
                                                                                                RRRPWCYVQVGLKPLVQECMVHDCADGKKPSSPPEE 96
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/label= X1
372..392
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Best Local Similarity
Matches 96; Conserv
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102..233
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WPI; 1995-015191/03.
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les 96; Conserv
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                                                                                                                                                            Sequence
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AAR66257
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                                                                                                                                                KTCYEGNGHFYRGKASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDN
      Bifunctional urokinase derivatives corresponding to the formula M4-X1-Y1 are claimed (see features table). Sequences AAR66244-R66266 are specific examples of such deriva, which have both improved fibrinolytic and thrombin-inhibiting activities, compared to known plasminogen activators or thrombin inhibitors. The proteins are useful as thrombolytic agents, e.g. for treatment of arterial occlusions, deep vein thrombosis, cardiac and cerebral infarction and pulmonary embolism.
(Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                             fibrinolysis; thrombin inhibition; thrombolytic; anti-thrombotic; urckinase; variant; mutein.
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                                                                                                             100.0%; Score 554; DB 16;
100.0%; Pred. No. 1.1e-44;
iive 0; Mismatches 0;
                                                                                                                                                                                   61 RRRPWCYVQVGLKPLVQECMVHDCADGKKPSSPPEE 96
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/label= X1
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(first entry)
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Les 96, Conservative
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New bifunctional urokinase derivs and related plasmids - with improved fibrinolytic and thrombin inhibiting activities, for treating cardiac and cerebral infarct, pulmonary embolism, etc
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1 KTCYEGNGHFYRGKASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDN 60
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                                                                                                                                                                                                                                                                                               Bifunctional urokinase derivatives corresponding to the formula M4-X1-Y1 are claimed (see features table). Sequences AAR66244-R66266 are specific examples of such derivs. Which have both improved fibrinolytic and thrombin-inhibiting activities, compared to known plasminogen activators or thrombin inhibitors. The proteins are useful as thrombolytic agents, e.g. for treatment of arterial occlusions, deep vein thrombosis, cardiac and cerebral infarction
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urokinase; variant; mutein.
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urokinase; variant; mutein.
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     'note= "unglycosylated prourokinase(Ser47-Leu411)"
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urokinase; variant; mutein.
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Region Region

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1 KTCYEGNGHFYRGKASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNFDN
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(Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                    /note= "unglycosylated prourokinase(Ser47-Leu411)"
                                                                                               thrombin inhibition; thrombolytic; anti-thrombotic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New bifunctional urokinase derivs and related plasmids - with improved fibrinolytic and thrombin inhibiting activities, for treating cardiac and cerebral infarct, pulmonary embolism, etc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 554; DB 16; Length 392; 100.0%; Pred. No. 1.1e-44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Steffens GJ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Schneider J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 1, Page 11 and Fig 1, 34pp; German.
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                                                               Bifunctional urokinase variant M30.
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/label= M4
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247..316
279..295
306..334
366..371
/label= X1
372..392
                                                                                                                   urokinase; variant; mutein.
                 (updated)
(first entry)
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Best Local Similarity
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                 25-MAR-2003
17-AUG-1995
                                                                                                                                                   Synthetic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KTCYEGNGHFYRGKASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bifunctional urokinase derivatives corresponding to the formula M4-X1-Y1 are claimed (see features table). Sequences AAR66244-R66266 are specific examples of such derivs. Which have both improved fibrinolytic and thrombin-inhibiting activities, compared to known plasminogen activators or thrombin inhibitors. The proteins are useful as thrombolytic agents, e.g. for treatment of arterial occlusions, deep vein thrombosis, cardiac and cerebral infarction
                                                                                                               'note= "unglycosylated prourokinase(Ser47-Leu411)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New bifunctional urokinase derivs and related plasmids - with improved fibrinolytic and thrombin inhibiting activities, for treating cardiac and cerebral infarct, pulmonary embolism, etc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Schneider J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and pulmonary embolism. (Updated on 25-MAR-2003 to correct PN field.)
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                                                               Location/Qualifiers
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                                                                              1..365
/label= M4
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/label= X1
372.392
/label= Y1
urokinase; variant; mutein
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Disulfide-b
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                               Synthetic
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Matches 96,
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61

AAR66263

RESULT 19 AAR66263

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Bifunctional urokinase derivatives corresponding to the formula M4-X1-Y1 are claimed (see features table). Sequences AAR66244-R66266 are specific examples of such derivs. Which have both improved fibriholytic and thrombin-inhibiting activities, compared to known plasminogen activators or thrombin inhibitors. The proteins are useful as thrombolytic agents, e.g. for treatment of arterial occlusions, deep vein thrombosis, cardiac and cerebral infarction
                                                                                                                                                                                           1. 365
/label= M4
/note= "unglycosylated prourokinase(Ser47-Leu411)"
                                                                                                                     fibrinolysis; thrombin inhibition; thrombolytic; anti-thrombotic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New bifunctional urokinase derivs and related plasmids - with improved fibrinolytic and thrombin inhibiting activities, for treating cardiac and cerebral infarct, pulmonary embolism, etc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 100.0%; Score 554; DB 16; Best Local Similarity 100.0%; Pred. No. 1.1e-44; Matches 96; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and pulmonary embolism.
(Updated on 25-MAR-2003 to correct PN field.)
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                                                                                                                                                                                   Location/Qualifiers
                                                                                             Bifunctional urokinase variant M31.
          AAR66264 standard; protein; 392 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           93DE-4323754
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151..222
249..295
306..334
366..371
17080= X1
1abel= X1
                                                                                                                                  urokinase; variant; mutein
                                                          (updated)
(first entry)
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25.67
56.80
102.233
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17-AUG-1995
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                                                                                                                                                          Synthetic
                                  AAR66264;
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AAR66264
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Indels

Length 392;

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                        2 KICYEGNGHFYRGKASTDIMGRFCLPWNSAIVLQQIYHAHRSDALQLGLGKHNYCRNPDN
1 KTCYEGNGHFYRGKASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note= "unglycosylated prourokinase(Ser47-Leu411)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             fibrinolysis, thrombin inhibition; thrombolytic; anti-thrombotic; urokinase; variant; mutein.
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                                                                                                                                 62 RRRPWCYVQVGLKPLVQECMVHDCADGKKPSSPPEE 97
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                                                                                                      RRRPWCYVQVGLKPLVQECMVHDCADGKKPSSPPEE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bifunctional urokinase variant M11.
                                                                                                                                                                                                                                                                                 AAR66244 standard; protein; 393 AA
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247..316
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366..374
1abel= X1
375..393
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'label= M4
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22-AUG-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic
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            compared to known
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4..85
are specific examples of such derivs. which have both improved this bibliohytic and thrombin-inhibiting activities, compared to know plasminogen activators or thrombin inhibitors. The proteins are useful as thrombolytic agents, e.g. for treatment of arterial acclusions, deep vein thrombosis, cardiac and cerebral infarction and pulmonary embolism. (Updated on 25-WAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                             fibrinolysis, thrombin inhibition, thrombolytic, anti-thrombotic, urokinase, variant, mutein.
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                                                                                                                Length 393;
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                                                                                                               100.0%; Score 554; DB 16;
100.0%; Pred. No. 1.1e-44;
ive 0; Mismatches 0;
                                                                                                                                                                                                          61 RRRPWCYVQVGLKPLVQECMVHDCADGKKPSSPPEE 96
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/label= M4
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/label= X1
373..393
/label= Y1
                                                                                                                                                                                                                                                                                                                                    (updated)
(first entry)
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Best Local Similarity 100.
Matches 96; Conservative
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                                                                                            393 AA;
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17-AUG-1995
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                                                                                            KTCYEGNGHFYRGKASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDN 61
                                                                              KTCYEGNGHFYRGKASTDIMGRPCLPWNSAIVLQQTYHAHRSDALQLGLGKHNYCRNPDN 60
                                                           Gaps
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M4-X1-Y1 are claimed (see features table). Sequences AAR66244-R66266
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| Aabel= M4
|/note= "unglycosylated prourokinase(Ser47-Leu411)"
                                                                                                                                                                                                                                                                                                            fibrinolysis, thrombin inhibition, thrombolytic, anti-thrombotic,
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                                    Length 393;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Schneider J, Steffens GJ;
                                                        Indels
                                 th 100.0%; Score 554; DB 16; Similarity 100.0%; Pred. No. 1.1e-44; 96; Conservative 0; Mismatches 0;
                                                                                                                                                97
                                                                                                                            RRRPWCYVQVGLKPLVQECMVHDCADGKKPSSPPEE 96
                                                                                                                                          RRRPWCYVQVGLKPLVQECMVHDCADGKKPSSPPEE
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Wnendt S,
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373..393
/label= Y1
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(first entry)
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279..295
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                                    Query Match
Best Local Similarity
              393 AA;
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                                                                                                                                                                                                     2 KTCYEGNGHFYRGKASTDIMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDN 61
                                         Bifunctional urokinase derivatives corresponding to the formula M4-X1-Y1 are claimed (see features table). Sequences AAR66244-R66266 are specific examples of such derivas, which have both improved fibrinolytic and thrombin-inhibiting activities, compared to known plasminogen activators or thrombin inhibitors. The proteins are useful as thrombolytic agents, e.g. for treatment of arrerial occlusions, deep vein thrombosis, cardiac and cerebral infarction and pulmonary embolism.
(Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                note= "unglycosylated prourokinase(Ser47-Leu411)"
                                                                                                                                                                                                                                                                                                                                                                        fibrinolysis; thrombin inhibition; thrombolytic; anti-thrombotic;
improved fibrinolytic and thrombin inhibiting activities, for treating cardiac and cerebral infarct, pulmonary embolism, etc
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                                                                                                                                                   100.0%; Score 554; DB 16; Length 393; larity 100.0%; Pred. No. 1.1e-44; Conservative 0; Mismatches 0; Indels 0;
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                         Example 1; Page 10 and Fig 1; 34pp; German
                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                         AAR66251 standard; protein; 393 AA
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/label= Y1
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/label= M4
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(first entry)
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/label= X1
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Matches 96; Conserv
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1 KTCYEGNGHFYRGKASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDN 60
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                                                                                                                                                                                                                                          Bifunctional urokinase derivatives corresponding to the formula M4-XI-YI are claimed (see features table). Sequences AAR66244-R66266 are specific examples of such derives, which have both improved fibrinolytic and thrombin-inhibiting activities, compared to known plasminogen activators or thrombin inhibitors. The proteins are useful as thrombolytic agents, e.g. for treatment of arterial and pulmonary embolism.
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/note= "unglycosylated prourokinase(Ser47-Leu411)"
4..85
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                                                                                                                                   improved fibrinolytic and thrombin inhibiting activities, for
treating cardiac and cerebral infarct, pulmonary embolism, etc
                                                                                                         New bifunctional urokinase derivs and related plasmids - with
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  Steffens
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  Schneider J,
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Heinzel-Wieland R, Saunders DJ,
Wnendt S;
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/label= X1
373..393
/label= Y1
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Les 96; Conservative
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151..222
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                                                                  WPI; 1995-015191/03
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         /label= X1
373..393
/label= Y1
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Best Local Similarity 100./
Matches 96; Conservative
366..372
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                                                                                                                                                                                                  Bifunctional uroxinase derivatives corresponding to the formula M4-X1-Y1 are claimed (see features table). Sequences AAR66244-R66266 are Specific examples of such derivs. Which have both improved fibrinolytic and thrombin-inhibiting activities, compared to known plasminogen activators or thrombin inhibitors. The proteins are useful as thrombolytic agents, e.g. for treatment of arterial occlusions, deep vein thrombosis, cardiac and cerebral infarction
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                                                                                                                                     New bifunctional urokinase derivs and related plasmids - with improved fibrinolytic and thrombin inhibiting activities, for treating cardiac and cerebral infarct, pulmonary embolism, etc
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                                                                                   Heinzel-Wieland R, Saunders DJ, Schneider J, Steffens GJ;
                                                                                                                                                                                                                                                                                                                                                                                                                  61 RRRPWCYVQVGLKPLVQECMVHDCADGKKPSSPPEE 96
                                                                                                                                                                                                                                                                                                                                                                                                                                      62 RRRPWCYVQVGLKPLVQECMVHDCADGKKPSSPPEE 97
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                                                                                                                                                                              Example 1; Page 10 and Fig 1; 34pp; German.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAR66253 standard; protein; 393 AA
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                     93DE-4323754
                                        93DE-4323754
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/label= M4
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(first entry)
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Best Local Similarity 100.1
                                                              CHEF ) GRUENENTHAL GMBH
                                                                                                                                                                                                                                                                            and pulmonary embolism.
                                                                                                                 WPI; 1995-015191/03
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17-AUG-1995
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1 KTCYEGNGHFYRGKASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDN 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bifunctional urokinase derivatives corresponding to the formula M4-X1-Y1 are claimed (see features table). Sequences AAR66244-R66266 are specific examples of such derive. Which have both improved fibrinolytic and thrombin-inhibiting activities, compared to known plasminogen activitors or thrombin inhibitors. The proteins are useful as thrombolytic agents, e.g. for treatment of arterial occlusions, deep vein thrombosis, cardiac and cerebral infarction
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Heinzel-Wieland R, Saunders DJ, Schneider J, Steffens GJ;
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100.0%; Pred. No. 1.1e-44;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                      Example 1; Page 10 and Fig 1; 34pp; German
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAR99885 standard; peptide; 393 AA
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05-JUN-1996

94DE-4440892

17-NOV-1994;

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Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 KICYEGNGHFYRGKASTDIMGRPCLPWNSATVLQQIYHAHRSDALQLGLGKGHYYCRNPDN 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (B) has hirdin or hirdin activities, or is derived from the human thrombin receptor, antistatin and/or the tick anticoagulant peptide. Most pref. are the 65 amino acid hirdin sequence or one of the six sequences given in AAR99879 to AAR99898.

Plasmids PWLT27 (MS1), pWS1 (MS112), pSE8 (M36) and pHW56 (M43) contain the sequences encoding AAR99885 to AAR99888, respectively. The products were tested in human citrated plasma (5 microg in 200 microl 1:10 diluted plasma). The thrombin time was then 1:2, 3, 2.8 and 1:2 times greater, repectively, than in the absence of the product.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Where T1= P or V, T2 = L or a bond; T3= O or OH.

(A) is pref. (pro)urokinase; tissue plasminogen activator (tPh), bat-PA (all opt. modified by deletion, substitution, insertion and/or addn.); streptokinase; staphylokinase; and/or APSAC (anisolated plasminogen streptokinase activator complex), esp. prourokinase (411 amino acids) or its Ser47 to Leu411 or Ser138 to Leu411 Liagments, or t-PA (527 amino acids) or its Ser89Arg to 527Pro or 1978 has highly acids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 KTCYEGNGHFYRGKASTDTMGRPCLPWNSATVLOQTYHAHRSDALQLGLGKHNYCRNPDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                       Proteins with fibrinolytic and anticoagulant activity - useful as
                                                                                                                                                                                                                                                                                                               New peptides (1) with fibrinolytic and anticoagulant activity comprise a plasminogen-activating amino acid sequence (A) fused at the N- and/Or C-terminus to a thrombin and/or factor Xa inhibiting amino acid sequence (B). Excluded from the claims are (I) where (A) is Ser47 to Leu411 of unglycosylated urokinase linked at the C-terminus to sequences (i) to (ii):
T1-RPPLISHORDEVEFFEDEEKNE
T1-RPSISFEEFEIDEEEK
(ii) (iii)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Thrombin; inhibition; thrombus; thrombolysis; chimeric protein; plasminogen activating sequence; fibrinolysis; infarction; angina pectoris; deep vein thrombosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ·.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 554; DB 17; Length 393; 100.0%; Pred. No. 1.1e-44; tive 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 RRRPWCYVQVGLKPLVQECMVHDCADGKKPSSPPEE 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63 RRRPWCYVQVGLKPLVQECMVHDCADGKKPSSPPEE 98
                                                                                                                Whendt S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chimeric protein M37 encoded by pSE9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAR99596 standard; Protein; 393 AA
                                                                                                                                                                                                                                                                          Disclosure; Fig 18; 59pp; German.
                                                                                                                Steffens GJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                (CHEF ) GRUENENTHAL GMBH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                             Heinzel-Wieland R,
                                                                                                                                                          WPI; 1996-240720/25
                                                                                                                                                                                                                                thrombolytic agents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 96; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              393 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             05-DEC-1996
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EP714982-A2 Synthetic

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3 KTCYEGNGHFYRGKASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDN 62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                      Example 1 describes the prodn. of plasmids pSE1 and pSE9 coneg. a DNA encoding a chimeric protein with fibrinolytic and thrombin-inhibiting properties.

pSE1 encodes the protein given in AAR99597 and pSE9 encodes the protein given in AAR99596.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Thrombin; inhibition; thrombus; thrombolysis; chimeric protein; plasminogen activating sequence; fibrinolysis; infarction; angina pectoris; deep vein thrombosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                 Length 393;
                                                                                                                                                                  Chimeric protein contg. plasminogen activating sequence and thrombin-inhibiting sequence - useful as thrombus-specific thrombolytic agent with rapid action
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chimeric protein contg. plasminogen activating sequence and thrombin-inhibiting sequence - useful as thrombus-specific thrombolytic agent with rapid action
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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                                                                                                    Whendt
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100.0%; Pred. No. 1.1e-44;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RRRPWCYVQVGLKPLVQECMVHDCADGKKPSSPPEE 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RRRPWCYVQVGLKPLVQECMVHDCADGKKPSSPPEE
                                                                                                    Steffens GJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Steffens GJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chimeric protein M38 encoded by pSE1.
                                                                                                                                                                                                                                         Example 1; Page 19-20; 37pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Z
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAR99597 standard; Protein; 393
                                                                                                    Janocha E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Heinzel-Wieland R, Janocha E,
95EP-0118050
                                94DE-4442665
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                 (CHEF ) GRUENENTHAL GMBH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                96; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (CHEF ) GRUENTHAL GMBH.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                    Heinzel-Wieland R,
                                                                                                                                   WPI; 1996-269715/28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1996-269715/28
                                                                                                                                                                                                                                                                                                                                                                                393 AA;
16-NOV-1995;
                                30-NOV-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-NOV-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-NOV-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            05-DEC-1996
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                                                                                                                                                                                                                                 1 KTCYEGNGHFYRGKASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDN 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      32 KICYEGNGHFYRGKASTDTMGRPCLPWNSAIVLQQTYHAHRSDALQLGLGKHNYCRNPDN 91
                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequences (AAQ55771-72) are pro-urokinase derivatives. The products have an inserted sugar moeity having an amino acid substituted, depleted or inserted variant around the thrombin cleavage site. They also have a long half-life allowing them to be used in the treatment of thrombosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pro-urokinase; half-life; thrombolytic; thrombosis; fibrinolytic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ô
                                       Example 1 describes the prodn. of plasmids pSE1 and pSE9 contg. a DNA encoding a chimeric protein with fibrinolytic and thrombin-inhibiting properties.

PSE1 encodes the protein given in AAR99597 and pSE9 encodes the protein given in AAR96969.
                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel human pro-urokinase derivs. having long half-life - with high thrombolytic activity, useful for treatment of thrombosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
100.0%; Score 554; DB 15; Length 395;
Best Local Similarity 100.0%; Pred. No. 1.1e-44;
Matches 96; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                   Length 393;
                                                                                                                                                                                                 Indels
                                                                                                                                                                  100.0%; Score 554; DB 17;
100.0%; Pred. No. 1.1e-44;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                              RRRPWCYVQVGLKPLVQECMVHDCADGKKPSSPPEE 98
                                                                                                                                                                                                                                                                                            61 RRRPWCYVQVGLKPLVQECMVHDCADGKKPSSPPEE 96
             Example 1; Page 21-22; 37pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 14; 29pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                        AAR47902 standard; Protein; 395 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                           Query Match
Best Local Similarity 100.0
Marches 96; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pro-urokinase derivative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1994-030907/04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           395 AA;
                                                                                                                                       393 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-DEC-1993
                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                      AAR47902;
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        Qy
        61 RRRPWCYVQVGLKPLVQECMVHDCADGKKPSSPPEE 96

        Db
        92 RRRPWCYVQVGLKPLVQECMVHDCADGKKPSSPPEE 127
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Search completed: December 3, 2003, 14:39:16 Job time : 16.1223 secs

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Sequence 9, Application US/09880503
Sequence 9, Application US/09880503
Sequence 9, Application US/09880503
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Sequence 9, Application US/09880503
Sequence 9, Application Sequence
Sequence 9, Application Sequence
Sequence 1 Title OF INVENTION: TISSUE CONTRACTABILITY
TITLE OF INVENTION: TISSUE CONTRACTABILITY
STILE REFERENCE: 9596-331
CURRENT FILING DATE: 2001-06-13
PRIOR APPLICATION NUMBER: US 60/212,847
SPRIOR PADLICATION NUMBER: US 60/212,847
SOFTWARE: PRENCE 10 NOS: 18
SOFTWARE: PRENCE IN VEY: 2.1
SEQUENCE 10 NOS: 18
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                           Sequence
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5 US-10-237.667-12

5 US-10-237.708-12

5 US-10-237.807-12

5 US-10-237.871-12

5 US-10-237.624-12

1 US-09-880-503-6

1 US-09-880-503-6

1 US-09-987.455-19

1 US-09-974.298-145

2 US-10-974.298-145

2 US-10-974.298-145

3 US-10-987.457-10

1 US-09-987.457-10

1 US-09-987.455-13

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 2
US-09-880-503-8
; Sequence 8, Application US/09880503
                                                                  TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           96;
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